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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:19:14 : Search time 56.7539 Seconds
(without alignments)
2920.093 Million cell updates/sec

Title: US-09-925-576C-6
Perfect score: 2854
Sequence: 1 AAFPNGTMMQYFEWYLPDDG.....TRPWTGEFVTRTEPLVAMP 515

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubppaa/PCF_NEW_PUB.pep:*
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- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2854	100.0	515	9 US-09-854-346-6	Sequence 6, Appl1
2	2854	100.0	515	9 US-09-918-543-6	Sequence 6, Appl1
3	2854	100.0	515	10 US-09-925-576C-6	Sequence 6, Appl1
4	2854	100.0	515	14 US-10-146-327-8	Sequence 8, Appl1
5	2854	100.0	515	16 US-10-477-725-6	Sequence 6, Appl1
6	2854	100.0	549	14 US-10-184-771-6	Sequence 6, Appl1
7	2847	99.8	514	12 US-10-644-187-6	Sequence 6, Appl1
8	2847	99.8	514	14 US-10-186-042-6	Sequence 6, Appl1
9	2836	99.4	549	14 US-10-081-872-104	Sequence 104, App
10	2836	99.4	549	15 US-10-385-305-104	Sequence 104, App
11	2832	99.2	549	14 US-10-081-872-92	Sequence 92, App
12	2832	99.2	549	15 US-10-385-305-92	Sequence 92, App
13	2787	97.7	515	9 US-09-795-211-4	Sequence 4, Appl1
14	2780	97.4	514	9 US-09-769-864-3	Sequence 3, Appl1
15	2780	97.4	514	9 US-09-902-188A-3	Sequence 3, Appl1

16	2780	97.4	514	12 US-10-665-667-3	Sequence 3, Appl1
17	2780	97.4	514	12 US-10-025-648-3	Sequence 3, Appl1
18	2780	97.4	514	12 US-10-327-837-3	Sequence 3, Appl1
19	2456	86.1	550	14 US-10-081-872-106	Sequence 106, App
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21	2426	85.0	472	14 US-10-081-872-88	Sequence 88, Appl1
22	2426	85.0	472	14 US-10-105-733-7	Sequence 7, Appl1
23	2426	85.0	472	14 US-10-081-739A-7	Sequence 7, Appl1
24	2426	85.0	472	15 US-10-385-305-88	Sequence 88, Appl1
25	2414	84.6	546	14 US-10-081-872-134	Sequence 134, App
26	2414	84.6	546	15 US-10-385-305-134	Sequence 134, App
27	2410	84.4	615	14 US-10-081-872-128	Sequence 128, App
28	2410	84.4	615	15 US-10-385-305-128	Sequence 128, App
29	2410	84.4	644	14 US-10-081-872-136	Sequence 136, App
30	2410	84.4	644	15 US-10-385-305-136	Sequence 136, App
31	2402	84.2	564	14 US-10-081-872-120	Sequence 120, App
32	2402	84.2	564	15 US-10-385-305-120	Sequence 120, App
33	1910.5	66.9	516	9 US-09-986-676A-2	Sequence 2, Appl1
34	1910.5	66.9	516	9 US-09-971-611-2	Sequence 2, Appl1
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37	1909.5	66.9	485	9 US-09-769-864-7	Sequence 7, Appl1
38	1909.5	66.9	485	9 US-09-854-346-2	Sequence 2, Appl1
39	1909.5	66.9	485	9 US-09-902-188A-1	Sequence 1, Appl1
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42	1909.5	66.9	485	10 US-09-925-576C-2	Sequence 2, Appl1
43	1909.5	66.9	485	12 US-10-665-667-1	Sequence 1, Appl1
44	1909.5	66.9	485	12 US-10-665-667-7	Sequence 7, Appl1
45	1909.5	66.9	485	12 US-10-025-648-1	Sequence 1, Appl1

ALIGNMENTS

US-09-854-346-6
Sequence 6, Application US/09854346
Patent No. US20020068352A1
GENERAL INFORMATION:
APPLICANT: No. US20020068352A1ozymes A/S
APPLICANT: Svendsen, Allan
APPLICANT: Jorgensen, Christel Thea
APPLICANT: Nielsen, Bjarne Ronfeldt
TITLE OR INVENTION: Alpha-amylase variants with altered 1,6 activity
FILE REFERENCE: 6140.200-US
CURRENT FILING DATE: 2001-05-11
CURRENT APPLICATION NUMBER: US/09/854,346
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 515
TYPE: PRT
ORGANISM: Bacillus stearothermophilus
US-09-854-346-6

Query Match 100.0%; Score 2854; DB 9; Length 515;
Best Local Similarity 100.0%; Pred. No. 1.8e-256;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	AAFPNGTMMQYFEWYLPDDGTLMTKVANEANNISLGLTALMPAYKGRSRVGGVY	60
QY	61	DLYDLGFNKGIVRTKYGTGAQYLOAIQAHAAGMVYADVVDHKGADGTEWDAVE	120
DB	61	DLYDLGFNKGIVRTKYGTGAQYLOAIQAHAAGMVYADVVDHKGADGTEWDAVE	120
QY	121	VNPSDRKQELISGTIOAQMTKFPFGKGNVYSSSKRWYHFDGVDMPESRLSLITYFERG	180
DB	121	VNPSDRKQELISGTIOAQMTKFPFGKGNVYSSSKRWYHFDGVDMPESRLSLITYFERG	180
QY	181	IGKAWDEVTENGNDYLYAVADLMDHPREVTELKMKGWYVNTTIDGFRDAVGHK	240

Db 181 IKGAMDWEVDTEKNGVADYLMYADLMDHBEVVTTELKNMGKMYVNTTNDGFLDAVKHIK 240
QY 241 FSEFPDMLSYVRSQSGKPLFTVGEYWSYDINCLAHYITTKDTGMSLFPAPLHNKFTYASK 300
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QY 301 SGGAPEMRLTMNTLMKDOPTLAFTVFNHDETPGQALOSWVDPWFKPLAFAFILLTROEG 360
Db 301 SGGAPEMRLTMNTLMKDOPTLAFTVFNHDETPGQALOSWVDPWFKPLAFAFILLTROEG 360
QY 361 YPCVFGDYGGIPQYNIPSLKSKIDPLLIARRDYAVGTQHDYLDHSDIIGWTRBEGTEKP 420
Db 361 YPCVFGDYGGIPQYNIPSLKSKIDPLLIARRDYAVGTQHDYLDHSDIIGWTRBEGTEKP 420
QY 421 GSGLAALITDGGGSKMYVKGQAHGKVFYDLTGNRSDTYVINSDGWGEFKNVNGGSVSW 480
Db 421 GSGLAALITDGGGSKMYVKGQAHGKVFYDLTGNRSDTYVINSDGWGEFKNVNGGSVSW 480
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Db 481 VPRKTTVSTIARPIITTRPMTGFEFVWTEPRLVAMP 515

RESULT 2
US-09-918-543-6
; Sequence 6, Application US/09918543
; Patent No. US20020155574A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020155574A1ozymes N/S
; APPLICANT: Thisted, Thomas
; APPLICANT: Kjaerulff, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Fuglsang, Claus Croone
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062.200-US
; CURRENT APPLICATION NUMBER: US/09/918.543
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 515
; TYPE: PR1
; ORGANISM: Bacillus stearothermophilus
US-09-918-543-6

Query Match 100.0%; Score 2854; DB 9; Length 515;
Best Local Similarity 100.0%; Pred. No. 1.8e-256;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEWYLPDDGTLMTKVNANNNLSIGITLMLPPAYKGTSRSDVGYGY 60
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Db 61 DLYDLGEFNQKGVTRKTKGTAKOYLQAIQAHAAGQVADVVDHKGADGETWDAVE 120
QY 121 VNSDRNOISGTYQIOAWTKDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
Db 121 VNSDRNOISGTYQIOAWTKDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
QY 181 IKGAMDWEVDTEKNGVADYLMYADLMDHBEVVTTELKNMGKMYVNTTNDGFLDAVKHIK 240
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Db 241 FSEFPDMLSYVRSQSGKPLFTVGEYWSYDINCLAHYITTKDTGMSLFPAPLHNKFTYASK 300
QY 301 SGGAPEMRLTMNTLMKDOPTLAFTVFNHDETPGQALOSWVDPWFKPLAFAFILLTROEG 360
Db 301 SGGAPEMRLTMNTLMKDOPTLAFTVFNHDETPGQALOSWVDPWFKPLAFAFILLTROEG 360

QY 361 YPCVFGDYGGIPQYNIPSLKSKIDPLLIARRDYAVGTQHDYLDHSDIIGWTRBEGTEKP 420
Db 361 YPCVFGDYGGIPQYNIPSLKSKIDPLLIARRDYAVGTQHDYLDHSDIIGWTRBEGTEKP 420
QY 421 GSGLAALITDGGGSKMYVKGQAHGKVFYDLTGNRSDTYVINSDGWGEFKNVNGGSVSW 480
Db 421 GSGLAALITDGGGSKMYVKGQAHGKVFYDLTGNRSDTYVINSDGWGEFKNVNGGSVSW 480
QY 481 VPRKTTVSTIARPIITTRPMTGFEFVWTEPRLVAMP 515
Db 481 VPRKTTVSTIARPIITTRPMTGFEFVWTEPRLVAMP 515

RESULT 3
US-09-925-576C-6
; Sequence 6, Application US/09925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borcherdt, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004.204-US
; CURRENT APPLICATION NUMBER: US/09/925.576C
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 515
; TYPE: PR1
; ORGANISM: Bacillus stearothermophilus
US-09-925-576C-6

Query Match 100.0%; Score 2854; DB 10; Length 515;
Best Local Similarity 100.0%; Pred. No. 1.8e-256;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEWYLPDDGTLMTKVNANNNLSIGITLMLPPAYKGTSRSDVGYGY 60
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Db 61 DLYDLGEFNQKGVTRKTKGTAKOYLQAIQAHAAGQVADVVDHKGADGETWDAVE 120
QY 121 VNSDRNOISGTYQIOAWTKDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
Db 121 VNSDRNOISGTYQIOAWTKDFPGRGNTYSSFKRWYHFDGVDWDESKLSRIYKFRG 180
QY 181 IKGAMDWEVDTEKNGVADYLMYADLMDHBEVVTTELKNMGKMYVNTTNDGFLDAVKHIK 240
Db 181 IKGAMDWEVDTEKNGVADYLMYADLMDHBEVVTTELKNMGKMYVNTTNDGFLDAVKHIK 240
QY 241 FSEFPDMLSYVRSQSGKPLFTVGEYWSYDINCLAHYITTKDTGMSLFPAPLHNKFTYASK 300
Db 241 FSEFPDMLSYVRSQSGKPLFTVGEYWSYDINCLAHYITTKDTGMSLFPAPLHNKFTYASK 300
QY 301 SGGAPEMRLTMNTLMKDOPTLAFTVFNHDETPGQALOSWVDPWFKPLAFAFILLTROEG 360
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Db 361 YPCVFGDYGGIPQYNIPSLKSKIDPLLIARRDYAVGTQHDYLDHSDIIGWTRBEGTEKP 420
QY 421 GSGLAALITDGGGSKMYVKGQAHGKVFYDLTGNRSDTYVINSDGWGEFKNVNGGSVSW 480
Db 421 GSGLAALITDGGGSKMYVKGQAHGKVFYDLTGNRSDTYVINSDGWGEFKNVNGGSVSW 480
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Db 481 VPRKTTVSTIARPIITTRPMTGFEFVWTEPRLVAMP 515

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RESULT 4
US-10-146-327-8
; Sequence 8, Application US/10146327
; Publication No. US20030044954A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/10/146,327
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/537,168
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PA 1999 00437
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/127,427
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 515
; TYPE: PRF
; ORGANISM: Bacillus stearothermophilus
US-10-146-327-8

Query Match          100.0%; Score 2854; DB 14; Length 515;
Best Local Similarity 100.0%; Pred. No. 1.8e-256;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFNGTMOQFEWYLPDDGTLMTKVNANNNLSIGITLMLPPAYKTSRSDVGYVY 60
DB 1 AAPFNGTMOQFEWYLPDDGTLMTKVNANNNLSIGITLMLPPAYKTSRSDVGYVY 60
QY 61 DLYDLGFNKGTVRTKYGTAQYLOAIQAHAAGMAYADVDFDHGAGDGTWVAVE 120
DB 61 DLYDLGFNKGTVRTKYGTAQYLOAIQAHAAGMAYADVDFDHGAGDGTWVAVE 120
QY 121 VNSDRNOEISGTQIOAMTKPDPGKNTYSSFKMWHYFDGVDWDESKLSITYFERG 180
DB 121 VNSDRNOEISGTQIOAMTKPDPGKNTYSSFKMWHYFDGVDWDESKLSITYFERG 180
QY 121 VNSDRNOEISGTQIOAMTKPDPGKNTYSSFKMWHYFDGVDWDESKLSITYFERG 180
DB 121 VNSDRNOEISGTQIOAMTKPDPGKNTYSSFKMWHYFDGVDWDESKLSITYFERG 180
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DB 181 IGRAMDEVDTEANGNDYLYADLDMDHPEVVELKMGKMYVNTNIDGFRDLAVAHIK 240
QY 181 IGRAMDEVDTEANGNDYLYADLDMDHPEVVELKMGKMYVNTNIDGFRDLAVAHIK 240
DB 181 IGRAMDEVDTEANGNDYLYADLDMDHPEVVELKMGKMYVNTNIDGFRDLAVAHIK 240
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DB 241 FSPFPDWLSYVSQTKPLFTVGEYMSYDINKLHNYITKTDTGMSLFDAPLANKFYTASK 300
QY 241 FSPFPDWLSYVSQTKPLFTVGEYMSYDINKLHNYITKTDTGMSLFDAPLANKFYTASK 300
DB 241 FSPFPDWLSYVSQTKPLFTVGEYMSYDINKLHNYITKTDTGMSLFDAPLANKFYTASK 300
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DB 301 SGCAFMDRTMTNTLMDQPTLAVTFVDNHDTEBQALQSWVDWPFPLAFAFLTROEG 360
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DB 301 SGCAFMDRTMTNTLMDQPTLAVTFVDNHDTEBQALQSWVDWPFPLAFAFLTROEG 360
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DB 361 YPCVFYGDYIGIPOYNIPLSKSIDPILLIARDYAGTQHDYLDHSDIIGTREGGTEKP 420
QY 421 GSGIALIITDGPSSKMYVKGQAHAKVFDLTGNRSDTYTINSDGGEFVNGSGSVW 480
DB 421 GSGIALIITDGPSSKMYVKGQAHAKVFDLTGNRSDTYTINSDGGEFVNGSGSVW 480
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DB 421 GSGIALIITDGPSSKMYVKGQAHAKVFDLTGNRSDTYTINSDGGEFVNGSGSVW 480
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DB 481 VPKRTVSTIARPIITTPWTEGFEFRWTEPRLVAMP 515

RESULT 5
US-10-477-725-6
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; Sequence 6, Application US/10477725
; Publication No. US20040096952A1
; GENERAL INFORMATION:
; APPLICANT: NOVOZYMES A/S
; APPLICANT: Svendsen, Carsten
; APPLICANT: Andersen, Christel
; APPLICANT: Thisted, Thomas
; APPLICANT: von der Osten, Claus
; TITLE OF INVENTION: Alpha-amylase variant with altered properties
; FILE REFERENCE: 10162.204-US
; CURRENT APPLICATION NUMBER: US/10/477,725
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 515
; TYPE: PRF
; ORGANISM: Bacillus stearothermophilus
US-10-477-725-6

Query Match          100.0%; Score 2854; DB 16; Length 515;
Best Local Similarity 100.0%; Pred. No. 1.8e-256;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAPFNGTMOQFEWYLPDDGTLMTKVNANNNLSIGITLMLPPAYKTSRSDVGYVY 60
DB 1 AAPFNGTMOQFEWYLPDDGTLMTKVNANNNLSIGITLMLPPAYKTSRSDVGYVY 60
QY 61 DLYDLGFNKGTVRTKYGTAQYLOAIQAHAAGMAYADVDFDHGAGDGTWVAVE 120
DB 61 DLYDLGFNKGTVRTKYGTAQYLOAIQAHAAGMAYADVDFDHGAGDGTWVAVE 120
QY 121 VNSDRNOEISGTQIOAMTKPDPGKNTYSSFKMWHYFDGVDWDESKLSITYFERG 180
DB 121 VNSDRNOEISGTQIOAMTKPDPGKNTYSSFKMWHYFDGVDWDESKLSITYFERG 180
QY 121 VNSDRNOEISGTQIOAMTKPDPGKNTYSSFKMWHYFDGVDWDESKLSITYFERG 180
DB 121 VNSDRNOEISGTQIOAMTKPDPGKNTYSSFKMWHYFDGVDWDESKLSITYFERG 180
QY 181 IGRAMDEVDTEANGNDYLYADLDMDHPEVVELKMGKMYVNTNIDGFRDLAVAHIK 240
DB 181 IGRAMDEVDTEANGNDYLYADLDMDHPEVVELKMGKMYVNTNIDGFRDLAVAHIK 240
QY 181 IGRAMDEVDTEANGNDYLYADLDMDHPEVVELKMGKMYVNTNIDGFRDLAVAHIK 240
DB 181 IGRAMDEVDTEANGNDYLYADLDMDHPEVVELKMGKMYVNTNIDGFRDLAVAHIK 240
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QY 241 FSPFPDWLSYVSQTKPLFTVGEYMSYDINKLHNYITKTDTGMSLFDAPLANKFYTASK 300
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QY 301 SGCAFMDRTMTNTLMDQPTLAVTFVDNHDTEBQALQSWVDWPFPLAFAFLTROEG 360
DB 301 SGCAFMDRTMTNTLMDQPTLAVTFVDNHDTEBQALQSWVDWPFPLAFAFLTROEG 360
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DB 301 SGCAFMDRTMTNTLMDQPTLAVTFVDNHDTEBQALQSWVDWPFPLAFAFLTROEG 360
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DB 421 GSGIALIITDGPSSKMYVKGQAHAKVFDLTGNRSDTYTINSDGGEFVNGSGSVW 480
QY 421 GSGIALIITDGPSSKMYVKGQAHAKVFDLTGNRSDTYTINSDGGEFVNGSGSVW 480
DB 421 GSGIALIITDGPSSKMYVKGQAHAKVFDLTGNRSDTYTINSDGGEFVNGSGSVW 480
QY 481 VPKRTVSTIARPIITTPWTEGFEFRWTEPRLVAMP 515
DB 481 VPKRTVSTIARPIITTPWTEGFEFRWTEPRLVAMP 515

RESULT 6
US-10-184-771-6
; Sequence 6, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
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;; PRIOR APPLICATION NUMBER: US/09/636,252
;; PRIOR FILING DATE: 2000-08-10
;; PRIOR APPLICATION NUMBER: 08/683,838
;; PRIOR FILING DATE: 1996-07-18
;; NUMBER OF SEQ ID NOS: 16
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 6
;; LENGTH: 549
;; TYPE: PRF
;; ORGANISM: B. stearothermophilus
US-10-184-771-6

Query Match 100.0%; Score 2854; DB 14; Length 549;
Best Local Similarity 100.0%; Pred. No. 2e-256;
Matches 515; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEWYLPDDGTLMTKVAANEANNTSLGITTALMLPPAYKTSRSDVGYGVY 60
DB 35 AAFNGTMMQYFEWYLPDDGTLMTKVAANEANNTSLGITTALMLPPAYKTSRSDVGYGVY 94
QY 61 DLYDLGEFNOKGTVRTKTKGTAQYLOAIQAHAAGMADVADVPDHKGADGTEWDAVE 120
DB 95 DLYDLGEFNOKGTVRTKTKGTAQYLOAIQAHAAGMADVADVPDHKGADGTEWDAVE 154
QY 121 VNPSDRNOEISGTYYQIQAWTKFDPFGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTYYQIQAWTKFDPFGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 214
QY 181 IGRAMDEVDTEENGNDYLYADLMDHPEVVTLEKMGKRYVNTNIDGRDLDAVHKIK 240
DB 215 IGRAMDEVDTEENGNDYLYADLMDHPEVVTLEKMGKRYVNTNIDGRDLDAVHKIK 274
QY 241 FSPFPDMLSYRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHKKFTYASK 300
DB 275 FSPFPDMLSYRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHKKFTYASK 334
QY 301 SGCAFDMRTMTNTLMKQDPTLAVTVDNHDTEPGALQSWVDPWFKPLAVALILTRQEG 360
DB 335 SGCAFDMRTMTNTLMKQDPTLAVTVDNHDTEPGALQSWVDPWFKPLAVALILTRQEG 394
QY 361 YPCVFGDYGYGIPOYNIPLSKSIDPLLIARRDYAGTGHYLDHSDIIGWTEEGTEKRP 420
DB 395 YPCVFGDYGYGIPOYNIPLSKSIDPLLIARRDYAGTGHYLDHSDIIGWTEEGTEKRP 454
QY 421 GSGLAALITDPPGSGKMVYGKQAHGKVFYDLTGNSDVTYITNSDGMGEFKVNGGSVSW 480
DB 455 GSGLAALITDPPGSGKMVYGKQAHGKVFYDLTGNSDVTYITNSDGMGEFKVNGGSVSW 514
QY 481 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAM 515
DB 515 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAM 549

RESULT 7
US-10-644-187-6

;; Sequence 6, Application US/10644187
;; Publication No. US20040048351A1
;; GENERAL INFORMATION:
;; APPLICANT: Svendsen, Allan
;; APPLICANT: Borchert, Torben
;; APPLICANT: Bisgaard-Frantzen, Henrik
;; TITLE OF INVENTION: Alpha-Amylase Mutants
;; FILE REFERENCE: 4796.204-US
;; CURRENT APPLICATION NUMBER: US/10/644,187
;; CURRENT FILING DATE: 2003-08-20
;; PRIOR APPLICATION NUMBER: 09/182,859
;; PRIOR FILING DATE: 1998-10-29
;; PRIOR APPLICATION NUMBER: 0515/96
;; PRIOR FILING DATE: 1996-04-30
;; PRIOR APPLICATION NUMBER: 0712/96
;; PRIOR FILING DATE: 1996-06-28
;; PRIOR APPLICATION NUMBER: 0775/96
;; PRIOR FILING DATE: 1996-07-11

;; PRIOR APPLICATION NUMBER: 1263/96
;; PRIOR FILING DATE: 1996-11-08
;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO: 6
;; LENGTH: 514
;; TYPE: PRF
;; ORGANISM: Bacillus stearothermophilus
US-10-644-187-6

Query Match 99.8%; Score 2847; DB 12; Length 514;
Best Local Similarity 100.0%; Pred. No. 8.1e-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAFNGTMMQYFEWYLPDDGTLMTKVAANEANNTSLGITTALMLPPAYKTSRSDVGYGVY 60
DB 1 AAFNGTMMQYFEWYLPDDGTLMTKVAANEANNTSLGITTALMLPPAYKTSRSDVGYGVY 60
QY 61 DLYDLGEFNOKGTVRTKTKGTAQYLOAIQAHAAGMADVADVPDHKGADGTEWDAVE 120
DB 61 DLYDLGEFNOKGTVRTKTKGTAQYLOAIQAHAAGMADVADVPDHKGADGTEWDAVE 120
QY 121 VNPSDRNOEISGTYYQIQAWTKFDPFGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
DB 121 VNPSDRNOEISGTYYQIQAWTKFDPFGRGNTYSSFKRWYHFDGVDWDESRKLSRIYKFRG 180
QY 181 IGRAMDEVDTEENGNDYLYADLMDHPEVVTLEKMGKRYVNTNIDGRDLDAVHKIK 240
DB 181 IGRAMDEVDTEENGNDYLYADLMDHPEVVTLEKMGKRYVNTNIDGRDLDAVHKIK 240
QY 241 FSPFPDMLSYRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHKKFTYASK 300
DB 241 FSPFPDMLSYRSQTKGKPLFTVGEYWSYDINKLHNYITKTDGTMSLFDAPLHKKFTYASK 300
QY 301 SGCAFDMRTMTNTLMKQDPTLAVTVDNHDTEPGALQSWVDPWFKPLAVALILTRQEG 360
DB 301 SGCAFDMRTMTNTLMKQDPTLAVTVDNHDTEPGALQSWVDPWFKPLAVALILTRQEG 360
QY 361 YPCVFGDYGYGIPOYNIPLSKSIDPLLIARRDYAGTGHYLDHSDIIGWTEEGTEKRP 420
DB 361 YPCVFGDYGYGIPOYNIPLSKSIDPLLIARRDYAGTGHYLDHSDIIGWTEEGTEKRP 420
QY 421 GSGLAALITDPPGSGKMVYGKQAHGKVFYDLTGNSDVTYITNSDGMGEFKVNGGSVSW 480
DB 421 GSGLAALITDPPGSGKMVYGKQAHGKVFYDLTGNSDVTYITNSDGMGEFKVNGGSVSW 480
QY 481 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAM 514
DB 481 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAM 514

RESULT 8
US-10-186-042-6

;; Sequence 6, Application US/10186042
;; Publication No. US20030171236A1
;; GENERAL INFORMATION:
;; APPLICANT: Svendsen, Allan
;; APPLICANT: Borchert, Torben
;; APPLICANT: Bisgaard-Frantzen, Henrik
;; TITLE OF INVENTION: Alpha-Amylase Mutants
;; FILE REFERENCE: 4796.204-US
;; CURRENT APPLICATION NUMBER: US/10/186,042
;; CURRENT FILING DATE: 2002-06-28
;; PRIOR APPLICATION NUMBER: 09/672,459
;; PRIOR FILING DATE: 2000-09-28
;; PRIOR APPLICATION NUMBER: 09/182,859
;; PRIOR FILING DATE: 1998-10-29
;; PRIOR APPLICATION NUMBER: 0515/96
;; PRIOR FILING DATE: 1996-04-30
;; PRIOR APPLICATION NUMBER: 0712/96
;; PRIOR FILING DATE: 1996-06-28
;; PRIOR APPLICATION NUMBER: 0775/96
;; PRIOR FILING DATE: 1996-07-11

;; PRIOR APPLICATION NUMBER: 1263/96
;; PRIOR FILING DATE: 1996-11-08
;; NUMBER OF SEQ ID NOS: 37
;; SOFTWARE: PastSeq for Windows Version 3.0
;; SEQ ID NO 6
;; LENGTH: 514
;; TYPE: PRT
;; ORGANISM: Bacillus stearothermophilus
US-10-186-042-6

Query Match 99.8%; Score 2847; DB 14; Length 514;
Best Local Similarity 100.0%; Pred. No. 8.1e-256;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 AAPNGMOMYFEFMYLPDDGTLMTKVNANNNSSIGITLMLPAPKGRSRSDVGVY 60
DB 1 AAPNGMOMYFEFMYLPDDGTLMTKVNANNNSSIGITLMLPAPKGRSRSDVGVY 60
QY 61 DLYDLGFNKGTVRTKGTGAQYLQAIQAHAAGMADVAVFPHKGADGTEWDAVE 120
DB 61 DLYDLGFNKGTVRTKGTGAQYLQAIQAHAAGMADVAVFPHKGADGTEWDAVE 120
QY 121 VNPSDRNOBISGTYQIQAWTKFDPGKRGNTYSSFKRWYHFDGVDMDSRKLSRIYKFRG 180
DB 121 VNPSDRNOBISGTYQIQAWTKFDPGKRGNTYSSFKRWYHFDGVDMDSRKLSRIYKFRG 180
QY 121 VNPSDRNOBISGTYQIQAWTKFDPGKRGNTYSSFKRWYHFDGVDMDSRKLSRIYKFRG 180
DB 121 VNPSDRNOBISGTYQIQAWTKFDPGKRGNTYSSFKRWYHFDGVDMDSRKLSRIYKFRG 180
QY 181 IGAAMDVEVTENGNDYLYADLMDHPEVTELKMGKMYVNTTIDGFRDVAVGHK 240
DB 181 IGAAMDVEVTENGNDYLYADLMDHPEVTELKMGKMYVNTTIDGFRDVAVGHK 240
QY 181 IGAAMDVEVTENGNDYLYADLMDHPEVTELKMGKMYVNTTIDGFRDVAVGHK 240
DB 181 IGAAMDVEVTENGNDYLYADLMDHPEVTELKMGKMYVNTTIDGFRDVAVGHK 240
QY 241 FSPFPDMLSYRSOTGKPLFTVGEYWSYDINKLHNYITKTIDGTMSLPDAPLHNFYASK 300
DB 241 FSPFPDMLSYRSOTGKPLFTVGEYWSYDINKLHNYITKTIDGTMSLPDAPLHNFYASK 300
QY 301 SGGA FDMRTMTMTLMKQPTLAVTFVNDHTEPGALQSWDPWFKPLAVAFILTRQEG 360
DB 301 SGGA FDMRTMTMTLMKQPTLAVTFVNDHTEPGALQSWDPWFKPLAVAFILTRQEG 360
QY 361 YPCVFYDYYGIGIQYNIPSLKSKIDPLLIARDYAYGTQHDYLDHSIIIGTREGGTEKP 420
DB 361 YPCVFYDYYGIGIQYNIPSLKSKIDPLLIARDYAYGTQHDYLDHSIIIGTREGGTEKP 420
QY 421 GSGLAALITGPGGSKMYVKGKHAGKVFYDLIGNRSDYITINS DGEFFKNGSGSVW 480
DB 421 GSGLAALITGPGGSKMYVKGKHAGKVFYDLIGNRSDYITINS DGEFFKNGSGSVW 480
QY 481 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAM 514
DB 481 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAM 514
```

RESULT 9
US-10-081-872-104
;; Sequence 104, Application US/10081872
;; Publication No. US20030125534A1
;; GENERAL INFORMATION:
;; APPLICANT: Callen, Walter
;; APPLICANT: Richardson, Toby
;; APPLICANT: Frey, Gerhard
;; APPLICANT: Short, Jay M.
;; APPLICANT: Mathur, Eric J.
;; APPLICANT: Gray, Kevin A.
;; APPLICANT: Kerovo, Janne S.
;; APPLICANT: Slupka, Malgorzata
;; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
;; FILE REFERENCE: 09010-108001
;; CURRENT APPLICATION NUMBER: US/10/081,872
;; CURRENT FILING DATE: 2002-02-21
;; PRIOR APPLICATION NUMBER: US 60/270,495
;; PRIOR FILING DATE: 2001-02-21
;; PRIOR APPLICATION NUMBER: US 60/270,496
;; PRIOR FILING DATE: 2001-02-21

;; PRIOR APPLICATION NUMBER: US 60/291,122
;; PRIOR FILING DATE: 2001-05-14
;; NUMBER OF SEQ ID NOS: 321
;; SOFTWARE: PastSeq for Windows Version 4.0
;; SEQ ID NO 104
;; LENGTH: 549
;; TYPE: PRT
;; ORGANISM: Environmental
US-10-081-872-104

Query Match 99.4%; Score 2836; DB 14; Length 549;
Best Local Similarity 99.4%; Pred. No. 9.4e-255;
Matches 512; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 AAPNGMOMYFEFMYLPDDGTLMTKVNANNNSSIGITLMLPAPKGRSRSDVGVY 60
DB 35 AAPNGMOMYFEFMYLPDDGTLMTKVNANNNSSIGITLMLPAPKGRSRSDVGVY 94
QY 61 DLYDLGFNKGTVRTKGTGAQYLQAIQAHAAGMADVAVFPHKGADGTEWDAVE 120
DB 95 DLYDLGFNKGTVRTKGTGAQYLQAIQAHAAGMADVAVFPHKGADGTEWDAVE 154
QY 121 VNPSDRNOBISGTYQIQAWTKFDPGKRGNTYSSFKRWYHFDGVDMDSRKLSRIYKFRG 180
DB 155 VNPSDRNOBISGTYQIQAWTKFDPGKRGNTYSSFKRWYHFDGVDMDSRKLSRIYKFRG 214
QY 181 IGAAMDVEVTENGNDYLYADLMDHPEVTELKMGKMYVNTTIDGFRDVAVGHK 240
DB 215 IGAAMDVEVTENGNDYLYADLMDHPEVTELKMGKMYVNTTIDGFRDVAVGHK 274
QY 241 FSPFPDMLSYRSOTGKPLFTVGEYWSYDINKLHNYITKTIDGTMSLPDAPLHNFYASK 300
DB 275 FSPFPDMLSYRSOTGKPLFTVGEYWSYDINKLHNYITKTIDGTMSLPDAPLHNFYASK 334
QY 301 SGGA FDMRTMTMTLMKQPTLAVTFVNDHTEPGALQSWDPWFKPLAVAFILTRQEG 360
DB 335 SGGA FDMRTMTMTLMKQPTLAVTFVNDHTEPGALQSWDPWFKPLAVAFILTRQEG 394
QY 361 YPCVFYDYYGIGIQYNIPSLKSKIDPLLIARDYAYGTQHDYLDHSIIIGTREGGTEKP 420
DB 395 YPCVFYDYYGIGIQYNIPSLKSKIDPLLIARDYAYGTQHDYLDHSIIIGTREGGTEKP 454
QY 421 GSGLAALITGPGGSKMYVKGKHAGKVFYDLIGNRSDYITINS DGEFFKNGSGSVW 480
DB 455 GSGLAALITGPGGSKMYVKGKHAGKVFYDLIGNRSDYITINS DGEFFKNGSGSVW 514
QY 481 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAM 515
DB 515 VPRKTVSTIARPIITRPWTGEFVRWTEPRLVAM 549
```

RESULT 10
US-10-385-305-104
;; Sequence 104, Application US/10385305
;; Publication No. US20040018607A1
;; GENERAL INFORMATION:
;; APPLICANT: Callen, Walter
;; APPLICANT: Richardson, Toby
;; APPLICANT: Frey, Gerhard
;; APPLICANT: Short, Jay M.
;; APPLICANT: Mathur, Eric J.
;; APPLICANT: Gray, Kevin A.
;; APPLICANT: Kerovo, Janne S.
;; APPLICANT: Slupka, Malgorzata
;; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
;; FILE REFERENCE: 09010-108001
;; CURRENT APPLICATION NUMBER: US/10/385,305
;; CURRENT FILING DATE: 2003-03-06
;; PRIOR APPLICATION NUMBER: US/10/081,872
;; PRIOR FILING DATE: 2002-02-21
;; PRIOR APPLICATION NUMBER: US 60/270,495
;; PRIOR FILING DATE: 2001-02-21

;; PRIOR APPLICATION NUMBER: US 60/270,496
;; PRIOR FILING DATE: 2001-02-21
;; PRIOR APPLICATION NUMBER: US 60/291,122
;; PRIOR FILING DATE: 2001-05-14
;; NUMBER OF SEQ ID NOS: 321
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 104
;; LENGTH: 549
;; TYPE: PRT
;; ORGANISM: Environmental
US-10-385-305-104

Query Match 99.4%; Score 2836; DB 15; Length 549;
Best Local Similarity 99.4%; Pred. No. 9.4e-255;
Matches 512; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 AAFNGTMMQYFEMYLPPDGTILMTKVAEANNLSIGITLMLPPAYKTSRSDVGCVY 60
DB 35 AAFNGTMMQYFEMYLPPDGTILMTKVAEANNLSIGITLMLPPAYKTSRSDVGCVY 94
QY 61 DLYDLGEFNOKGTVRTKTKGKAOYLQAIQAHAAGMOYADVFDHKGADGTEWDAYE 120
DB 95 DLYDLGEFNOKGTVRTKTKGKAOYLQAIQAHAAGMOYADVFDHKGADGTEWDAYE 154
QY 121 VNPSDRNOEISGTYYQIQAMTKFDPGRGNTYSSFKRWYHFDGVDMDESRKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTYYQIQAMTKFDPGRGNTYSSFKRWYHFDGVDMDESRKLSRIYKFRG 214
QY 181 IGRAMDVEVTENGENYDYLMTADLMDHPEVYTELKNMGKMYVNTNIDGFRDLDAVKHIK 240
DB 215 IGRAMDVEVTENGENYDYLMTADLMDHPEVYTELKNMGKMYVNTNIDGFRDLDAVKHIK 274
QY 241 FSFPPDMLSYRSQTKGKPLFTVGEYMSYDINKLHNYITKTDGMSLFDAPLNHKFTYASK 300
DB 275 FSFPPDMLSYRSQTKGKPLFTVGEYMSYDINKLHNYITKTDGMSLFDAPLNHKFTYASK 334
QY 301 SGGAFDMRTLMTNTLTKMDQPTLAVTFVDNHDPTEGQALQSWDVPWPKPLAAYAFILTRQEG 360
DB 335 SGGAFDMRTLMTNTLTKMDQPTLAVTFVDNHDPTEGQALQSWDVPWPKPLAAYAFILTRQEG 394
QY 361 YPCVFYGDYIGIPQYNIPLSKSKIDPLLIARRDYAGTQHDYLDHSDIIGWTRREGTEKXP 420
DB 395 YPCVFYGDYIGIPQYNIPLSKSKIDPLLIARRDYAGTQHDYLDHSDIIGWTRREGTEKXP 454
QY 421 GSGLAALITDGPGGSKMYVYKQAHAKVYDITGNRSDVTYINSDGWGEFKNVNGGSVSW 480
DB 455 GSGLAALITDGPGGSKMYVYKQAHAKVYDITGNRSDVTYINSDGWGEFKNVNGGSVSW 514
QY 481 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAMP 515
DB 515 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAMP 549
```

RESULT 11
US-10-081-872-92
;; Sequence 92, Application US/10081872
;; Publication No. US20030125534A1
;; GENERAL INFORMATION:
;; APPLICANT: Callen, Walter
;; APPLICANT: Richardson, Toby
;; APPLICANT: Frey, Gerhard
;; APPLICANT: Short, Jay M.
;; APPLICANT: Mathur, Eric J.
;; APPLICANT: Gray, Kevin A.
;; APPLICANT: Kervuuo, Janne S.
;; APPLICANT: Slupeka, Malgorzata
;; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
;; FILE REFERENCE: 09010-108001
;; CURRENT APPLICATION NUMBER: US/10/081,872
;; PRIOR FILING DATE: 2002-02-21
;; PRIOR APPLICATION NUMBER: US 60/270,495
;; PRIOR FILING DATE: 2001-02-21

;; PRIOR APPLICATION NUMBER: US 60/270,496
;; PRIOR FILING DATE: 2001-02-21
;; PRIOR APPLICATION NUMBER: US 60/291,122
;; PRIOR FILING DATE: 2001-05-14
;; NUMBER OF SEQ ID NOS: 321
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 92
;; LENGTH: 549
;; TYPE: PRT
;; ORGANISM: Bacterial
US-10-081-872-92

Query Match 99.2%; Score 2832; DB 14; Length 549;
Best Local Similarity 99.4%; Pred. No. 2.2e-254;
Matches 512; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 AAFNGTMMQYFEMYLPPDGTILMTKVAEANNLSIGITLMLPPAYKTSRSDVGCVY 60
DB 35 AAFNGTMMQYFEMYLPPDGTILMTKVAEANNLSIGITLMLPPAYKTSRSDVGCVY 94
QY 61 DLYDLGEFNOKGTVRTKTKGKAOYLQAIQAHAAGMOYADVFDHKGADGTEWDAYE 120
DB 95 DLYDLGEFNOKGTVRTKTKGKAOYLQAIQAHAAGMOYADVFDHKGADGTEWDAYE 154
QY 121 VNPSDRNOEISGTYYQIQAMTKFDPGRGNTYSSFKRWYHFDGVDMDESRKLSRIYKFRG 180
DB 155 VNPSDRNOEISGTYYQIQAMTKFDPGRGNTYSSFKRWYHFDGVDMDESRKLSRIYKFRG 214
QY 181 IGRAMDVEVTENGENYDYLMTADLMDHPEVYTELKNMGKMYVNTNIDGFRDLDAVKHIK 240
DB 215 IGRAMDVEVTENGENYDYLMTADLMDHPEVYTELKNMGKMYVNTNIDGFRDLDAVKHIK 274
QY 241 FSFPPDMLSYRSQTKGKPLFTVGEYMSYDINKLHNYITKTDGMSLFDAPLNHKFTYASK 300
DB 275 FSFPPDMLSYRSQTKGKPLFTVGEYMSYDINKLHNYITKTDGMSLFDAPLNHKFTYASK 334
QY 301 SGGAFDMRTLMTNTLTKMDQPTLAVTFVDNHDPTEGQALQSWDVPWPKPLAAYAFILTRQEG 360
DB 335 SGGAFDMRTLMTNTLTKMDQPTLAVTFVDNHDPTEGQALQSWDVPWPKPLAAYAFILTRQEG 394
QY 361 YPCVFYGDYIGIPQYNIPLSKSKIDPLLIARRDYAGTQHDYLDHSDIIGWTRREGTEKXP 420
DB 395 YPCVFYGDYIGIPQYNIPLSKSKIDPLLIARRDYAGTQHDYLDHSDIIGWTRREGTEKXP 454
QY 421 GSGLAALITDGPGGSKMYVYKQAHAKVYDITGNRSDVTYINSDGWGEFKNVNGGSVSW 480
DB 455 GSGLAALITDGPGGSKMYVYKQAHAKVYDITGNRSDVTYINSDGWGEFKNVNGGSVSW 514
QY 481 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAMP 515
DB 515 VPRKTVSTIARPIITTRPWTGEFVRWTEPRLVAMP 549
```

RESULT 12
US-10-385-305-92
;; Sequence 92, Application US/10385305
;; Publication No. US20040018607A1
;; GENERAL INFORMATION:
;; APPLICANT: Callen, Walter
;; APPLICANT: Richardson, Toby
;; APPLICANT: Frey, Gerhard
;; APPLICANT: Short, Jay M.
;; APPLICANT: Mathur, Eric J.
;; APPLICANT: Gray, Kevin A.
;; APPLICANT: Kervuuo, Janne S.
;; APPLICANT: Slupeka, Malgorzata
;; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
;; FILE REFERENCE: 09010-108001
;; CURRENT APPLICATION NUMBER: US/10/385,305
;; PRIOR FILING DATE: 2003-03-06
;; PRIOR APPLICATION NUMBER: US/10/081,872
;; PRIOR FILING DATE: 2002-02-21

```

; PRIOR APPLICATION NUMBER: US 60/270,495
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/270,496
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/291,122
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Bacterial
; US-10-385-305-92

```

```

Query Match          99.2%; Score 2832; DB 15; Length 549;
Best Local Similarity 99.4%; Pred. No. 2,2e-254;
Matches 512; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 AAFNGTMQYFEMYLDDGTLMTKVNANNNLSLIGITLMLPPAYKGTSRSDVGYGY 60
DB 35 AAFNGTMQYFEMYLDDGTLMTKVNANNNLSLIGITLMLPPAYKGTSRSDVGYGY 94
QY 61 DLYDLGFNKGKGVRTKYGKAYLOAIQAHAAGMAYADVDPDHKGADGTEWDVAE 120
DB 95 DLYDLGFNKGKGVRTKYGKAYLOAIQAHAAGMAYADVDPDHKGADGTEWDVAE 154
QY 121 VNPSDRNOEISGTQIOAMTKFDPGKGNYSFKRMWHFDDVDMDSRKLRIYKFRG 180
DB 155 VNPSDRNOEISGTQIOAMTKFDPGKGNYSFKRMWHFDDVDMDSRKLRIYKFRG 214
QY 181 IGRAMDVEVDTEGNNDYLYADLMDHPEVTELEKMGKMYVTNNIDGFRDLAVGHIK 240
DB 215 IGRAMDVEVDTEGNNDYLYADLMDHPEVTELEKMGKMYVTNNIDGFRDLAVGHIK 274
QY 241 FSEFPDMLSYRSQTKGKPLFTVGBYSYDINKLHNYITKTDGWSLFDAPLHNFYASK 300
DB 275 FSEFPDMLSYRSQTKGKPLFTVGBYSYDINKLHNYITKTDGWSLFDAPLHNFYASK 334
QY 301 SGGAFDRLTMTNTLMDOPTLAVTFVNDHTEBGQALQSWDPWFKPLAVALTLTQEG 360
DB 335 SGGAFDRLTMTNTLMDOPTLAVTFVNDHTEBGQALQSWDPWFKPLAVALTLTQEG 394
QY 361 YPCVFYGDYIGIPOYNIPLSKSKIDPLIARDAVYTOHDYLDHSDIIGTREGTEKP 420
DB 395 YPCVFYGDYIGIPOYNIPLSKSKIDPLIARDAVYTOHDYLDHSDIIGTREGTEKP 454
QY 421 GSGIALLITDGPSSKMYVKGQAHGKVFYDLTGNRSDDVTYINSDGGEFVNGGSYSVW 480
DB 455 GSGIALLITDGPSSKMYVKGQAHGKVFYDLTGNRSDDVTYINSDGGEFVNGGSYSVW 514
QY 481 VPKRTVSTIARPTTTPWTGEPFRWTEPRVLVAMP 515
DB 515 VPKRTVSTIARPTTTPWTGEPFRWTEPRVLVAMP 549

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RESULT 13
US-09-795-211-4
; Sequence 4, Application US/09795211
; Publication No. US20020183226A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Kasturi, Chandrika
; APPLICANT: Wandersat, Mark E.
; APPLICANT: Song, Brian X.
; TITLE OF INVENTION: LIQUID DETERGENT COMPOSITION EXHIBITING ENHANCED a-AMYLASE ENZY
; FILE REFERENCE: Detergent Composition
; CURRENT APPLICATION NUMBER: US/09/795,211
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent version 3.1
; SEQ ID NO 4
; LENGTH: 515

```

```

; TYPE: PRT
; ORGANISM: alkaliphilicbaciillus
; US-09-795-211-4

```

```

Query Match          97.7%; Score 2787; DB 9; Length 515;
Best Local Similarity 98.1%; Pred. No. 3.1e-250;
Matches 505; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

```

```

QY 1 AAFNGTMQYFEMYLDDGTLMTKVNANNNLSLIGITLMLPPAYKGTSRSDVGYGY 60
DB 1 AAFNGTMQYFEMYLDDGTLMTKVNANNNLSLIGITLMLPPAYKGTSRSDVGYGY 60
QY 61 DLYDLGFNKGKGVRTKYGKAYLOAIQAHAAGMAYADVDPDHKGADGTEWDVAE 120
DB 61 DLYDLGFNKGKGVRTKYGKAYLOAIQAHAAGMAYADVDPDHKGADGTEWDVAE 120
QY 121 VNPSDRNOEISGTQIOAMTKFDPGKGNYSFKRMWHFDDVDMDSRKLRIYKFRG 180
DB 121 VNPSDRNOEISGTQIOAMTKFDPGKGNYSFKRMWHFDDVDMDSRKLRIYKFRG 180
QY 181 IGRAMDVEVDTEGNNDYLYADLMDHPEVTELEKMGKMYVTNNIDGFRDLAVGHIK 240
DB 181 IGRAMDVEVDTEGNNDYLYADLMDHPEVTELEKMGKMYVTNNIDGFRDLAVGHIK 240
QY 241 FSEFPDMLSYRSQTKGKPLFTVGBYSYDINKLHNYITKTDGWSLFDAPLHNFYASK 300
DB 241 FSEFPDMLSYRSQTKGKPLFTVGBYSYDINKLHNYITKTDGWSLFDAPLHNFYASK 300
QY 301 SGGAFDRLTMTNTLMDOPTLAVTFVNDHTEBGQALQSWDPWFKPLAVALTLTQEG 360
DB 301 SGGAFDRLTMTNTLMDOPTLAVTFVNDHTEBGQALQSWDPWFKPLAVALTLTQEG 360
QY 361 YPCVFYGDYIGIPOYNIPLSKSKIDPLIARDAVYTOHDYLDHSDIIGTREGTEKP 420
DB 361 YPCVFYGDYIGIPOYNIPLSKSKIDPLIARDAVYTOHDYLDHSDIIGTREGTEKP 420
QY 421 GSGIALLITDGPSSKMYVKGQAHGKVFYDLTGNRSDDVTYINSDGGEFVNGGSYSVW 480
DB 421 GSGIALLITDGPSSKMYVKGQAHGKVFYDLTGNRSDDVTYINSDGGEFVNGGSYSVW 480
QY 481 VPKRTVSTIARPTTTPWTGEPFRWTEPRVLVAMP 515
DB 481 VPKRTVSTIARPTTTPWTGEPFRWTEPRVLVAMP 515

```

```

RESULT 14
US-09-769-864-3
; Sequence 3, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Bacillus stearothermophilus
; US-09-769-864-3

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Query Match          97.4%; Score 2780; DB 9; Length 514;
Best Local Similarity 98.1%; Pred. No. 1.4e-249;
Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

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1 AAPENGTMQYFEWYLPDDGTLMTKVANEANNLSLIGITALMLPPAYKTSRSDVGYY 60
1 AAPENGTMQYFEWYLPDDGTLMTKVANEANNLSLIGITALMLPPAYKTSRSDVGYY 60
61 DLYDLGEFNOKGAVRTKTKGAKOYLQAIQAHAAGQVYADVFPDHKGADGTEWDAVE 120
61 DLYDLGEFNOKGAVRTKTKGAKOYLQAIQAHAAGQVYADVFPDHKGADGTEWDAVE 120
121 VNPSRNOEISGTQYIOAWTKFDPGKNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180
121 VNPSRNOEISGTQYIOAWTKFDPGKNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180
181 IGRAMDWEVDTEGNVYLYMADLMDHPEVTELKNGKMYVNTNIDGFRDLAVKHK 240
181 IGRAMDWEVDTEGNVYLYMADLMDHPEVTELKNGKMYVNTNIDGFRDLAVKHK 240
241 FSPFPDMLSVRSQTKGKPLFTVGEYWSYDINKLHNYITKTGTMSLPDAPLHNKFTYASK 300
241 FSPFPDMLSVRSQTKGKPLFTVGEYWSYDINKLHNYITKTGTMSLPDAPLHNKFTYASK 300
301 SGGAFFDMKTLMTNTLMKQPTLAATFVNDHTEPGALQSWDVPWFKPLAFAFILTROEG 360
301 SGGAFFDMKTLMTNTLMKQPTLAATFVNDHTEPGALQSWDVPWFKPLAFAFILTROEG 360
361 YPCVFYGDYGIPOYNIPSLKSIDPLLIARDYAGTQHDYLDHSDIIGWTRREGTEKP 420
361 YPCVFYGDYGIPOYNIPSLKSIDPLLIARDYAGTQHDYLDHSDIIGWTRREGTEKP 420
421 GSGLAALITDGPBGSKMYVKGAKVFDLTGNRSDVTYINSDGWGEFKNVGSVSW 480
421 GSGLAALITDGPBGSKMYVKGAKVFDLTGNRSDVTYINSDGWGEFKNVGSVSW 480
481 VPRKTVSTIARPIITRRPWTGEFVRWTEPRLVAM 514
481 VPRKTVSTIARPIITRRPWTGEFVRWTEPRLVAM 514

RESULT 15
US-09-902-188A-3
Sequence 3, Application US/09902188A
Patent No. US2002009896A1
GENERAL INFORMATION:
APPLICANT: Bisgard-Frantzen, Henrik
Svendsen, Allan
Borchert, Torben Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. US2002009896A1o No. US2002009896A1disk of No. US2002009896A1
STREET: 405 Lexington Avenue, Suite 6400
City: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/902,188A
FILING DATE: 10-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/354,191
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318, 204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123

TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-902-188A-3
Query Match 97.4%; Score 2780; DB 9; Length 514;
Best Local Similarity 98.1%; Pred. No. 1,4e-249;
Matches 504; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
1 AAPENGTMQYFEWYLPDDGTLMTKVANEANNLSLIGITALMLPPAYKTSRSDVGYY 60
1 AAPENGTMQYFEWYLPDDGTLMTKVANEANNLSLIGITALMLPPAYKTSRSDVGYY 60
61 DLYDLGEFNOKGAVRTKTKGAKOYLQAIQAHAAGQVYADVFPDHKGADGTEWDAVE 120
61 DLYDLGEFNOKGAVRTKTKGAKOYLQAIQAHAAGQVYADVFPDHKGADGTEWDAVE 120
121 VNPSRNOEISGTQYIOAWTKFDPGKNTYSSFKRWYHFDGVDWDSRKLRIYKFRG 180
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181 IGRAMDWEVDTEGNVYLYMADLMDHPEVTELKNGKMYVNTNIDGFRDLAVKHK 240
241 FSPFPDMLSVRSQTKGKPLFTVGEYWSYDINKLHNYITKTGTMSLPDAPLHNKFTYASK 300
241 FSPFPDMLSVRSQTKGKPLFTVGEYWSYDINKLHNYITKTGTMSLPDAPLHNKFTYASK 300
301 SGGAFFDMKTLMTNTLMKQPTLAATFVNDHTEPGALQSWDVPWFKPLAFAFILTROEG 360
301 SGGAFFDMKTLMTNTLMKQPTLAATFVNDHTEPGALQSWDVPWFKPLAFAFILTROEG 360
361 YPCVFYGDYGIPOYNIPSLKSIDPLLIARDYAGTQHDYLDHSDIIGWTRREGTEKP 420
361 YPCVFYGDYGIPOYNIPSLKSIDPLLIARDYAGTQHDYLDHSDIIGWTRREGTEKP 420
421 GSGLAALITDGPBGSKMYVKGAKVFDLTGNRSDVTYINSDGWGEFKNVGSVSW 480
421 GSGLAALITDGPBGSKMYVKGAKVFDLTGNRSDVTYINSDGWGEFKNVGSVSW 480
481 VPRKTVSTIARPIITRRPWTGEFVRWTEPRLVAM 514
481 VPRKTVSTIARPIITRRPWTGEFVRWTEPRLVAM 514

Search completed: October 7, 2004, 00:57:27
Job time : 57.7539 secs

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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:45:37 ; Search time 58.3101 Seconds
(without alignments)
2340.424 Million cell updates/sec

Title: US-09-925-576C-8
Perfect score: 2666
Sequence: 1 ANINGTLMIQFVWYMPNDQ.....SEGWGEFVNQGSVSIVQR 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2666	100.0	483	2	AAR72447
2	2666	100.0	483	2	AAR78267
3	2666	100.0	483	2	AAW31404
4	2666	100.0	483	2	AAV15418
5	2666	100.0	483	2	AAV29852
6	2666	100.0	483	2	AAV07384
7	2666	100.0	483	3	AAV99605
8	2666	100.0	483	3	AAV97545
9	2666	100.0	483	5	ABW06936
10	2666	100.0	483	5	AAU12152
11	2666	100.0	483	5	AAE26534
12	2666	100.0	483	5	ABW47853
13	2666	100.0	483	5	ABW76589
14	2666	100.0	531	2	AAR98007
15	2666	100.0	630	2	AAW22523
16	2666	100.0	630	2	AAW23603
17	2663	99.9	483	2	AAW57985
18	2663	99.9	483	2	AAW88438
19	2663	99.9	483	2	AAW81475
20	2663	99.9	483	2	AAW14498
21	2663	99.9	483	2	AAW39742
22	2663	99.9	483	4	AAW65876
23	2663	99.9	487	2	AAW57987
24	2663	99.9	487	2	AAW80189
25	2663	99.9	487	4	AAW65881

26	2663	99.9	512	1	AAW70753	AAW70753
27	2663	99.9	512	2	AAW73509	AAW73509
28	2663	99.9	512	2	AAW00769	AAW00769
29	2663	99.9	512	4	AAW07097	AAW07097
30	2663	99.9	512	4	AAW65875	AAW65875
31	2663	99.9	512	4	AAW65877	AAW65877
32	2661	99.8	483	5	AAU12165	AAU12165
33	2661	99.8	483	5	AAU12161	AAU12161
34	2660	99.8	483	2	AAW58000	AAW58000
35	2660	99.8	483	2	AAW58002	AAW58002
36	2660	99.8	483	2	AAW57992	AAW57992
37	2660	99.8	483	2	AAW80192	AAW80192
38	2660	99.8	483	5	AAU12162	AAU12162
39	2660	99.8	483	5	AAU12163	AAU12163
40	2660	99.8	487	2	AAW80215	AAW80215
41	2660	99.8	487	2	AAW80191	AAW80191
42	2660	99.8	487	2	AAW57437	AAW57437
43	2659	99.7	483	2	AAW10576	AAW10576
44	2659	99.7	483	2	AAW58007	AAW58007
45	2659	99.7	483	2	AAW58007	AAW58007

ALIGNMENTS

RESULT 1	AAW72447	standard; protein; 483 AA.
ID	AAW72447	
XX	AAW72447	
AC	AAW72447	
XX	25-MAR-2003 (revised)	
DT	01-DEC-1995 (first entry)	
DT	01-DEC-1995	
XX	Bacillus licheniformis alpha amylase (mature protein).	
DE	Bacillus licheniformis alpha amylase (mature protein).	
XX	Alpha amylase; variant; enzyme; detergent; additive; dishwashing;	
KW	washing; Bacillus licheniformis; Bacillus amyloliquefaciens;	
KW	Bacillus stearothermophilus; dyeing; bleaching; scouring; textile;	
KW	thermostable.	
XX	Bacillus licheniformis.	
OS	Bacillus licheniformis.	
XX	WO9510603-A1.	
PN	20-APR-1995.	
PD	05-OCT-1994; 94WO-DK000370.	
PF	08-OCT-1993; 93DK-00001133.	
XX	02-FEB-1994; 94DK-00000140.	
PR	(NOVO) NOVO-NORDISK AS.	
PA	Borchert TV, Bisgard-Frantzen H, Svendsen A, Thellersen M;	
PI	Van Der Zee P;	
XX	WPI; 1995-161790/21.	
XX	N-PSDB; AA088066.	
DR	New Bacillus derived alpha-amylase variants - having amino acid	
XX	modifications to improve washing and/or dishwashing performance.	
PT	Claim 6; Page 72; 105pp; English.	
XX	Variant alpha amylase enzymes which have improved washing and/or as	
XX	detergent additives. The enzymes have one or more amino acid residues	
CC	added, deleted or substituted. The variants can also be used for textile	
CC	desizing prior to scouring, bleaching and dyeing. The variants have	
CC	improved thermostability, acid/alkaline stability, low temperature	
CC	optimum; pH optimum; higher hydrolysis velocity and improved tolerance	
CC	to other composition constituents, e.g. oxidation agents. (Updated on 25-MAR	
CC	-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)	

XX Sequence 483 AA;
SQ
Query Match 100.0%; Score 2666; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 1,7e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANLNGTLMQYFEWYMPNDGQHWRRLOQDSAYLAHGGITAVWIPPAVKGTSQADVGYGAYD 60
DB 1 ANLNGTLMQYFEWYMPNDGQHWRRLOQDSAYLAHGGITAVWIPPAVKGTSQADVGYGAYD 60
QY 61 LYDGEFHQKGTVRTKTKGTGELQSAIKSLHSRDINVGDVVYNHKGADATEDVTAVEV 120
DB 61 LYDGEFHQKGTVRTKTKGTGELQSAIKSLHSRDINVGDVVYNHKGADATEDVTAVEV 120
QY 121 DPADRNRVISGEHLIKAMTHFFHPGRGSTYSDPKMWHYHFDGTDWDESRKLNRIYKFGQK 180
DB 121 DPADRNRVISGEHLIKAMTHFFHPGRGSTYSDPKMWHYHFDGTDWDESRKLNRIYKFGQK 180
QY 181 AMDWEVSNGENVYDLYMADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKHIFSF 240
DB 181 AMDWEVSNGENVYDLYMADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKHIFSF 240
QY 241 LRDVNVHVRREKTKGEMFTVAEYQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGG 300
DB 241 LRDVNVHVRREKTKGEMFTVAEYQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGG 300
QY 301 GYDMRKILNGTVVSKPLKSVTFVDNHDTPQGSLSTVQWPKPLAFAFILTBESGYPO 360
DB 301 GYDMRKILNGTVVSKPLKSVTFVDNHDTPQGSLSTVQWPKPLAFAFILTBESGYPO 360
QY 361 VFYGDWYGTGDSQREIPALKHKIEPIILKARKQYAGAOHDYFDHHDIVGWTREGDSSVA 420
DB 361 VFYGDWYGTGDSQREIPALKHKIEPIILKARKQYAGAOHDYFDHHDIVGWTREGDSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSEGMGEFHVNGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSEGMGEFHVNGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483
RESULT 2
ID AAR78267 standard; protein; 483 AA.
XX AAR78267;
XX 17-JAN-1996 (first entry)
DT 17-JAN-1996 (first entry)
XX Bacillus licheniformis alpha amylase (mature protein).
DE Bacillus licheniformis alpha amylase (mature protein).
XX Alpha amylase; oxidation; desizing; scouring; bleaching; fabric; starch;
KM thermostable; methionine; Bacillus licheniformis;
KW Bacillus amyloliquefaciens; Bacillus stearothermophilus.
XX Bacillus licheniformis.
OS WO9521247-A1.
PN WO9521247-A1.
XX 10-AUG-1995.
PD 10-AUG-1995.
XX 05-OCT-1994; 94WO-DK000371.
PF 05-OCT-1994; 94WO-DK000371.
XX 02-FEB-1994; 94DK-00000141.
PR 02-FEB-1994; 94DK-00000141.
XX (NOVO) NOVO-NORDISK AS.
PA (NOVO) NOVO-NORDISK AS.
XX Tofte AH, Marcher D, Pedersen HH, Nilsson TE;
PI Tofte AH, Marcher D, Pedersen HH, Nilsson TE;
XX WPI; 1995-283767/37.
DR

DR N-PSDB; AAQ95031.
XX Use of an oxidation stable alpha-amylase - for simultaneous desizing and
XX PT bleaching or scouring of fabrics contg. starch or starch derivs.
XX PT bleaching or scouring of fabrics contg. starch or starch derivs.
XX PS Claim 6; Page 22; 37pp; English.
XX Oxidation stable alpha amylases can be used for the simultaneous desizing
CC and bleaching or scouring of a fabric comprising starch or starch
CC derivatives. They exhibit a better heat stability, especially in the
CC presence of oxidising agents. They are obtained from a parent alpha
CC amylase by replacing one or more methionine residues with any amino acid
CC different from Cys or Met, preferably Leu, Thr, Ala, Gly, Ser, Ile or
CC Asp. The parent alpha amylase is derived from a Bacillus species. This is
CC the wild type (unmodified) alpha amylase
XX
SQ Sequence 483 AA;
Query Match 100.0%; Score 2666; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 1,7e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANLNGTLMQYFEWYMPNDGQHWRRLOQDSAYLAHGGITAVWIPPAVKGTSQADVGYGAYD 60
DB 1 ANLNGTLMQYFEWYMPNDGQHWRRLOQDSAYLAHGGITAVWIPPAVKGTSQADVGYGAYD 60
QY 61 LYDGEFHQKGTVRTKTKGTGELQSAIKSLHSRDINVGDVVYNHKGADATEDVTAVEV 120
DB 61 LYDGEFHQKGTVRTKTKGTGELQSAIKSLHSRDINVGDVVYNHKGADATEDVTAVEV 120
QY 121 DPADRNRVISGEHLIKAMTHFFHPGRGSTYSDPKMWHYHFDGTDWDESRKLNRIYKFGQK 180
DB 121 DPADRNRVISGEHLIKAMTHFFHPGRGSTYSDPKMWHYHFDGTDWDESRKLNRIYKFGQK 180
QY 181 AMDWEVSNGENVYDLYMADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKHIFSF 240
DB 181 AMDWEVSNGENVYDLYMADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKHIFSF 240
QY 241 LRDVNVHVRREKTKGEMFTVAEYQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGG 300
DB 241 LRDVNVHVRREKTKGEMFTVAEYQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGG 300
QY 301 GYDMRKILNGTVVSKPLKSVTFVDNHDTPQGSLSTVQWPKPLAFAFILTBESGYPO 360
DB 301 GYDMRKILNGTVVSKPLKSVTFVDNHDTPQGSLSTVQWPKPLAFAFILTBESGYPO 360
QY 361 VFYGDWYGTGDSQREIPALKHKIEPIILKARKQYAGAOHDYFDHHDIVGWTREGDSSVA 420
DB 361 VFYGDWYGTGDSQREIPALKHKIEPIILKARKQYAGAOHDYFDHHDIVGWTREGDSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSEGMGEFHVNGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSEGMGEFHVNGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483
RESULT 3
ID AAW31404 standard; protein; 483 AA.
XX AAW31404;
XX AAW31404;
XX 17-OCT-2003 (revised)
DT 17-OCT-2003 (revised)
XX 11-MAY-1996 (first entry)
DT 11-MAY-1996 (first entry)
XX Bacillus licheniformis Termamyl alpha-amylase.
DE Bacillus licheniformis Termamyl alpha-amylase.
XX Termamyl; alpha-amylase; enzyme engineering; protein engineering; starch;
KW liquefaction; saccharification; sweetener; textile desizing;
KM detergent additive.

XX OS *Bacillus licheniformis*, strain ATCC 27811.
 XX PN WO9741213-A1.
 XX PD 06-NOV-1997.
 XX PF 30-APR-1997; 97WO-DK000197.
 XX PR 30-APR-1996; 96DK-00000515.
 XX PR 28-JUN-1996; 96DK-00000712.
 XX PR 11-JUL-1996; 96DK-00000775.
 XX PR 08-NOV-1996; 96DK-00001263.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX PI Svendsen A, Borchert TV, Bisgaard-Frantzen H;
 XX DR WPI; 1997-549718/50.
 XX DR N-PSDB; AAV02471.
 XX PT Termamyl-like alpha-amylase variants with improved properties - e.g.
 XX PT increased stability at low pH and low calcium, useful as detergent
 XX PT additives and in industrial starch processing e.g. liquefaction.
 XX PS Claim 1; Page 82; 101pp; English.
 CC This protein comprises Termamyl alpha-amylase (see AAW31404) of *Bacillus*
 CC *licheniformis* ATCC 27811. The invention relates to novel variants
 CC (mutants) of Termamyl-like alpha-amylases that have alpha-amylase
 CC activity and exhibit an alteration in at least one property selected
 CC from: substrate specificity; binding or cleavage pattern; thermal
 CC stability; pH/activity or pH/stability profile; stability towards
 CC oxidation; Ca²⁺ dependency and specific activity. The variant has one or
 CC more mutations selected from: (a) the mutations A181E, D, Q, N, V; I201
 CC (bulkier amino acid) including I201W, F, L; Y203Q, Q9K, L, E; F11R, K, E;
 CC E12Q; D100N, L; V101H, R, K, D, E, F, V102A, T; I103H, K; N104R, K, D;
 CC H105R, K, D, E, W, F; L196R, K, D, E, F, Y; I212R, K, D, E; L230H, K, I;
 CC A232G, H, F, S, V; V233D, K234L, E; I236R, K, N, H, D, E; L241R, K, D, E,
 CC F; A260S; W263H; Q264R, D, K, E; N265K, R, D; A269R, K, D, E; L270R, K,
 CC H, D, E; V283H, D; F284H; D285N, L; V286R, K, H, D, E; Y290R, E, K;
 CC I212R, K, D, E; F323H; D325N; N326K, H, D, L; H327Q, N, E, D, F; Q220L, E
 CC G333D; Q333R, K, H, E, L; S334A, V, T, L, I, D; L335G, A, S, T, N,
 CC E336R + R375E; T337D, K, T338D, E; T338D, Q360K, R, E; D365N; G371D, R;
 CC (b) substitutions at positions H68, H91, H247, R305, K306, H382, K389,
 CC H405, H406, H450 or R483; (c) the mutations H140Y, H142Y, H159Y, H140D +
 CC H142R, H140K + H142D; or H142Y + H156Y; (d) deletion of 3 amino acids
 CC within the partial sequence from T369 to I377, including K370-D372 or
 CC D372-Q374; (e) replacement of T369-I377 by IPTHSV, IPTHGV or IQVNT; (f)
 CC substitutions at positions R169 or R173, including R169T, L, F, T or
 CC R173I, L, F, T; (g) the mutations H156D, I201F, I212F, A209L or T, or
 CC V208I; (h) substitutions at positions N172, A181, N188, N190, H205, D207,
 CC A209, A210, E211, Q264 or N265, including N172R, H, K; A181T, N188P, D207,
 CC N190L, F; H205C; D207Y; A209L, T, V; A210S, E211Q, Q264A, E, L, K, S, T;
 CC N265A, S, T, Y, or (Q264S + N265Y); and (i) the mutations H156Y + A181T +
 CC A209V; H156Y + A181T + N190F + A209V + Q264S; A1* + N2* + L3V + M1ST +
 CC R23K + S29A + A30E + Y31H + A33S + E34D + H35I + H156Y + A209V
 CC (where * indicates deletion of the amino acid residue); A1* + N2* + L3V +
 CC M1ST + R23K + S29A + A30E + Y31H + A33S + E34D + H35I + H156Y + A181T +
 CC N90F + A209V; or A1* + N2* + L3V + M1ST + R23K + S29A + A30E + Y31H +
 CC A33S + E34D + H35I + H156Y + A181T + N190F + A209V + Q264S. Also claimed
 CC are constructs comprising DNA (see AAV02471) encoding such a variant, and
 CC recombinant expression vectors and transformed cells containing the DNA.
 CC The alpha-amylase variant is useful as a detergent additive and can also
 CC be used in industrial starch processing e.g. liquefaction (claimed) or
 CC saccharification to produce sweeteners, and in textile desizing (claimed) or
 CC (claimed). (Updated on 17-OCT-2003 to standardise OS field)
 XX SQ Sequence 483 AA;
 Query Match 100.0%; Score 2666; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1,7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANINGTLMQYFENYMPNDQGMRLQNDASVLAHEGTTAVWIPPAYGTSQADVGAYD 60
 DB 1 ANINGTLMQYFENYMPNDQGMRLQNDASVLAHEGTTAVWIPPAYGTSQADVGAYD 60
 QY 61 LYLDFEHOFGKGTTRTKYGTGELQSAIKSLHSRDINVGQVNVNHHKGAATETVAVEV 120
 DB 61 LYLDFEHOFGKGTTRTKYGTGELQSAIKSLHSRDINVGQVNVNHHKGAATETVAVEV 120
 QY 121 DPADRRNVISGEHLIKAMTHFFPGRGSTSDPEKMHVHFDGTDWDSRKLRIYKFGK 180
 DB 121 DPADRRNVISGEHLIKAMTHFFPGRGSTSDPEKMHVHFDGTDWDSRKLRIYKFGK 180
 QY 181 AMDMEVSNENGNVDYLMYADIDYDHPVAAEIKRMGTWVANELODGFRLDAVHKIFSP 240
 DB 181 AMDMEVSNENGNVDYLMYADIDYDHPVAAEIKRMGTWVANELODGFRLDAVHKIFSF 240
 QY 241 LRDVNHVREKTKGEMFTVAEYQNDIGALENTYKTNFNVHSDVPLHIOFHAASTQGG 300
 DB 241 LRDVNHVREKTKGEMFTVAEYQNDIGALENTYKTNFNVHSDVPLHIOFHAASTQGG 300
 QY 301 GYDMRKLLNGTVVSKHPLKSVTPVDNHDTPQGSLESTVQTPWPKLAFILTESSGPQ 360
 DB 301 GYDMRKLLNGTVVSKHPLKSVTPVDNHDTPQGSLESTVQTPWPKLAFILTESSGPQ 360
 QY 361 VFYGDWYGTGDSQREIPALKHKIEPIIKARKQYAYGAQHDYEDHDI VGTWREGDSSVA 420
 DB 361 VFYGDWYGTGDSQREIPALKHKIEPIIKARKQYAYGAQHDYEDHDI VGTWREGDSSVA 420
 QY 421 NSGLAALITDGPAGKAMVYGRONAGETWHDITGNREBPVINSGEVPHVNGSVSIY 480
 DB 421 NSGLAALITDGPAGKAMVYGRONAGETWHDITGNREBPVINSGEVPHVNGSVSIY 480
 QY 481 VOR 483
 DB 481 VOR 483
 RESULT 4
 AAV15418
 ID AAV15418 standard; protein; 483 AA.
 AC AAV15418;
 XX 22-JUL-1999 (first entry)
 DT 22-JUL-1999 (first entry)
 DE *Bacillus licheniformis* alpha-amylase protein.
 XX *Bacillus licheniformis* alpha-amylase variant; washing; dishwashing; production;
 KW sweetener; ethanol; starch; textile desizing; starch liquefaction;
 KM saccharification process.
 OS *Bacillus licheniformis*.
 XX WO9923211-A1.
 XX 14-MAY-1999.
 PD 30-OCT-1998; 98WO-DK000471.
 PF 30-OCT-1998; 98WO-DK000471.
 PR 30-OCT-1997; 97DK-00001240.
 PR 14-JUL-1998; 98DK-00000936.
 PA (NOVO) NOVO-NORDISK AS.
 XX Borchert TV, Svendsen A, Andersen C, Nielsen BR, Nielsen TL;
 PI Kjærulff S;
 XX WPI; 1999-326987/27.
 DR New Termamyl-like alpha-amylase variants.
 XX Claim 38; Page 82-84; 115pp; English.

XX The specification describes termamyl-like alpha-amylase variants that
 CC have altered amino acid sequences to improve properties. The variants are
 CC produced by creating one or more of the following mutations in amino acid
 CC sequence of the parent termamyl-like alpha-amylase: T144, K142, F143,
 CC D144, F145, P146, G147, R148, Q174, R181, G182, D183, G184, K185,
 CC A186, W189, S193, N195, H107, K108, G109, D166, W167, D168, Q169, S170,
 CC R171, Q172, F173, F267, W268, K269, N270, D271, L272, G273, A274, L275,
 CC K311, R346, K385, G456, F458, P459, G460, T461, V462, T463. The
 CC variants can be used for washing and/or dishwashing. They can also be
 CC used in the production of sweeteners and ethanol from starch, and/or for
 CC textile desizing, and in starch liquefaction and/or saccharification
 CC processes. The present amylase can function as the parent sequence in the
 CC production of the variants of the invention

XX Sequence 483 AA;

Query Match 100.0%; Score 2666; DB 2; Length 483;

Best Local Similarity 100.0%; Pred. No. 1.7e-224;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEWMPNDGQWRLQNDSDATLAHGTIAWIPPAKYGTSQADVGYGAYD 60
 DB 1 ANLNGTLMQYFEWMPNDGQWRLQNDSDATLAHGTIAWIPPAKYGTSQADVGYGAYD 60
 QY 61 LYDGEFHQKGTVRTKYGKELQSAIKSLHSRDINVGDVVNHKGGADATEDVTAVEV 120
 DB 61 LYDGEFHQKGTVRTKYGKELQSAIKSLHSRDINVGDVVNHKGGADATEDVTAVEV 120
 QY 121 DPADRRNVISGEHLIKAWTHFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNIYKFGQK 180
 DB 121 DPADRRNVISGEHLIKAWTHFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNIYKFGQK 180
 QY 121 DPADRRNVISGEHLIKAWTHFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNIYKFGQK 180
 DB 121 DPADRRNVISGEHLIKAWTHFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNIYKFGQK 180
 QY 181 AMDWEVSENGNNTYLYMADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVXHKIFSF 240
 DB 181 AMDWEVSENGNNTYLYMADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVXHKIFSF 240
 QY 241 LRDMVNHVREKTKEMFTVAEYQNDLGALENTYLNKTNFNSVFDVPLHYQFHAASQGG 300
 DB 241 LRDMVNHVREKTKEMFTVAEYQNDLGALENTYLNKTNFNSVFDVPLHYQFHAASQGG 300
 QY 301 GYDMRKILNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTWFKPLAFAFLITRESGYPQ 360
 DB 301 GYDMRKILNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTWFKPLAFAFLITRESGYPQ 360
 QY 361 VFYGDWYGTGDSQREIPALKKHIEPIILKARKQYAGAODYFDHDIIVGWTREGSSVA 420
 DB 361 VFYGDWYGTGDSQREIPALKKHIEPIILKARKQYAGAODYFDHDIIVGWTREGSSVA 420
 QY 421 NSGLAALITDGPAGAKRMVYGRONAGEFTWHDITGNRSEPVVINSBGGEFHVNGSVSIT 480
 DB 421 NSGLAALITDGPAGAKRMVYGRONAGEFTWHDITGNRSEPVVINSBGGEFHVNGSVSIT 480
 QY 481 VQR 483
 DB 481 VQR 483

RESULT 5
 ID AAY29852 standard; protein; 483 AA.

XX AAY29852;

XX 18-NOV-1999 (first entry)

XX Bacillus licheniformis Termamyl-like alpha-amylase Val54.

XX Alpha-amylase; Termamyl-like alpha-amylase; glucose syrup; starch.

XX Bacillus licheniformis.

XX MO9946399-A1.

XX 16-SEP-1999.
 PD 08-MAR-1999; 99MO-DK000114.
 PF 09-MAR-1998; 98DK-00000321.
 PR (NOVO) NOVO-NORDISK AS.
 PI Norman BE, Hendriksen HV;
 XX WPI; 1999-551422/46.
 DR N-PSDB; AAZ21078.
 PT Preparation of a glucose syrup, using a Termamyl-like alpha-amylase.

XX Claim 8, Page 26-28; 36pp; English.

CC A method has been developed for the preparation of a glucose syrup using
 CC a Termamyl-like alpha-amylase containing a substitution at Val(54). The
 CC glucose syrup obtained by the process is useful as an ingredient in food
 CC products. The Termamyl-like alpha-amylase facilitates the preparation of
 CC glucose syrups suitable for the food industry, previously only possible
 CC using acid hydrolysis. The present sequence represents Bacillus
 CC licheniformis Termamyl-like alpha-amylase

XX Sequence 483 AA;

Query Match 100.0%; Score 2666; DB 2; Length 483;

Best Local Similarity 100.0%; Pred. No. 1.7e-224;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEWMPNDGQWRLQNDSDATLAHGTIAWIPPAKYGTSQADVGYGAYD 60
 DB 1 ANLNGTLMQYFEWMPNDGQWRLQNDSDATLAHGTIAWIPPAKYGTSQADVGYGAYD 60
 QY 61 LYDGEFHQKGTVRTKYGKELQSAIKSLHSRDINVGDVVNHKGGADATEDVTAVEV 120
 DB 61 LYDGEFHQKGTVRTKYGKELQSAIKSLHSRDINVGDVVNHKGGADATEDVTAVEV 120
 QY 121 DPADRRNVISGEHLIKAWTHFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNIYKFGQK 180
 DB 121 DPADRRNVISGEHLIKAWTHFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNIYKFGQK 180
 QY 121 DPADRRNVISGEHLIKAWTHFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNIYKFGQK 180
 DB 121 DPADRRNVISGEHLIKAWTHFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNIYKFGQK 180
 QY 181 AMDWEVSENGNNTYLYMADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVXHKIFSF 240
 DB 181 AMDWEVSENGNNTYLYMADIDYDHPDVAEIKRWGTWYANLQDGFRLDAVXHKIFSF 240
 QY 241 LRDMVNHVREKTKEMFTVAEYQNDLGALENTYLNKTNFNSVFDVPLHYQFHAASQGG 300
 DB 241 LRDMVNHVREKTKEMFTVAEYQNDLGALENTYLNKTNFNSVFDVPLHYQFHAASQGG 300
 QY 301 GYDMRKILNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTWFKPLAFAFLITRESGYPQ 360
 DB 301 GYDMRKILNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTWFKPLAFAFLITRESGYPQ 360
 QY 361 VFYGDWYGTGDSQREIPALKKHIEPIILKARKQYAGAODYFDHDIIVGWTREGSSVA 420
 DB 361 VFYGDWYGTGDSQREIPALKKHIEPIILKARKQYAGAODYFDHDIIVGWTREGSSVA 420
 QY 421 NSGLAALITDGPAGAKRMVYGRONAGEFTWHDITGNRSEPVVINSBGGEFHVNGSVSIT 480
 DB 421 NSGLAALITDGPAGAKRMVYGRONAGEFTWHDITGNRSEPVVINSBGGEFHVNGSVSIT 480
 QY 481 VQR 483
 DB 481 VQR 483

RESULT 6
 ID AAY07384 standard; protein; 483 AA.

XX AAY07384

AAV07384;
 16-JUL-1999 (first entry)
 Wild type Termamyl (RTM)-like alpha-amylase protein #4.
 Variant; Termamyl; alpha-amylase; mutation; Bacillus; detergent;
 dishwashing; laundry; textile; desizing; starch liquefaction; sweetener;
 ethanol.
 Bacillus sp.
 Key Location/Qualifiers
 Misc-difference 190 /note= "optionally altered to any amino acid except an
 Asn residue"
 Misc-difference 201 /note= "optionally altered to any amino acid except an
 Ile residue"
 Misc-difference 211 /note= "optionally altered to any amino acid except an
 Asp residue"
 Misc-difference 214 /note= "optionally altered to any amino acid except a Glu
 residue"
 Misc-difference 264 /note= "optionally altered to any amino acid except a Glu
 residue"
 WO9919467-A1.
 22-APR-1999.
 13-OCT-1998; 98WO-DK000444.
 13-OCT-1997; 97DK-00001172.
 (NOVO) NOVO-NORDISK AS.
 Svendsen A, Borchert TV, Bisgaard-Frantzen H;
 WPI; 1999-277632/23.
 Variant alpha-amylases - useful as detergents or for textile desizing or
 starch liquefaction.
 Claim 1; Page 67-68; 93pp; English.
 This sequence represents the parent sequence for new variants of a parent
 Termamyl-like alpha-amylase with alpha-amylase activity. The variants
 comprise mutations in 2-6 regions/positions relative to an alpha-amylase
 from either of two Bacillus species in WO9526397, B. stercoriorumophilus,
 B. licheniformis, B. amyloliquefaciens or Bacillus sp. #707. The alpha-
 amylase variants are detergent additives for use in detergents for
 dishwashing, manual or automatic laundry. The variants can also be used
 for textile desizing or starch liquefaction (e.g. for production of
 sweeteners or ethanol)
 Sequence 483 AA;
 Query Match 100.0%; Score 2666; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DPADNRNVISGEHLIKAWTHFFPGSGTYSDFKMWYHFDGTDWDSRKLNRITYKFGK 180
 121
 AMDMEVSENGNVDYLMYADIDYDHPVAAEIKRMGTWYANEIQDGFRLDAVGHIFSF 240
 181
 AMDMEVSENGNVDYLMYADIDYDHPVAAEIKRMGTWYANEIQDGFRLDAVGHIFSF 240
 181
 LRDVNVHREKTKGEMETVAEYQNDIGALENYLNTKTNFHSVPDPLHYQFHAATQGG 300
 241
 LRDVNVHREKTKGEMETVAEYQNDIGALENYLNTKTNFHSVPDPLHYQFHAATQGG 300
 241
 LRDVNVHREKTKGEMETVAEYQNDIGALENYLNTKTNFHSVPDPLHYQFHAATQGG 300
 241
 GYDMRKILNGTVVSKHPLKSVTFVDNHDTPGQSLBSTVQTFKPLAARILRESGYPQ 360
 301
 GYDMRKILNGTVVSKHPLKSVTFVDNHDTPGQSLBSTVQTFKPLAARILRESGYPQ 360
 301
 VFYGDWGTGDSOREIPALKHPIELKARKOYAGAOHDYFDHDIYGTREGDSVA 420
 361
 VFYGDWGTGDSOREIPALKHPIELKARKOYAGAOHDYFDHDIYGTREGDSVA 420
 361
 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSGEFFHVGGSYSIY 480
 421
 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSGEFFHVGGSYSIY 480
 421
 VQR 483
 481
 VQR 483
 481
 VQR 483

RESULT 7
 AAY9605
 ID AAY9605 standard; protein; 483 AA.
 AAY9605;
 04-SEP-2000 (first entry)
 Bacillus licheniformis Termamyl alpha-amylase.
 Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
 K_m saccharification; muten; mutanc; enzyme stability; hybrid.
 Bacillus licheniformis.
 WO200029560-A1.
 25-MAY-2000.
 16-NOV-1999; 99WO-DK000628.
 16-NOV-1998; 98DK-00001495.
 (NOVO) NOVO-NORDISK AS.
 Svendsen A, Kjaerulff S, Bisgaard-Frantzen H, Andersen C;
 WPI; 2000-38777/33.
 N-PSDB; AAA46483.
 Variant of parent termamyl-like alpha amylase useful for washing, textile
 desizing and starch liquefaction, comprising alterations in one or more
 solvent exposed amino acid residues.
 Claim 8; Page 58-59; 80pp; English.
 The present sequence is a parent alpha-amylase from which mutants with
 increased stability at acidic pH, low calcium concentration and high
 temperatures have been derived. The enzyme is commercially available as
 Termamyl. A variant may contain mutations in one or more solvent exposed
 amino acid residues to increase the overall hydrophobicity of the enzyme
 or the overall number of methyl groups in the side chains of exposed
 residues may be increased. The mutations can be incorporated by site-
 directed mutagenesis or by random mutagenesis. As a result of their
 increased stability, the variants are suitable for the industrial

processing of starch, i.e. starch liquefaction and saccharification. They may also be useful for washing, dishwashing and textile desizing. Hybrid alpha-amylases comprising partial amino acid sequences derived from two or more alpha-amylases have also been created in order to increase enzyme stability

Sequence 483 AA;

Query Match 100.0%; Score 2666; DB 3; Length 483;

Best Local Similarity 100.0%; Pred. No. 1.7e-224; Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANLNGTLMQYFEWYMPNDGQHMRLQNDSAVLAHEGITAFAWVIPPAYKTSQADVGYGAYD 60
DB 1 ANLNGTLMQYFEWYMPNDGQHMRLQNDSAVLAHEGITAFAWVIPPAYKTSQADVGYGAYD 60
QY 61 LYDGEFHQKGTVRTKYGKGELOSALKSLSRDINVGDVVYNHKGADATEDVTAVEV 120
DB 61 LYDGEFHQKGTVRTKYGKGELOSALKSLSRDINVGDVVYNHKGADATEDVTAVEV 120
QY 121 DPADRRNVISGEHLIKAWTHFHFPGRGSTYSDFKMHYHFDGTDWDSRKLNRITYKQK 180
DB 121 DPADRRNVISGEHLIKAWTHFHFPGRGSTYSDFKMHYHFDGTDWDSRKLNRITYKQK 180
QY 181 AMDWEVSNGENVYLYMADIDYDHPDVAAEIKKGTWYANELQDGFRLDAVGHKFSF 240
DB 181 AMDWEVSNGENVYLYMADIDYDHPDVAAEIKKGTWYANELQDGFRLDAVGHKFSF 240
QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENVYLNKTNFNSVDFVPLHYQFHAASQGG 300
DB 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENVYLNKTNFNSVDFVPLHYQFHAASQGG 300
QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQWFKPLAYAFILTRSGYRQ 360
DB 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQWFKPLAYAFILTRSGYRQ 360
QY 361 VFYGDWYTKGDSQREIPALKKIEPIILAKKOYAGAHQYFDHHDIVGWTREGDSSVA 420
DB 361 VFYGDWYTKGDSQREIPALKKIEPIILAKKOYAGAHQYFDHHDIVGWTREGDSSVA 420
QY 421 NSGLAALITDGPQAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFHVNGSVSY 480
DB 421 NSGLAALITDGPQAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFHVNGSVSY 480
QY 481 VQR 483
DB 481 VQR 483
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RESULT 8

AAV97545

ID AAV97545 standard; protein; 483 AA.

AAV97545;

12-FEB-2001 (first entry)

B. licheniformis termamyl-like alpha amylase.

Termamyl-like alpha-amylase; variant; starch liquefaction; fuel; detergent composition; laundry cleaning composition; ethanol production; dish washing cleaning composition; hard surface cleaning composition; industrial ethanol production; textile desizing.

Bacillus licheniformis.

WO200060059-A2.

12-OCT-2000.

28-MAR-2000; 2000WO-DK000148.

30-MAR-1999; 99DK-00000437.

XX (NOVO) NOVO NORDISK AS.

XX Andersen C, Jorgensen CT, Bisgard-Frantzen H, Svendsen A;

XX Kjaeralff S;

DR WPI: 2001-015656/02.

XX N-PSDB; AAA37849.

PT New variants of parent Termamyl-like alpha-amylase, useful in starch liquefaction, in detergent compositions and in ethanol production, exhibit altered cleavage pattern relative to the parent.

PS Claim 1; Page 60-62; 78pp; English.

CC This sequence represents a termamyl-like alpha amylase. The invention relates to a variant (I) of parent Termamyl-like alpha-amylase comprising alteration at one or more of the positions W13, G48, T49, S50, O51, A52, D53, V54, G57, G107, G108, A111, S168 and M197. The alterations in (I) are independently an insertion of an amino acid downstream of the amino acid which occupies the position or deletion or substitution of the amino acid which occupies the position with a different amino acid. The variant has alpha-amylase activity. (I) or compositions containing it are useful in starch liquefaction, in detergent composition such as laundry, dish washing and hard surface cleaning compositions, ethanol production such as fuel, drinking and industrial ethanol production, desizing of textiles, fabrics or garments. (I) exhibits a reduced capability of cleaving a substrate close to the branching point, and further exhibits improved substrate specificity and/or improved specific activity relative to the parent alpha-amylase

XX Sequence 483 AA;

Query Match 100.0%; Score 2666; DB 4; Length 483;

Best Local Similarity 100.0%; Pred. No. 1.7e-224; Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ANLNGTLMQYFEWYMPNDGQHMRLQNDSAVLAHEGITAFAWVIPPAYKTSQADVGYGAYD 60
DB 1 ANLNGTLMQYFEWYMPNDGQHMRLQNDSAVLAHEGITAFAWVIPPAYKTSQADVGYGAYD 60
QY 61 LYDGEFHQKGTVRTKYGKGELOSALKSLSRDINVGDVVYNHKGADATEDVTAVEV 120
DB 61 LYDGEFHQKGTVRTKYGKGELOSALKSLSRDINVGDVVYNHKGADATEDVTAVEV 120
QY 121 DPADRRNVISGEHLIKAWTHFHFPGRGSTYSDFKMHYHFDGTDWDSRKLNRITYKQK 180
DB 121 DPADRRNVISGEHLIKAWTHFHFPGRGSTYSDFKMHYHFDGTDWDSRKLNRITYKQK 180
QY 181 AMDWEVSNGENVYLYMADIDYDHPDVAAEIKKGTWYANELQDGFRLDAVGHKFSF 240
DB 181 AMDWEVSNGENVYLYMADIDYDHPDVAAEIKKGTWYANELQDGFRLDAVGHKFSF 240
QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENVYLNKTNFNSVDFVPLHYQFHAASQGG 300
DB 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENVYLNKTNFNSVDFVPLHYQFHAASQGG 300
QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQWFKPLAYAFILTRSGYRQ 360
DB 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQWFKPLAYAFILTRSGYRQ 360
QY 361 VFYGDWYTKGDSQREIPALKKIEPIILAKKOYAGAHQYFDHHDIVGWTREGDSSVA 420
DB 361 VFYGDWYTKGDSQREIPALKKIEPIILAKKOYAGAHQYFDHHDIVGWTREGDSSVA 420
QY 421 NSGLAALITDGPQAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFHVNGSVSY 480
DB 421 NSGLAALITDGPQAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFHVNGSVSY 480
QY 481 VQR 483
DB 481 VQR 483
```

RESULT 9
 ABB06936
 ID ABB06936 standard; protein; 483 AA.
 XX
 AC ABB06936;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 DE B. licheniformis termamyl-like alpha-amylase protein SEQ ID NO:8.
 XX
 KW Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
 KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
 KW washing; sweetener; ethanol; starch.
 XX
 OS Bacillus licheniformis.
 XX
 PN WO200166712-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 07-MAR-2001; 2001WO-DK000144.
 XX
 PR 08-MAR-2000; 2000DK-00000376.
 PR 15-MAR-2000; 2000US-0189857P.
 PR 23-FEB-2001; 2001DK-00000303.
 PR 26-FEB-2001; 2001US-0271382P.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Andersen C, Borchert TV, Nielsen BR,
 XX
 DR WPI; 2002-239612/29.
 DR N-PSDB; ABL50567.
 XX
 PT Novel variant of parent termamyl-like alpha-amylase useful as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Claim 8; Page 142-143; 153pp; English.
 XX
 CC The present invention describes a variant of a parent termamyl-like alpha
 CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
 CC positions of a group of 31 possible amino acid positions. The alteration
 CC in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,
 CC Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
 CC Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
 CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
 CC washing and/or dishwashing, textile desizing, and starch liquefaction.
 CC (I) is useful as a component in hard surface cleaning detergent
 CC composition, and for producing sweeteners and ethanol from starch. (I)
 CC has altered solubility, preferably increased solubility, in particular
 CC under washing, dish washing or hard surface cleaning conditions. The
 CC present sequence represents a Bacillus licheniformis termamyl-like alpha-
 CC amylase which is used in the exemplification of the present invention
 XX
 SQ Sequence 483 AA;
 XX
 Query Match 100.0%; Score 2666; DB 5; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1.7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 ANLNGTLMQYFEMWMPNDQHMRLQNDSDAYIAEHGITAIVIPYKGTSGADVGYAYD 60
 XX
 DB 1 ANLNGTLMQYFEMWMPNDQHMRLQNDSDAYIAEHGITAIVIPYKGTSGADVGYAYD 60
 XX
 QY 61 LYDLGEFPOKGTVRKYGTGKGLQSAIKSLHSRDLNVYGVVINKKGADATEDVTAVEV 120
 XX
 DB 61 LYDLGEFPOKGTVRKYGTGKGLQSAIKSLHSRDLNVYGVVINKKGADATEDVTAVEV 120
 XX
 QY 121 DPADNRNRYISGEHLIKAWTHFHPGRGSTYSDPKMWHYHFDGTDWDESKLRIRYKFOOK 180
 XX
 DB 121 DPADNRNRYISGEHLIKAWTHFHPGRGSTYSDPKMWHYHFDGTDWDESKLRIRYKFOOK 180
 XX

RESULT 10
 AAU12152
 ID AAU12152 standard; protein; 483 AA.
 XX
 AC AAU12152;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Bacillus TERMAMYL alpha-amylase.
 XX
 KW TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing;
 KW starch liquefaction; ethanol production; hard surface cleaner; sweetener;
 KW amylpectin; limit dextrin; NOVAMYL.
 XX
 OS Bacillus licheniformis.
 XX
 PN WO200188107-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 10-MAY-2001; 2001WO-DK000323.
 XX
 PR 12-MAY-2000; 2000DK-00000779.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Svendsen A, Jorgensen CT, Nielsen BR,
 XX
 DR WPI; 2002-106123/14.
 DR N-PSDB; AAS20025.
 XX
 PT New variant of parent Termamyl-like alpha-amylase for use as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Claim 5; Fig 1; 84pp; English.
 XX
 CC The invention relates to a variant of parent TERMAMYL-like alpha-amylase
 CC comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
 CC or at position 234, where the variant has alpha-amylase activity and each
 CC position corresponds to a position of a parent Termamyl-like alpha-
 CC amylase sequence having a Bacillus licheniformis alpha-amylase sequence
 CC of 483 amino acids, given in specification. The variant alpha-amylase, a
 CC detergent additive comprising the variant or a detergent composition
 CC comprising the variant, is useful for washing and/or dishwashing or
 CC textile desizing. The alpha-amylase is useful for starch liquefaction or
 CC ethanol production and as a component in a hard surface cleaning

CC detergent composition, and for producing sweeteners from starch. The
CC variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage
CC activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic
CC branch linkage cleavage activity of amylopectin or a limit dextrin
CC prepared by TERNAMYL (RSM) or NOVAMYL (RSM). The present sequence is the
CC TERNAMYL alpha-amyase upon which the variants of the invention are based
XX
XX Sequence 483 AA;

Query Match 100.0%; Score 2666; DB 5; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.7e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMOYFEWYMPNDGQHMRLQNDASAYLAHEGITAAMIIPRAYKTSQADVGAYD 60
Db 1 ANLNGTLMOYFEWYMPNDGQHMRLQNDASAYLAHEGITAAMIIPRAYKTSQADVGAYD 60
QY 61 LYDGEFHQKGTVRTKTKGSELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
Db 61 LYDGEFHQKGTVRTKTKGSELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
QY 121 DPADRNRYISGEHLIKAWTHFHPGRGSTYSDPKMWHYFPGTDMDESRKLNRIYKPOGK 180
Db 121 DPADRNRYISGEHLIKAWTHFHPGRGSTYSDPKMWHYFPGTDMDESRKLNRIYKPOGK 180
QY 181 AMDWEVSNENGNVDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
Db 181 AMDWEVSNENGNVDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
QY 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNISVFDVPLHYQFHAASTOGG 300
Db 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNISVFDVPLHYQFHAASTOGG 300
QY 301 GYDMRKLNGLTVVSKPLKSVTFVDNHDTPQGSLSTVQWTFKPLAFAFLITRESGPQ 360
Db 301 GYDMRKLNGLTVVSKPLKSVTFVDNHDTPQGSLSTVQWTFKPLAFAFLITRESGPQ 360
QY 361 VFYGDWYGTGDSQREIPALKHKIEPIIKARKQYAYGAQHDYFDHDI VGTWREGDSVA 420
Db 361 VFYGDWYGTGDSQREIPALKHKIEPIIKARKQYAYGAQHDYFDHDI VGTWREGDSVA 420
QY 421 NSGIALALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
Db 421 NSGIALALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
QY 481 VQR 483
Db 481 VQR 483

RESULT 11
AAE26534
ID AAE26534 standard; protein; 483 AA.

XX AAE26534;

XX 13-DEC-2002 (first entry)

XX DE Bacillus licheniformis alpha-amyase protein.

XX KW Alpha amyase; alpha-1,4-glucan-4-glucanohydrolase; EC 3.2.1.1;
XX KM dishwashing; textile desizing; detergent; paper; starch liquefaction;
XX laundry; alcohol production; ethanol production; pulp; beer; brewing;
XX sweetener; enzyme.

XX OS Bacillus licheniformis.

XX PN WO200231124-A2.

XX 18-APR-2002.

XX 12-OCT-2001; 2001WO-DK000668.

PR 13-OCT-2000; 2000DK-00001533.
PR 23-OCT-2000; 2000US-0242692P.
PR 02-OCT-2001; 2001DK-00001442.
PR 03-OCT-2001; 2001US-0326752P.

XX (NOVO) NOVOZYMES AS.

XX Andersen C;

XX WPI: 2002-463264/49.

DR N-PSDB; AAD44363.

PT KSM-K36 or KSM-K38 variant from Bacillus for cleaning dishes, textile
PT desizing, starch liquefaction and ethanol production has alpha-amyase
PT activity.

PS Disclosure; Page 60-62; 69pp; English.

CC The present invention relates to KSM-K36 or KSM-K38 variant of parent
CC alpha-amyases (alpha-1,4-glucan-4-glucanohydrolases, EC 3.2.1.1) from
CC Bacillus. The variants have alpha-amyase activity and exhibit an amino
CC acid alteration such as an insertion, deletion or substitution of the
CC parent alpha-amyase. The variants are useful for washing and/or dish-
CC washing, textile desizing, starch liquefaction and alcohol production,
CC particularly ethanol production. They are also useful as components in
CC detergent compositions for e.g. laundry, dishwashing and hard surface cleaning
CC in beer making and in production of sweeteners. The present sequence is Bacillus
CC licheniformis alpha-amyase protein

XX Sequence 483 AA;

Query Match 100.0%; Score 2666; DB 5; Length 483;
Best Local Similarity 100.0%; Pred. No. 1.7e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMOYFEWYMPNDGQHMRLQNDASAYLAHEGITAAMIIPRAYKTSQADVGAYD 60
Db 1 ANLNGTLMOYFEWYMPNDGQHMRLQNDASAYLAHEGITAAMIIPRAYKTSQADVGAYD 60
QY 61 LYDGEFHQKGTVRTKTKGSELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
Db 61 LYDGEFHQKGTVRTKTKGSELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
QY 121 DPADRNRYISGEHLIKAWTHFHPGRGSTYSDPKMWHYFPGTDMDESRKLNRIYKPOGK 180
Db 121 DPADRNRYISGEHLIKAWTHFHPGRGSTYSDPKMWHYFPGTDMDESRKLNRIYKPOGK 180
QY 181 AMDWEVSNENGNVDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
Db 181 AMDWEVSNENGNVDYLMYADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
QY 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNISVFDVPLHYQFHAASTOGG 300
Db 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNISVFDVPLHYQFHAASTOGG 300
QY 301 GYDMRKLNGLTVVSKPLKSVTFVDNHDTPQGSLSTVQWTFKPLAFAFLITRESGPQ 360
Db 301 GYDMRKLNGLTVVSKPLKSVTFVDNHDTPQGSLSTVQWTFKPLAFAFLITRESGPQ 360
QY 361 VFYGDWYGTGDSQREIPALKHKIEPIIKARKQYAYGAQHDYFDHDI VGTWREGDSVA 420
Db 361 VFYGDWYGTGDSQREIPALKHKIEPIIKARKQYAYGAQHDYFDHDI VGTWREGDSVA 420
QY 421 NSGIALALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
Db 421 NSGIALALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
QY 481 VQR 483
Db 481 VQR 483

RESULT 12
 AAB47853
 ID AAB47853 standard; protein; 483 AA.
 XX
 AC AAB47853;
 XX
 DT 02-APR-2002 (first entry)
 XX
 DE Bacillus termamyl alpha amylase.
 XX
 KM Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;
 KM starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
 KM bakery; cereal bar; ice cream; coffee whitener; salad dressing;
 KM cured meat; fermented meat; spice.
 XX
 OS Bacillus licheniformis.
 XX
 PN W0200196537-A2.
 PD 20-DEC-2001.
 XX
 PF 13-JUN-2001; 2001WO-DK000404.
 XX
 PR 14-JUN-2000; 2000DK-00000917.
 PR 20-JUN-2000; 2000US-0212852P.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Nielsen BR, Weibye M;
 XX
 DR WPI; 2002-098064/13.
 DR N-PSDB; AAI72214.
 XX
 PT New modified alpha-amylase derived from the genus Bacillus and/or is a
 PT Termamyl-like alpha-amylase, which has been pre-oxidized for producing
 PT maltodextrin or glucose syrup.
 XX
 PS Claim 5; Page 36-37; 47pp; English.
 XX
 CC The sequences given in AAB47850-56 show modified alpha-amylases derived
 CC from the genus Bacillus. These alpha amylases are Termamyl-like alpha-
 CC amylase and they have been pre-oxidized. The alpha amylase is useful for
 CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
 CC oxidized alpha-amylase until a product with a DE between 5-45 has been
 CC provided and/or until a product with a molecular weight of between 5-30
 CC kDa has been provided. The product comprises a maltodextrin with a DE of
 CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The
 CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
 CC where the glucose syrup is useful as an ingredient in food, feed or
 CC pharmaceuticals. Glucose syrup is useful in confectionery such as
 CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
 CC dairy and ice cream such as coffee whiteners, conventional foods such as
 CC salad dressings, and food ingredients and preparations such as cured
 CC meat, fermented meat, spices and seasoning encapsulated flavours
 XX
 SQ Sequence 483 AA;
 Query Match 100.0%; Score 2666; DB 5; Length 483;
 Best Local Similarity 100.0%; Pred. No. 1,7e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ANLNGTLMOYFEWMPNDGQWRLQNDASVLAHGTAWIPPAKYKTSQADVGXAYD 60
 DB 1 ANLNGTLMOYFEWMPNDGQWRLQNDASVLAHGTAWIPPAKYKTSQADVGXAYD 60
 QY 61 LYDGEFHQKGTVTYTKGELQSAIKSLSRDINVDVINHHKGADATEDVTAVEV 120
 DB 61 LYDGEFHQKGTVTYTKGELQSAIKSLSRDINVDVINHHKGADATEDVTAVEV 120
 QY 121 DPADNRVYSGEHLIKATWTHHFPGRGSTYSDFKWMTYHFGDTWDESRKLNRIYKFGK 180
 DB 121 DPADNRVYSGEHLIKATWTHHFPGRGSTYSDFKWMTYHFGDTWDESRKLNRIYKFGK 180

QY 181 AMDWEVSNGENDYDLYMYADIDYDHPVAAEIKKWTWYANELQDGRFLDAVHKIKSF 240
 DB 181 AMDWEVSNGENDYDLYMYADIDYDHPVAAEIKKWTWYANELQDGRFLDAVHKIKSF 240
 QY 241 LRDVNVHVRREKTKGEMTVAEWYQNDGALENYLNKTNFNHVSVDVPLHYGFHAASVTOGG 300
 DB 241 LRDVNVHVRREKTKGEMTVAEWYQNDGALENYLNKTNFNHVSVDVPLHYGFHAASVTOGG 300
 QY 301 GYDWRKILNGTVVSKHPLKSTFTVDNHDTPQGSLESTVQTFWFLAYAFILITRESGPQ 360
 DB 301 GYDWRKILNGTVVSKHPLKSTFTVDNHDTPQGSLESTVQTFWFLAYAFILITRESGPQ 360
 QY 361 VFYGDWYGTGDSQREIPALKHKEPILKARKQYAYAGQHDYFDHDIIVGWTREGDSVA 420
 DB 361 VFYGDWYGTGDSQREIPALKHKEPILKARKQYAYAGQHDYFDHDIIVGWTREGDSVA 420
 QY 421 NSGIAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINEGGEFFVNGSVISY 480
 DB 421 NSGIAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINEGGEFFVNGSVISY 480
 QY 481 VQR 483
 DB 481 VQR 483
 RESULT 13
 ABB76589
 ID ABB76589 standard; protein; 483 AA.
 XX
 AC ABB76589;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Termamyl-like-alpha-amylase #4.
 XX
 KM Termamyl; alpha amylase; starch liquefaction; ethanol production;
 KM textile desizing; detergent; enzyme.
 XX
 OS Bacillus licheniformis.
 XX
 PN W0200210355-A2.
 PD 07-FEB-2002.
 XX
 PF 12-JUL-2001; 2001WO-DK000488.
 XX
 PR 01-AUG-2000; 2000DK-00001160.
 PR 12-SEP-2000; 2000DK-00001354.
 PR 10-NOV-2000; 2000DK-00001687.
 PR 26-APR-2001; 2001DK-00000655.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;
 XX
 DR WPI; 2002-280633/32.
 DR N-PSDB; ABL96210.
 XX
 PT Variant of parent Termamyl-like alpha amylase, useful in detergent
 PT compositions, for starch liquefaction, ethanol production, washing and/or
 PT dish washing, and textile desizing.
 XX
 PS Claim 1; Fig 4; 90pp; English.
 XX
 CC This invention relates to variants of a parent Termamyl-like alpha-
 CC amylases. These are used for starch liquefaction, ethanol production,
 CC detergent, and textile desizing. The amylases have altered stability,
 CC particularly at high temperatures from 70-120pH and low pH in the
 CC range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-
 CC amylase
 XX
 SQ Sequence 483 AA;

Query Match	100.0%;	Score 2666;	DB 5;	Length 483;
Best Local Similarity	100.0%;	Pred. No. 1.7e-224;		
Matches 483;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ANLNGTLMQYFEWYMPNDGQHWRLQNDSAVLAHEGITAWMIPPAVKGTSGADVGYAYD	60	
DB	1	ANLNGTLMQYFEWYMPNDGQHWRLQNDSAVLAHEGITAWMIPPAVKGTSGADVGYAYD	60	
QY	61	LYDLGEFHOKGTVRTKYGKTELQSAIKSLHSRDINVGDVVNNHKGADATEDVTAVEV	120	
DB	61	LYDLGEFHOKGTVRTKYGKTELQSAIKSLHSRDINVGDVVNNHKGADATEDVTAVEV	120	
QY	121	DPADRRNRVISEGHLIKAWTHFHPGRGSTYSPFKMWHYFDGTWDESRKLNRIYKFGQK	180	
DB	121	DPADRRNRVISEGHLIKAWTHFHPGRGSTYSPFKMWHYFDGTWDESRKLNRIYKFGQK	180	
QY	181	AMDWEVSNENGYDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIFSF	240	
DB	181	AMDWEVSNENGYDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIFSF	240	
QY	241	LRDWVNHREKTKGEMFTVAEYMONDLAGLENYLNKTNFNHSVPDVPLHYQFHAASQCG	300	
DB	241	LRDWVNHREKTKGEMFTVAEYMONDLAGLENYLNKTNFNHSVPDVPLHYQFHAASQCG	300	
QY	301	GYDMRKILNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTMFKPLAYAFILTRBSGYPQ	360	
DB	301	GYDMRKILNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTMFKPLAYAFILTRBSGYPQ	360	
QY	361	VFYGDMYTKGDSQREIPALKHKIEPILKARKQVAYGAQHDYFDHHDIVGWTREGDSVA	420	
DB	361	VFYGDMYTKGDSQREIPALKHKIEPILKARKQVAYGAQHDYFDHHDIVGWTREGDSVA	420	
QY	421	NSGLAALITDGPQAKRMVYGRONAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY	480	
DB	421	NSGLAALITDGPQAKRMVYGRONAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY	480	
QY	481	VQR 483		
DB	481	VQR 483		

RESULT 14
AAR98007
ID AAR98007 standard; protein; 531 AA.

AC	AAR98007;			
DT	27-AUG-2003 (revised)			
DT	16-OCT-1996 (first entry)			
XX	Pe1B signal-Termamyl-leucine zipper.			
XX				
KW	Allergen; allergy; self-oligomerising polypeptide; Termamyl;			
XX	alpha-amylase; leucine zipper; detergent.			
OS	Synthetic.			
OS	unspecified organism.			
OS	Chimeric.			
XX				
XX	Key	Location/Qualifiers		
FT	Protein	1..482		
FT	Region	/label= Termamyl		
FT	Domain	483..489		
FT		/label= linker		
FT		490..531		
XX		/label= leucine_zipper		
XX				
XX	WO9616177-A1.			
XX	30-MAY-1996.			
XX	23-NOV-1995;	95WO-DK000463.		
XX				

PR	24-NOV-1994;	94DK-00001343.		
XX				
XX	(NOVO) NOVO-NORDISK AS.			
PI	Bjornvad ME, Prento A;			
XX				
DR	WPI; 1996-268613/27.			
DR	N-PSDB; AAT33228.			
XX				
XX	Prodn. of self-oligomerising peptide(s) with reduced allergenicity - used			
PT	in household and personal cleaning prods., and in food and feeds etc.			
XX				
PS	Disclosure; Page 61-63; 85pp; English.			
CC				
CC	A polypeptide (AAR98007) is composed of Termamyl alpha-amylase, a linker			
CC	derived from the IgG3 hinge domain and a leucine zipper from the GCN4			
CC	yeast transcription factor. It was produced by PCR amplification of the			
CC	Termamyl gene and ligation of synthetic oligonucleotides (see also			
CC	AAT33229-32) encoding the leucine zipper and linker. Upon expression in			
CC	E. coli, using a vector including the pelB signal sequence, the Termamyl			
CC	product self-oligomerised into a dimer that was secreted into the			
CC	periplasm. The method constitutes an industrially applicable process for			
CC	producing a biologically active polypeptide that self-oligomerises owing			
CC	to the presence of leucine zippers, the enlarged size of the resulting			
CC	polypeptide leading to a reduction in its allergenicity. (Updated on 27-			
CC	AUG-2003 to correct OS field.)			
XX				
SO	Sequence 531 AA;			

Query Match 100.0%; Score 2666; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. No. 1.9e-224;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ANLNGTLMQYFEWYMPNDGQHWRLQNDSAVLAHEGITAWMIPPAVKGTSGADVGYAYD	60	
DB	1	ANLNGTLMQYFEWYMPNDGQHWRLQNDSAVLAHEGITAWMIPPAVKGTSGADVGYAYD	60	

QY	61	LYDLGEFHOKGTVRTKYGKTELQSAIKSLHSRDINVGDVVNNHKGADATEDVTAVEV	120	
DB	61	LYDLGEFHOKGTVRTKYGKTELQSAIKSLHSRDINVGDVVNNHKGADATEDVTAVEV	120	

QY	121	DPADRRNRVISEGHLIKAWTHFHPGRGSTYSPFKMWHYFDGTWDESRKLNRIYKFGQK	180	
DB	121	DPADRRNRVISEGHLIKAWTHFHPGRGSTYSPFKMWHYFDGTWDESRKLNRIYKFGQK	180	

QY	181	AMDWEVSNENGYDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIFSF	240	
DB	181	AMDWEVSNENGYDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIFSF	240	

QY	241	LRDWVNHREKTKGEMFTVAEYMONDLAGLENYLNKTNFNHSVPDVPLHYQFHAASQCG	300	
DB	241	LRDWVNHREKTKGEMFTVAEYMONDLAGLENYLNKTNFNHSVPDVPLHYQFHAASQCG	300	

QY	301	GYDMRKILNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTMFKPLAYAFILTRBSGYPQ	360	
DB	301	GYDMRKILNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTMFKPLAYAFILTRBSGYPQ	360	

QY	361	VFYGDMYTKGDSQREIPALKHKIEPILKARKQVAYGAQHDYFDHHDIVGWTREGDSVA	420	
DB	361	VFYGDMYTKGDSQREIPALKHKIEPILKARKQVAYGAQHDYFDHHDIVGWTREGDSVA	420	

QY	421	NSGLAALITDGPQAKRMVYGRONAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY	480	
DB	421	NSGLAALITDGPQAKRMVYGRONAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY	480	

QY	481	VQR 483		
DB	481	VQR 483		

RESULT 15
AAW22523
ID AAW22523 standard; protein; 630 AA.

XX AAM2523;
 AC 17-OCT-2003 (revised)
 DT 08-FEB-1998 (first entry)
 XX
 DE Alpha-amylase-Cena cellulose binding domain hybrid enzyme.
 XX
 KM Desizing; cellulose; fabric; enzyme hybrid; Termamyl; alpha-amylase;
 KM cellulose binding domain; Cena; Bacillus licheniformis;
 KM Cellulomonas fiml; protein secretion.
 XX
 OS Bacillus licheniformis.
 OS Cellulomonas fiml; strain ATCC 484.
 OS Chimeric.
 XX
 FH Key location/Qualifiers
 FT Peptide 1..29
 FT /label= Sig_peptide
 FT /note= "Termamyl signal peptide"
 FT Protein 20..630
 FT /label= Mat_protein
 FT /note= "CBD (aa29-147)-Termamyl (aa148-630) hybrid"
 FT
 XX MO9728256-A1.
 PN 07-AUG-1997.
 XX
 XX 29-JAN-1997; 97WO-DK000041.
 XX
 XX 29-JAN-1996; 96DK-00000093.
 XX
 PA (NOVO) NOVO-NORDISK AS.
 FI Von Der Osten C, Bjornvad M, Vind J, Raemussen MD;
 XX
 DR WPI; 1997-402610/37.
 DR N-PSDB; AAT77063.
 XX
 PT Desizing cellulose-containing fabric or textile using an enzyme hybrid -
 PT which comprises a catalytically active amino acid sequence of a non-
 PT cellulolytic enzyme linked to an amino acid sequence comprising a
 PT cellulose binding domain.
 XX
 PS Example 3; Page 60; 72pp; English.
 XX
 CC This protein sequence comprises a hybrid enzyme in which Bacillus
 CC licheniformis alpha-amylase (Termamyl) signal peptide is linked to the
 CC cellulose binding domain (CBD) of Cellulomonas fiml Cena, which is
 CC further linked to mature Termamyl polypeptide. The CBD-Termamyl fusion
 CC has been expressed and secreted as an approx. 85 kDa protein in Bacillus
 CC subillis Pl2306 transformants. A claimed process for desizing cellulose-
 CC containing fabric or textile comprises treating the fabric or textile
 CC with a modified enzyme (enzyme hybrid) comprising a non-cellulolytic
 CC enzyme linked to a CBD. The process gives improved enzyme performance by
 CC modifying the enzyme so as to increase its affinity for cellulosic
 CC fabric. A desizing composition suitable for use in the process comprises
 CC the enzyme hybrid and a wetting agent. (Updated on 17-Oct-2003 to
 CC standardise OS field)
 CC
 SQ Sequence 630 AA;

Query Match 100.0%; Score 2666; DB 2; Length 630;
 Best Local Similarity 100.0%; Pred. No. 2.5e-224;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLNQYFEWYMPNDGQHRRLONDSAYLAHGITAWWIPPAYKGTSDADVGYGAYD 60
 DB 148 ANLNGTLNQYFEWYMPNDGQHRRLONDSAYLAHGITAWWIPPAYKGTSDADVGYGAYD 207
 QY 61 LYDLGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGVDVVIINHGAGADATEDVTAAVEV 120
 DB 208 LYDLGEFHQKGTVRTKYGKGLQSAIKSLHSRDINVGVDVVIINHGAGADATEDVTAAVEV 267

QY 121 DPADRRNVISGEHLIKAWTHFHPGRGSTYSDFKMHWHFDGTDWDSRKLNRITKFOGK 180
 DB 268 DPADRRNVISGEHLIKAWTHFHPGRGSTYSDFKMHWHFDGTDWDSRKLNRITKFOGK 327
 QY 181 AMDWEVSNGENYDYLMTADIDYDHPVAABIKRWGTWYANLQDGFRLDAVGHIFSF 240
 DB 328 AMDWEVSNGENYDYLMTADIDYDHPVAABIKRWGTWYANLQDGFRLDAVGHIFSF 387
 QY 241 LRDMVNHVRKTKGEMFTVAEYQNDLGALNTYLNKTNFHNSVYDVPALHYQFHAASTOGG 300
 DB 388 LRDMVNHVRKTKGEMFTVAEYQNDLGALNTYLNKTNFHNSVYDVPALHYQFHAASTOGG 447
 QY 301 GYDMRKLNGTVVSKHPLKSVTVFVDNNDITQPGSLBESTVQTMFKPLAATILTRREGTYPQ 360
 DB 448 GYDMRKLNGTVVSKHPLKSVTVFVDNNDITQPGSLBESTVQTMFKPLAATILTRREGTYPQ 507
 QY 361 VFYGDWYGTGDSOREIPALKHKIEPILKARKOYAYGAOHDPDHDIVGWTREGDSSVA 420
 DB 508 VFYGDWYGTGDSOREIPALKHKIEPILKARKOYAYGAOHDPDHDIVGWTREGDSSVA 567
 QY 421 NSGLAALITDGPQGAQKMYVGRQNAGETWHDITGNRSEPVVINSSEGVGFHVNGGSVSIY 480
 DB 568 NSGLAALITDGPQGAQKMYVGRQNAGETWHDITGNRSEPVVINSSEGVGFHVNGGSVSIY 627
 QY 481 VQR 483
 DB 628 VQR 630

Search completed: October 7, 2004, 00:12:20
 Job time : 62.3101 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:01:38 / Search time 14.8246 Seconds
(without alignments)
3134.012 Million cell updates/sec

Title: US-09-925-576C-8

Perfect score: 2666
Sequence: 1 ANLNGTLMOQFEMWYMPMDQ.....SEGWGEPHYVNGSVSYVQR 483

Scoring table: BLOSUM62
Gapop 10.0, Gapept 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 78:*

1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2654	99.5	512	1	ALBSL
2	2184	81.9	514	1	ALBSN
3	1879	70.5	518	1	A27705
4	1786.5	67.0	549	1	A54541
5	1780.5	66.8	549	1	A24549
6	1776.5	66.6	549	1	A24436
7	1715	64.3	548	1	ALBSF
8	1262	47.3	493	2	S15713
9	1244	46.7	492	2	AH2079
10	1233	46.2	484	2	G95160
11	1228	46.1	484	2	P98026
12	1108	41.6	491	2	C86781
13	1091.5	40.9	506	2	G98247
14	1090	40.9	495	2	AD3038
15	1060	39.8	494	1	B45738
16	1053	39.5	494	2	AD0751
17	1047	39.3	495	1	A45738
18	1047	39.3	495	2	B50962
19	1028	38.6	495	2	B85810
20	524	19.7	217	2	A19506
21	340	12.8	1196	2	A29130
22	321	12.0	826	2	B96720
23	311.5	11.7	421	2	S10514
24	310	11.6	404	2	A55861
25	304	11.4	440	2	S14958
26	302.5	11.3	437	2	S1478
27	300	11.3	437	2	S14956
28	298	11.2	713	2	S09196
29	294	11.0	713	1	ALBSG1

30	292.5	11.0	413	1	ALMT3	alpha-amylase (EC
31	292	11.0	718	1	ALBSGC	cyclomaltoextrin
32	291.5	10.9	718	1	ALBSG6	cyclomaltoextrin
33	290.5	10.9	437	2	JC7138	alpha-amylase (EC
34	290	10.9	437	2	JT0946	alpha-amylase 3B -
35	289	10.8	438	2	S14957	alpha-amylase (EC
36	288	10.8	712	1	ALBSG3	cyclomaltoextrin
37	286	10.7	713	2	A58800	cyclomaltoextrin
38	284.5	10.7	423	2	T09942	alpha-amylase (EC
39	281	10.5	435	2	S12625	alpha-amylase (EC
40	280	10.5	435	2	JC7137	alpha-amylase (EC
41	279	10.5	713	1	ALBSG7	cyclomaltoextrin
42	277.5	10.4	710	2	S63598	cyclomaltoextrin
43	276.5	10.4	718	1	ALBSMX	cyclomaltoextrin
44	275.5	10.3	439	2	T02956	alpha-amylase (EC
45	271.5	10.2	528	1	ALBSK	alpha-amylase (EC

ALIGNMENTS

RESULT 1

ALBSL
alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus licheniformis
C:Date: 30-Jun-1987 #sequence revision 24-Apr-1998 #text change 15-Sep-2000
C:Accession: A91997; B24549; A91796; A21663; I39774; I39772; A26151; S53788; A00844
J:Yuuki, T.; Nomura, T.; Tezuka, H.; Tsudol, A.; Yamagata, H.; Teukagoshi, N.; Uda, S.
J: Biochem. 98, 1147-1156, 1985
J: Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amylase deduced from the DNA sequences.
A:Reference number: A91997; MUID:86111694; PMID:2418011
A:Accession: A91997
A:Molecule type: DNA
A:Residues: 1-162; 'R', 164-512 <YDU>
A:Cross-references: GB:X03236; NID:g39551; PIDN:CAA26981.1; PID:g39552
A:Experimental source: ATCC 27811
R:Gray, G.L.; Mainzer, S.E.; Ray, M.W.; Lama, M.H.; Kindle, K.L.; Carmona, C.; Reguadt, J. Bacteriol. 166, 635-643, 1986
J: Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus
A:Reference number: A91817; MUID:86195857; PMID:3009417
A:Accession: B24549
A:Molecule type: DNA
A:Residues: 1-338; 'G', 340-348; 'S', 350-512 <GRA>
A:Cross-references: GB:M13256; NID:g142510; PIDN:AAA2240.1; PID:g142511
A:Experimental source: NCIB 8061
R:Stephens, M.A.; Orlepp, S.A.; Ollington, J.F.; McConnell, D.J.
J: Bacteriol. 158, 369-372, 1984
J: Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase
A:Reference number: A91796; MUID:84185455; PMID:6609154
A:Accession: A91796
A:Molecule type: DNA
A:Residues: 1-104 <STE>
A:Cross-references: GB:K01984; NID:g142432; PIDN:AAA22193.1; PID:g142433
R:Sibakov, M.; Palva, I.
Eur. J. Biochem. 145, 567-572, 1984
J: Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-amylase
A:Reference number: A21663; MUID:85076654; PMID:6334606
A:Accession: A21663
A:Molecule type: DNA
A:Residues: 1-3; 'H', 5-12; 'P', 14-47; 'R', 49-61; 'V', 63; 'D', 65-67; 'VA', 70-71; 'S', 73-80; 'D', 82
A:Experimental source: Chromosomal DNA of ATCC 14580
A:Note: The authors translated the codon GGT for residue 48 as Gly and GAC for residue 66
R:laide, B.M.; Chambliss, G.H.; McConnell, D.J.
J: Bacteriol. 171, 2435-2442, 1989
J: Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent
A:Reference number: I39773; MUID:89213924; PMID:2540150
A:Accession: I39774
A:Molecule type: DNA
A:Status: translated from GB/EMBL/DBJ
A:Residues: 1-29 <LAO>
A:Cross-references: GB:M26412; NID:g341477; PIDN:AAA22237.1; PID:g516590


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Qy 63 DLGEFHOKGTVRKTKYKSGELQSAIKSLHSRDINVGDVVINKHGADATEDVTAAYVDP 122
D 92 DLGEFHOKGTVRKTKYKSGELQSAIKSLHSRDINVGDVVINKHGADATEDVTAAYVDP 151
Qy 123 ADNRNVIAGEHLIAKMTFHHPGRGSTYSPDKMWHYFDGTDWDESKLARIYF--GK 180
D 152 ANRQOETSEBYQIAKMTDFPRPGNGTYSDFKMHYFDDGADWDESKRISIFKFRGEK 211
Qy 181 AMDVEVSENGNVDYLYMADIDVHDHPVAEIKRWGTYANELQDGFRLDAYKHIFSF 240
D 212 AMDVEVSENGNVDYLYMADIDVHDHPVAEIKRWGTYANELQDGFRLDAYKHIFSF 271
Qy 241 LRDVNVHREKTKEMETVAEYMONDGLALENTLNKTNFHSVPDVLHYQFHAASQGG 300
D 272 LRDVNVHREKTKEMETVAEYMONDGLALENTLNKTNFHSVPDVLHYQFHAASQGG 331
Qy 301 GYDMRKLINGTVSKHPLKSVTFVDNHDTPGQSLSTVQTFWPKLAPAFILITRESGPQ 360
D 332 GYDMRKLINGTVSKHPLKSVTFVDNHDTPGQSLSTVQTFWPKLAPAFILITRESGPQ 391
Qy 361 VFYGDWYGTGKDSOREIPALKKHIEPIIKARKQVYGAQHDYFDHHDIVGWTREGDSS 420
D 392 VFYGDWYGTGKDSOREIPALKKHIEPIIKARKQVYGAQHDYFDHHDIVGWTREGDSS 451
Qy 421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVYINSEGMGEFHVNGSVSY 480
D 452 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVYINSEGMGEFHVNGSVSY 511
Qy 481 VQR 483
D 512 VQR 514

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RESULT 3

```

alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase
C:Species: Bacillus sp.
C:Date: 31-Mar-1999 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
R:Accession: A27705
R:Tokamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A:Title: Nucleotide sequence of the maltotetraose-producing amylase gene from an alkalophilic
A:Reference number: A27705; MUID:88162814; PMID:3258152
A:Accession: A27705
A:Molecule type: DNA
A:Residues: 1-518 <TSU>
A:Cross-references: GB:M18862; NID:G142496; PID:NAA22231.1; PID:G142497
A:Experimental source: chromosomal DNA of strain 707
A:Note: amino end of mature protein also determined
C:Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloglycofasciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F:1-33/Domain: signal sequence #status predicted <SIG>
F:334-518/Product: alpha-amylase #status experimental <MAT>
F:236-369/Domain: alpha-amylase core homology <AMY>
F:139,228,273/Binding site: calcium (Asn, Asp, His) #status predicted
F:269,299,366/Active site: Asp, Glu, Asp #status predicted

```

```

Query Match 70.5%; Score 1879; DB 1; Length 518;
Best Local Similarity 67.8%; Pred. No. 1e-125;
Matches 329; Conservative 67; Mismatches 79; Indels 10; Gaps 4;

```

```

Qy 4 NGTLMQYFEMTENDGQWRRLQNDASVLAHGTAVWIPPAKYKTSQADVGYGYAYD 63
D 39 NGTLMQYFEMTENDGQWRRLQNDASVLAHGTAVWIPPAKYKTSQADVGYGYAYD 98
Qy 64 LGFHFQKGTVRKTKYKSGELQSAIKSLHSRDINVGDVVINKHGADATEDVTAAYVDP 123
D 64 LGFHFQKGTVRKTKYKSGELQSAIKSLHSRDINVGDVVINKHGADATEDVTAAYVDP 151

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D 99 LGFHFQKGTVRKTKYKSGELQSAIKSLHSRDINVGDVVINKHGADATEDVTAAYVDP 158
Qy 124 DNRNVIAGEHLIAKMTFHHPGRGSTYSPDKMWHYFDGTDWDESKLARIYF--GK 180
D 159 NRQOETSEBYQIAKMTDFPRPGNGTYSDFKMHYFDDGADWDESKRISIFKFRGEK 218
Qy 181 AMDVEVSENGNVDYLYMADIDVHDHPVAEIKRWGTYANELQDGFRLDAYKHIFSF 240
D 219 AMDVEVSENGNVDYLYMADIDVHDHPVAEIKRWGTYANELQDGFRLDAYKHIFSF 278
Qy 241 LRDVNVHREKTKEMETVAEYMONDGLALENTLNKTNFHSVPDVLHYQFHAASQGG 300
D 279 LRDVNVHREKTKEMETVAEYMONDGLALENTLNKTNFHSVPDVLHYQFHAASQGG 338
Qy 301 GYDMRKLINGTVSKHPLKSVTFVDNHDTPGQSLSTVQTFWPKLAPAFILITRESGPQ 360
D 339 GYDMRKLINGTVSKHPLKSVTFVDNHDTPGQSLSTVQTFWPKLAPAFILITRESGPQ 398
Qy 361 VFYGDWYGTGKDSOREIPALKKHIEPIIKARKQVYGAQHDYFDHHDIVGWTREGDSS 418
D 399 VFYGDWYGTGKDSOREIPALKKHIEPIIKARKQVYGAQHDYFDHHDIVGWTREGDSS 453
Qy 419 VANSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVYINSEGMGEFHVNGSVSY 478
D 454 VANSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVYINSEGMGEFHVNGSVSY 513
Qy 479 IYVQR 483
D 514 IYVQR 518

```

RESULT 4

```

alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DNI792)
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Bacillus stearothermophilus
C:Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
R:Accession: A54541
R:Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEBS Microbiol. Lett. 77, 271-276, 1991
A:Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
A:Reference number: A54541
A:Accession: A54541
A:Molecule type: DNA
A:Residues: 1-549 <JOR>
A:Cross-references: GB:X59476
A:Experimental source: chromosomal DNA of strain DNI792
C:Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C:Genetics:
A:Start codon: GTG
C:Function:
A:Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A:Pathway: glycogen/starch degradation
C:Superfamily: alpha-amylase, amyloglycofasciens type; alpha-amylase core homology
C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-549/Product: alpha-amylase #status predicted <MAT>
F:235-368/Domain: alpha-amylase core homology <AMY>
F:139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F:269,298,365/Active site: Asp, Glu, Asp #status predicted

```

```

Query Match 67.0%; Score 1786.5; DB 1; Length 549;
Best Local Similarity 64.7%; Pred. No. 4e-119;
Matches 314; Conservative 68; Mismatches 98; Indels 5; Gaps 2;

```

```

Qy 1 ANLNGTLMQYFEMTENDGQWRRLQNDASVLAHGTAVWIPPAKYKTSQADVGYGYAYD 60
D 36 ANLNGTLMQYFEMTENDGQWRRLQNDASVLAHGTAVWIPPAKYKTSQADVGYGYAYD 95
Qy 61 LGFHFQKGTVRKTKYKSGELQSAIKSLHSRDINVGDVVINKHGADATEDVTAAYVDP 120
D 96 LGFHFQKGTVRKTKYKSGELQSAIKSLHSRDINVGDVVINKHGADATEDVTAAYVDP 155

```

Qy	121	PADNRNIRISGEHLIKAMTHHFRPGSGSTYSDPFKHHWHFOGTDMDESRKLNIITYKO--	178
Dd	156	NPSDNOBISGYYQIQAWTKFDPPGRGNITSSFPKRWHPGVMDBSRKLRIYKFGXI	215
Qy	179	GKAMDWENSNGENDIYLMTADIDYDHDPVAEIERMGWTWYANELQLGFRLDAVKHKF	238
Dd	216	GKAMWMEVDTEANGNDIYLMTADLDMDHBEVYTELKMKGWKYNTNNIDGFLDAVKHKF	275
Qy	239	SPLRDWNHVBEKTGKEMFVAEYWQNDLGALENYLNTKNFNHSVFVDVLHYOFHAASQTQ	298
Dd	276	SFFPDMLSIVYSQTSKPLFTVGWEYWSYDIINKLHNITKTGDGMSLPDAPLNHKFYTASKS	335
Qy	299	GGGYDMRKLTNGTYVVSKHPLKSVTFVNDHNPQPGSLSESYQTWPKPLAVALFILTRREGY	358
Dd	336	GGAEPMLTLMNTNLTKODPFLAVTFVDNHDTPEPGALOSWDPMWKPLAVALFILTRREGY	395
Qy	359	POVFPGMDYGTKGDSOREIPALKHEIPLILAKROYAGAODHYDHDHDITAGMTRREGSS	418
Dd	396	PCVFRTGDIYGI---PQYNIPSLSKSIDPILARKROYAAGTDQDYDHSDDILGMTRREGSTE	452
Qy	419	VANSGLALLITDGPACRAMYVGRONAGEYTHMDITGNSEBPVINSSEGMEPHYNGGSVS	478
Dd	453	KPGSLALLITDGPESKMYTVGKQHAKXVPYDDLGNNSDVIYTINSDOMGEFXYNGGSVS	512
Qy	479	IYYOR 483	
Dd	513	VMVR 517	

RESULT 5
A24549
alpha-amylase (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* (strain NZ-3)
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: *Bacillus stearothermophilus*
C/Date: 30-Jun-1988 #sequence revision 18-Aug-1995 #text_change 18-Jun-1999
C/Accession: A24549; 139501; 139770
J/Grey, G.L.; Maltzer, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Regardt, J.
J. Bacteriol. 166, 635-643, 1986
A/Title: Structural genes encoding the thermophilic alpha-amylases of *Bacillus stearothermophilus*
A/Reference number: A91817; MUID:86195857; PMID:3009417
A/Accession: A24549
A/Molecule type: DNA
A/Residues: 1-549 (GRA>
A/Cross-references: GB:M1325; NID:g142512; PIDN:AAA22241.1; PID:g142513
A/Experimental source: genomic DNA of strain NZ-3
J/Satcho, H.; Nishida, H.; Igono, K.
J. Bacteriol. 170, 1034-1040, 1988
A/Title: Evidence for movement of the alpha-amylase gene into two phylogenetically distant
A/Reference number: 139501; MUID:88139156; PMID:3257753
A/Accession: 139501
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 536-549 <RES>
A/Cross-references: GB:M29577; NID:g142476; PIDN:AAA2225.1; PID:g142478
A/Experimental source: strain DY-5
A/Accession: 139770
A/Status: translated from GB/EMBL/DBJ
A/Residues: 536-549 <RE2>
A/Cross-references: GB:M29578; NID:g142484; PIDN:AAA22228.1; PID:g142486
A/Experimental source: strain 799
C/Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C/Genetics:
A/Start codon: GTG
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide
F:1-34/Domin: signal sequence #status predicted <SIG>
F:35-549/Product: alpha-amylase #status predicted <MAT>
F:235-368/Domin: alpha-amylase core homology <MTY>
F:139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted

F,268,298,365/Active site: Asp, Glu, Asp #status predicted	
Query Match	66.8%, Score 1780.5; DB 1; Length 549;
Best Local Similarity	64.7%; Pred. No. 1,1e-118;
Matches 314; Conservative 67; Mismatches 99; Indels 5; Gaps 2	

QY 1 ANLNGTLMQFEMWPMNDQGHMRRLDNDSDAYLHGHGTAVIIPPAKYGTQADVGAYD 60
 Db 36 APFNGTMOQFEMWLPDDGTILTKRVANEANNSSLGITLMLPEPAIKGIRSDVGGAYD 95
 QY 61 LYDIEGFHQKGYVTKYGTGYGELQSAIKSLHSRBDINVYGDVIVNHKGADATEDVTAVEY 120
 Db 96 LYDIEGFENQKGYVTKYGTGAOYLQAIQAHAAGMOYVADVVFDDHKGADGETWDAVEY 155
 QY 121 DPADRNVISGEHLIKAWTHFHPGSGSTSDAKPMHMYHDDGDMDBSRKLINEYFKQ-- 178
 Db 156 NPSRBNQIEIGTYQIQAMTKFDPNRCGNITSSFKMRMYHFDGADMBESRKLSTIYFRGI 215
 QY 179 GKADMDVSNENGNYYDYLMATADIDYDHPDYAAEIKKWGTVYANELOLDGFRDLAVHRIK 238
 Db 216 GKADMDVEVDJENGNYYDYLMATADLDMDHPELVTELKQWGGKXYVNTJNIDGFRDLAVHRIK 275
 QY 239 SFLRDMVNNHREKTGKEMFTVAEYQNDLGALENNYLANKTNPFNHSVDVPLHYFHASTQ 298
 Db 276 SFPEDMISTVYRSQTKPLFTVGEWYSYDINKLNHYITKTNGTMSLDAPALHNKFYAAKSS 335
 QY 299 GGGDYMKELNGTVVSNKHPLKSVTFVDNHDTPQGQSLESTVQTWFRPLAYAFILTEESGY 358
 Db 336 GGAEDMSTLNNNTLMMKQOPLTAVTFVDNHDTEBGQALQGSVMDPFRPLAVAFILTRQEGY 395
 QY 359 POWFYGMGTGKQDSQREIPALGHKTEPILIAKQOYAYGAQHYFPHHDIWGTREGDSS 418
 Db 396 PCVFGYGYGI---PQINIPSLKSKIDPDLIARDYAYGQHDYLDHSIDIWGTREGVTE 452
 QY 419 VANSGLAALLTTDGPAGKAKRYVGRONAGETWHDITGNRSBPVYINSBGGEFFHNGGSYS 478
 Db 453 KPQSGLAALLTDPGGSKMYYVKGQHAQKAFYDLTGNRSDTYIINSDGNGEPRVNGGSYS 512
 QY 479 IYVOR 483
 Db 513 VVWVR 517

RESULT 6
A24436
alpha-amylase (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* plasmid pAT5
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: *Bacillus stearothermophilus*
C/Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #ext_change 18-Jun-1999
C/Accession: A24436; J39777
R/Nakajima, R.; Imanaka, T.; Aiba, S.
J. Bacteriol. 163, 401-406, 1985
A/Reference number: A24436; PMID:85234394; PMID:3924897
A/Accession: A24436
A/Molecule type: DNA
A/Residues: 1-549 <NAK>
A/Cross-references: GB:M11450
A/Experimental source: plasmid pAT5
A/Note: amino end of the mature protein also determined
R/Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Didrichsen, B.
Gene 96, 37-41, 1990
A/Title: In vivo genetic engineering: homologous recombination as a tool for plasmid construction
A/Reference number: J39772; PMID:91092499; PMID:2265757
A/Accession: J39777
A/Status: preliminary; translated from GB/EMBL/DDBT
A/Molecule type: DNA
A/Residues: 1-45 <RSS>
A/Cross-references: GB:M62638; NTD:G142514; PTDN:AAA2242.1; PTD:G142515
C/Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C/Genetics:
A/Genes: amyS
A/Genome: plasmid
A/Start codon: GTG

C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F/1-34/Domain: signal sequence #status predicted <SIG>
F/35-549/Product: alpha-amylase #status experimental <MAT>
F/235-368/Domain: alpha-amylase core homology <AMY>
F/139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F/268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 66.6%; Score 1776.5; DB 1; Length 549;
Best Local Similarity 64.7%; Pred. No. 2,1e-118;
Matches 314; Conservative 66; Mismatches 100; Indels 5; Gaps 2;

```
QY 1 ANLNGTLMQYFEWMPNDGQWRLQNDASVLAHGTAWIPRAYKGTSGADVGYAYD 60
DB 36 APFGTMMQYFEWLPDGLMTVANEANLSSIGITALMLPPRAYKGTSDVGYGYD 95
QY 61 LYDGEFHQKGTATKTKGTGELQSAIKSLHSDINYGDVVNHKGGADATEDVTAVEV 120
DB 96 LYDGEFNQKAVTKTKGTQYQYLAIAAAGQYADVPFHKGAGDTEWVDAVEV 155
QY 121 DPADRNVISGEHLIKAWTFHFPGRGTYSDFKMWHYHFDGTDWDSRKLRIYKQ-- 178
DB 156 NPSDRNGEISGTQIQAWTKDFPGRGNTYSSFKMRYHFDGVDMDSRKLRIYKRG 215
QY 179 GKAMDVEVSNENGYDYLMTADIDYHPDVAELKRGTYANLQDGRDLAVKIKF 238
DB 216 GKAMDVEVDENGYDYLMADIDMDHPEVTELSKMGKMYVNTNIDGFRDLAVKIKF 275
QY 239 SFLADWNVHREKTKGKMFVAEYQNDLGALENYLNKTNFNSVFPVPLHYOFHA 298
DB 276 SFPEDMLSTYRSQTKPLFTVGEYWSYDINKLHNYINKTNGTMSLFPALPNKRYT 335
QY 299 GGGYDMRKLNGTVSKPLKSVTFVDNHDTPQGSLESTVQTFKPLAAYAFILTR 358
DB 336 GGTDMETMTNLTMLKQPTLAVTFVDNHDTPQALQSWDPFKPLAAYAFILTR 395
QY 359 PÖVFGDMYGTGDSQREIPALKEIPILKARKQYAGAHYFDHHDIVGWTREG 418
DB 396 PCVFGYGDYGI---PÖYNIPLSKIDPLIARDYVAGTQHDYLDHSDIIGWTR 452
QY 419 VANSGLAALTDDGGKAKMYVGRONAGETMHDITGNRSEPVVNSGGEFHN 478
DB 453 KPSGGLAALTDDGGKAKMYVGRONAGETMHDITGNRSDVTITNSGGEFHN 512
QY 479 IYVOR 483
DB 513 VWVPR 517
```

RESULT 7
ALBSF
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DY-5) plasmid

N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: Bacillus stearothermophilus
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Feb-1997
C/Accession: A91999; B91999; A91804; A00845
R/Ihara, H.; Sasaki, T.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uda, S.
J. Biochem. 98, 95-103, 1985
A/Title: Complete nucleotide sequence of a thermophilic alpha-amylase gene: homology bet
A/Reference number: A91999; MUID:86008166; PMID:3876333
A/Accession: A91999
A/Molecule type: DNA
A/Residues: 1-548 <IH1>
A/Cross-references: GB:X02769
A/Experimental source: plasmid pHI300 from strain DY-5
A/Accession: B91999
A/Molecule type: protein
A/Residues: 35-48 <IH2>
A/Experimental source: strain DY-5
R/Tsukagoshi, N.; Iritani, S.; Sasaki, T.; Takemura, T.; Ihara, H.; Idota, Y.; Yamagata,

J. Bacteriol. 164, 1182-1187, 1985
A/Title: Efficient synthesis and secretion of a thermophilic alpha-amylase by protein-pr
A/Reference number: A91804; MUID:86059211; PMID:2999073
A/Contents: B9A01
A/Accession: A91804
A/Molecule type: DNA
A/Residues: 1-29, 'Q', '31-75', 'W', '77-122' <TSU>
A/Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C/Genetics:
A/Genome: plasmid
A/Scat. codon: GTG
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F/1-34/Domain: signal sequence #status predicted <SIG>
F/35-548/Product: alpha-amylase #status experimental <MAT>
F/235-368/Domain: alpha-amylase core homology <AMY>
F/139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F/268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 64.3%; Score 1715; DB 1; Length 548;
Best Local Similarity 63.1%; Pred. No. 4.8e-114;
Matches 306; Conservative 67; Mismatches 106; Indels 6; Gaps 3;

```
QY 1 ANLNGTLMQYFEWMPNDGQWRLQNDASVLAHGTAWIPRAYKGTSGADVGYAYD 60
DB 36 APFGTMMQYFEWLPDGLMTVANEANLSSIGITALSLPPRAYKGTSDVGYGYD 95
QY 61 LYDGEFHQKGTATKTKGTGELQSAIKSLHSDINYGDVVNHKGGADATEDVTAVEV 120
DB 96 LYDGEFNQKAVTKTKGTQYQYLAIAAAGQYADVPFHKGAGDTEWVDAVEV 155
QY 121 DPADRNVISGEHLIKAWTFHFPGRGTYSDFKMWHYHFDGTDWDSRKLRIYKQ-- 178
DB 156 NPSDRNGEISGTQIQAWTKDFPGRGNTYSSFKMRYHFDGVDMDSRKLRIYKRG 215
QY 179 GKAMDVEVSNENGYDYLMTADIDYHPDVAELKRGTYANLQDGRDLAVKIKF 238
DB 216 GKAMDVEVDENGYDYLMADIDMDHPEVTELSKMGKMYVNTNIDGFRDLAVKIKF 275
QY 239 SFLADWNVHREKTKGKMFVAEYQNDLGALENYLNKTNFNSVFPVPLHYOFHA 298
DB 276 SFPEDMLSTYRSQTKPLFTVGEYWSYDINKLHNYINKTNGTMSLFPALPNKRYT 335
QY 299 GGGYDMRKLNGTVSKPLKSVTFVDNHDTPQGSLESTVQTFKPLAAYAFILTR 358
DB 336 GGAFTDMTMTNLTMLKQPTLAVTFVDNHDTPAKRC-SHGRPFKPLAAYAFILTR 394
QY 359 PÖVFGDMYGTGDSQREIPALKEIPILKARKQYAGAHYFDHHDIVGWTREG 418
DB 395 PCVFGYGDYGI---PÖYNIPLSKIDPLIARDYVAGTQHDYLDHSDIIGWTR 451
QY 419 VANSGLAALTDDGGKAKMYVGRONAGETMHDITGNRSEPVVNSGGEFHN 478
DB 452 KPSGGLAALTDDGGKAKMYVGRONAGETMHDITGNRSDVTITNSGGEFHN 511
QY 479 IYVOR 483
DB 512 VWVPR 516
```

RESULT 8

alpha-amylase (EC 3.2.1.1) - Bacillus circulans
C/Species: Bacillus circulans
C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C/Accession: S15713
R/Marcel, T.
submitted to the EMBL Data Library, May 1991
A/Reference number: S15713
A/Accession: S15713


```

Qy 64 LGEEHOKGVTKYGTKEGLOSAIKSLHSRDINVGAVINHGKADATEDVTAVEVPA 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 LGEEHOKGVTKYGTKEGLOSAIKSLHSRDINVGAVINHGKADATEDVTAVEVPA 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 124 DRNVIHGEHLIKAWTHFHPGSGTYSDFKMHYHFDGTDWDSRKLNRITYKQG--KA 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 DRNVIHGEHLIKAWTHFHPGSGTYSDFKMHYHFDGTDWDSRKLNRITYKQG--KA 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 182 WDME--VSNENGVNDYLMVADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHKFS 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 WANEELVDNENGVNDYLMVADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIDSF 242
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 240 FLRDMVHVRKTKGEMFTVAEYQNDLGALNTKTNFNSHVFDPVPLHYQFHAASQOG 299
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 243 FMRNFIIDMEKYGDDYVGEFPMNPKDEANLDLEKTEEHFIDLVDRLHONLFEASQAG 302
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 300 GGYDMRKLNGTVVSKPLKSVTFVDNHDTPQGSLSTVQWTFKPLAYAFILTRSGYR 359
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 303 ANYDLRGIFFTSLVELKPKDAVTFVDNHDTPQGSLSTVQWTFKPLAYAFILTRSGYR 362
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 360 QVEFGDMYGTGDSQREIPALKHKEPILKARKQAYAGAHYEDHNDIVGWTREGDSSV 419
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 363 CVFYGDYGGISGQYAOE--DFKEILDRLLAIRKDLAYGEQNDYFDHANCIGWVSGAEN- 419
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 420 ANSGALALITDGPAGAKMYVGRONAGETWHDITGNRSEPVINSBGMGEFHNAGSVSI 479
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 420 -QSPFIAVLISNDQNSKSMFVGQEMTQTFVDLIGNHQGVTTIDEGYGFPPVARSYSV 478
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 480 Y 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 479 W 479
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 11

```

P98026
alpha-amylase (EC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C:Accession: P98026
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Balaz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: P98026
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-484 <KTR>
A:Cross-references: GB:AE007317; PIDN:AL00043.1; PID:915458876; GSPDB:GN00174
A:Gene: amy
C:Genetics:
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase

```

```

Query Match 46.1%; Score 1228; DB 2; Length 484;
Best Local Similarity 48.2%; Pred. No. 1.5e-79;
Matches 232; Conservative 75; Mismatches 166; Indels 8; Gaps 4;
Qy 4 NGTLMQFEWMPNDGQHWRRLQNDASVLAHEGITAIVWIPRAYKGSQADVGYAYLDYD 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 NGTLMQFEWMPNDGQHWRRLQNDASVLAHEGITAIVWIPRAYKGSQADVGYAYLDYD 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 64 LGEEHOKGVTKYGTKEGLOSAIKSLHSRDINVGAVINHGKADATEDVTAVEVPA 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 LGEEHOKGVTKYGTKEGLOSAIKSLHSRDINVGAVINHGKADATEDVTAVEVPA 122
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 124 DRNVIHGEHLIKAWTHFHPGSGTYSDFKMHYHFDGTDWDSRKLNRITYKQG--KA 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 DRNVIHGEHLIKAWTHFHPGSGTYSDFKMHYHFDGTDWDSRKLNRITYKQG--KA 182
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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```

Qy 182 WDME--VSNENGVNDYLMVADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHKFS 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 WANEELVDNENGVNDYLMVADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIDSF 242
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 240 FLRDMVHVRKTKGEMFTVAEYQNDLGALNTKTNFNSHVFDPVPLHYQFHAASQOG 299
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 243 FMRNFIIDMEKYGDDYVGEFPMNPKDEANLDLEKTEEHFIDLVDRLHONLFEASQAG 302
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 300 GGYDMRKLNGTVVSKPLKSVTFVDNHDTPQGSLSTVQWTFKPLAYAFILTRSGYR 359
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 303 ANYDLRGIFFTSLVELKPKDAVTFVDNHDTPQGSLSTVQWTFKPLAYAFILTRSGYR 362
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 360 QVEFGDMYGTGDSQREIPALKHKEPILKARKQAYAGAHYEDHNDIVGWTREGDSSV 419
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 363 CVFYGDYGGISGQYAOE--DFKEILDRLLAIRKDLAYGEQNDYFDHANCIGWVSGAEN- 419
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 420 ANSGALALITDGPAGAKMYVGRONAGETWHDITGNRSEPVINSBGMGEFHNAGSVSI 479
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 420 -QSPFIAVLISNDQNSKSMFVGQEMTQTFVDLIGNHQGVTTIDEGYGFPPVARSYSV 478
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 480 Y 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 479 W 479
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 12

```

C86781
alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: C86781
R:Boletín, A.; Mincker, P.; Manger, S.; Jallón, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: C86781
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-491 <STO>
A:Cross-references: GB:AE005176; PID:912724224; PIDN:AAK05349.1; GSPDB:GN00146
A:Experimental source: strain IL1403
A:Genetics:
A:Gene: amyL
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

```

```

Query Match 41.6%; Score 1108; DB 2; Length 491;
Best Local Similarity 41.7%; Pred. No. 5e-71;
Matches 204; Conservative 93; Mismatches 168; Indels 24; Gaps 7;
Qy 6 TLMQFEWMPNDGQHWRRLQNDASVLAHEGITAIVWIPRAYKGSQADVGYAYLDYD 64
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 TLMQFEWMPNDGQHWRRLQNDASVLAHEGITAIVWIPRAYKGSQADVGYAYLDYD 62
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 65 GEEHOKGVTKYGTKEGLOSAIKSLHSRDINVGAVINHGKADATEDVTAVEVPA 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 GEEHOKGVTKYGTKEGLOSAIKSLHSRDINVGAVINHGKADATEDVTAVEVPA 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 124 DRNVIHGEHLIKAWTHFHPGSGTYSDFKMHYHFDGTDWDSRKLNRITYKQG--KA 181
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 EDNHLNHNENKKTVEVMTKTFPGRQKYNVYIWTMNFICIDYDERKNOEILFEFGHE 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 182 WDMEVSNENGVNDYLMVADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHKFS 241
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 WDMEVSNENGVNDYLMVADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHKFS 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 242 RDVNVHVRKTKGEMFTVAEYQNDLGALNTKTNFNSHVFDPVPLHYQFHAASQOG 301
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 240 DKLMEQAKQDLRKLFLVIGYMSDDLKLYLEQSSDRQLRPVPLHFMKKEASSTNGE 299
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 302 YDMRKLNGTVVSKPLKSVTFVDNHDTPQGSLSTVQWTFKPLAYAFILTRSGYR 361
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 FMRNFIIDMEKYGDDYVGEFPMNPKDEANLDLEKTEEHFIDLVDRLHONLFEASQAG 359
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```


[illegible]

RESULT 13

cytoplasmic alpha-amylase (1,4-alpha-D-glucan glucanohydrolase) [imported] - Agrobacterium
C:Species: Agrobacterium tunnei
C:Date: 22-Oct-2001 Sequence Revision 22-Oct-2001 #text_change 18-Nov-2002
C:Accession: G98247
R:Goodner, B.; Hinkley, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tunnei
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: G98247
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1506 <KDP>
A:Cross-references: GB:AE007870; PIDN:AAK9505.1; PID:G15159379; GSFDB:GN00170
C:Genetics:
A:Gene: AGR_L_1863
A:Map position: linear chromosome
A:Superfamily: alpha-amylase, amyloliqueficans type; alpha-amylase core homology

	Score	Length
Query Match	40.9%	506
Best Local Similarity	44.3%	
Matches 219; Conservative	80; Mismatches 178;	Indels 17; Gaps 6;

```

Qy 2 NUNG- TLMOQYEWYMPNDGQHWRRRLONDSAYLAHEGILTVMIRPAYKTSQA- DVGXGAY 59
Dh 11 NMAGTLLLOFFHMYYPDDGCKLSEVAKESASLAKMGITVWMLPPAYKGAAGYSVGDYTY 70
Qy 60 DLYDGEFFQKCTVYTKYGTKEGELQSAISLHSRDINXYGDVYVHNKGGADATEDYTAVE 119
Dh 71 DLFDJGEBPDQKTVAKTGDRALEBHAQKTLKONGIRVJHDDVVLNHNKMGADKEKQVRR 130
Qy 120 VDPADRNRYISEHNIKAWTHFHPFPGSGTUSD FKNHWYHPDGTDMDESRKLNRIKYGOG 179
Dh 131 VNPDRTRTDDBDFPALATYTRTFEPRNKGKHSFTYDLKCFSGVDHIEEBTEBGIRLVN 190
Qy 180 K---AMDWEYSNENGANDYLMYADIDYHPDVAAEIKKWTWYANELOLDGERLDAVXG 235
Dh 191 EYGDGEWMBEVDQENGONFDYLMGADYVEFRNRAVYBELKTYWGRWLSBQVYDQGRFLDAAGX 250
Qy 236 IKFSLRDMVNVHREKTKGEMFTVAEYMONDGALENIYLNKTNFNHSVDPYRPHYOFNAA 295
Dh 251 IPAMFFRDMVGHMRRETVDPDLFVVAEYWMPDLEALKSYELVDKQMLDPLVALHHSFHRA 310
Qy 296 STOGGSGYMRKLNJNGVYSKHPILKSTVPJNDNDHOGSGSLSTVQWMPFLVAYALITRE 355
Dh 311 SKQGGDFEFDKRSIFDSLSVSAVDPDHATVLDVNDHDTLOGLSLEAVEBEMFPLAYAILLKE 370
Qy 356 SGYPQVGFYGDMMGTK-----GDSQREI PALKHIEF ILKARKOYAGAQCHDYFDHND 407
Dh 371 EGVPCVFFPDLFGTISTYTDGTGNDGNEKXIDIPALE-CLPRLTIERSKSFANGPOQDIDDDAS 429
Qy 408 IVGWTRGSDSVANSGLAALITDGPGARMYVGVGNAGETWHDITGNSEPVVINSSEGN 467
Dh 430 CIAFIRHGTADA- PGCVVVWMSNGSBGEKQADLGPERRASVWRDPLGHREHEHTLDESCK 487
Qy 468 GEFHNGSGSVSLIYV 481
Dh 488 GTFPTNGSGSVSVWV 501

```

RESULT 14
AD3038

RESULT 14

alpha-amylase amya [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: ADJ038
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, P.; Grant, C.; Guenther, D.; Kutyavlin, T.; Levy, R.; Li, M.; McClellan,
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.

A: Accessi

A:status: preliminary
A:molecule type: DNA
A:Residues: 1-495 <KDR>
A:Cross-preferences: GM:A800689; PIDN:AAL44722.1; PID:gi17742354; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: amya
A:map position: linear chromosome
C:Superfamily: alpha-amy-lase, amyloid-efaciens type: alpha-amy-lase core homology

Query Match: 40.9%; Score 1030; DB 2; Length 485;
 Best Local Similarity 44.4%; Pred. No. 9.6e-70;
 Matches 217; Conservative 79; Mismatches 177; Indels 16; Gaps 5.

```
QY      6 TLMQFEWYNPDGQHRRRLONDSATLAEHGTAVWLPRAYKTSQA-DVGYAYDLYL 64
        ||:|||||:::|||||||:::|||||||
Db       5 TLDFHWYPDGCKLMSEVAEKAESIAKMGITDVMLPRAKGAGGISVGPTDYDLFPL 64
```

QY 65 GEFHQKGTWRTKYGTGELGSAIKSLHSRDINVGDVVINHGGADATEDVTANEVDPAD 12
 ||| ||| ||| : : : ||| : ||| ||| ||| : : |||
 DB 65 GEFQDKGTVAITYGDPALAEHAGKTLKDNGIRVIHVDVVLNKKMGADAEKEKVRVRRVNPDD 12

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QY      125  RNRVTSGEHLIKAWTHFHFPPKGSITSDFKMWVYHFGSDIWESKRLKRLKQK-----180
          |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      125  RTDIDDEDFFALAYTRPTFPGRNGKSKSFINDLKCFSGVDHIEPTEDGIFRLVNBXGDC 180

```

QY 181 AMDWEVSNEGNIYDILMTIAUDIDIHDPVAAEINRWGIMIANLQLDDGRKDAVAHINISF
| : | | | | | | | : : : | : | | | | | |
Db 185 EKNSEVDQENGNFYLMGADVEFRNNAVYEELKYWGRLSEQVQVDDGERLDAAKHIPAMF 24

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241 LRDNVNHVKRNLGKAMF I VAD I MGNLQVALLN I LNKLNFNISV FVDFVNI I QFTHMAG I QGG
245 FRDWGMRETVDPDLFVVAEYWHPRDLKLSYELVDKQLMLFDVALTHSFHDASKGG 30

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[illegible]

365 VFPPDLFGISTYDTGNDGNEYKIDIPAIE-CLPKLIEARSRFANGPQIDIFDDASCIARF 422

424 RHGTADA--PGCVVYMSNGEFGKQADLPERRAGSVKRFLLGHRREHITLDESGKGTFFT 481

Db 482 NGSYSVMV 490

RESULT 15

B45738
 alpha-amylase (EC 3.2.1.1), cytosolic - *Salmonella typhimurium*
 N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C:Species: *Salmonella typhimurium*

C>Date: 07-Apr-1994 #sequence revision 18-Aug-1995 #text change 18-Jun-1999
C/Accession: B45738
R/Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.
J. Bacteriol. 174, 6644-6652, 1992
A/Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyA.
A/Reference number: A45738; MUID:93015717; PMID:1400215
A/Accession: B45738
A/Molecule type: DNA
A/Residues: 1-494 <RAH>
A/Cross-references: GB:L01643; NID:g154043; PIDN:AAA27110.1; PID:g154045
C/Genetics:
A/Gene: amyA
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C/Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation
F/202-335/Domain: alpha-amylase core homology <AMY>
F/239,265,332/Active site: His, Glu, Asp #status predicted

Query Match 39.8%; Score 1060; DB 1; Length 494;
Best Local Similarity 42.4%; Pred. No. 1.3e-67;
Matches 208; Conservative 88; Mismatches 179; Indels 16; Gaps 6;

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QY 4 NGTLMQYFEWYMPNDQGMRLQNDSDAYLAHGITAVWIPRAYKTSQA-DVGYGAYDLY 62
Db 3 NPTLLQYFHWYYPDGKLMSELARADGLNDIGINMWLPACKAGSGYSGYDTYDLF 62
QY 63 DLGEFHOKGTVRYTGTGELQSAIKSLHSRDINVGDVYINHGADATEDVTAVEYDP 122
Db 63 DLGEFDQKGTATATYCKGRQLTATDALKKNINAVLLDVVVVNHKGADDEKERIRVQRVNQ 122
QY 123 ADNRKRVSGEHLIAWTHFHPGSGSTYSDPKMTHHPDGTMDSESKLRITYK---FQ 178
Db 123 DDRTOIDNITIECGWTRRYTFPARAGQSNFTWYHCGSGIDHIENPEDGIFKIYNDYT 182
QY 179 GKAWDMEVSNENGNVDYLMYADIDYDHPVNAEIKRWGTWYANELQDGFRLDAVKIKF 238
Db 183 GDDGNDQVDDMGNFDYLMGENDIFRNHAYTEEIKYARWMEQTHCDGFRLLDAVKIIPA 242
QY 239 SFLDWNVNVAREKTKGEMFTVAEYWNQDLGALENYLNKTNFNHSGVDFVPLHYQFHAATQ 298
Db 243 WFYKEMWIEHQAQVAPKPLFIYAEEYSHSHVDLQTYIDQVDGKTMLPDALQMKFHEASRQ 302
QY 299 GCGGDMKRLNGTVSKHPLKSVTFVNDHDPQGSLESTVQTWEKPLAVAFILTRSEGY 358
Db 303 GAEDYMRHIFGTGLVEADPFHAYVTLVANHDTPQLALEAPVEPWFKPLAYALILRENGV 362
QY 359 POFVYGMVGT-----KGDQR-ETPALGKIEPILKAKQAYGAGQHDYFDHDIYV 410
Db 363 PSVTFYPLDYGASVDSGSENGETCRVDMVT-NQLDRLLIARQRFAGIQTLFFDHPCIA 421
QY 411 WTRGDSVANSGLAALITDGPGAQKMYVGRONAGETMDITGNRSEPVVINSEGWGEF 470
Db 422 FSRSGTEE--NPGCVVVLNSDDEKKTILLGDNYANKTWRFSGNRDEYVVTNDGEATF 479
QY 471 HVGGSVSIYV 481
Db 480 FCNAGSVSVWV 490
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Search completed: October 7, 2004, 00:20:44
Job time : 15.8246 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:46:32 ; Search time 8.47121 Seconds

(without alignments)
2968.867 Million cell updates/sec

Title: US-09-925-576C-8

Perfect score: 2666
Sequence: 1 ANANGTLMQYFEWYMPNDQ.....SEGKGFHVGGSVSIYQR 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2648	99.3	512	1 AMY_BACLI	P06278 bacillus 11
2	2184	81.9	514	1 AMY_BACAM	P06927 bacillus am
3	1879	70.5	518	1 AMY6_BACS7	P19571 bacillus sp
4	1776.5	66.6	549	1 AMY_BACST	P06279 bacillus st
5	1058	39.7	494	1 AMY2_SALTY	P26613 salmonella
6	1047	39.3	495	1 AMY2_ECOLI	P26612 escherichia
7	340	12.8	1196	1 AMYB_PABPO	P21543 paenibacilli
8	311.5	11.7	421	1 AMYA_VIGMU	P17859 vigna mungo
9	304	11.4	440	1 AM3A_ORYSA	P27932 oryza sativ
10	300	11.3	437	1 AM3C_ORYSA	P27938 oryza sativ
11	298	11.2	713	1 CDGT_BAC8	P17692 bacillus sp
12	294	11.0	713	1 CDGT_BAC80	P05618 bacillus sp
13	292.5	11.0	413	1 AMY3_WHEAT	P08117 triticum ae
14	292	11.0	718	1 CDGT_BACCI	P30920 bacillus ci
15	291.5	10.9	718	1 CDGT_BACSS	P13747 bacillus sp
16	290	10.9	437	1 AM3E_ORYSA	P27934 oryza sativ
17	289	10.8	438	1 AM3B_ORYSA	P27937 oryza sativ
18	288	10.8	713	1 CDGT_BAC3	P09121 bacillus sp
19	286	10.7	712	1 CDGU_BACCI	P43379 bacillus ci
20	281	10.5	435	1 AM3D_ORYSA	P27933 oryza sativ
21	279	10.5	713	1 CDGT_BACSP	P10921 bacillus sp
22	277.5	10.4	710	1 CDGT_THERU	P26827 thermocae
23	276.5	10.4	718	1 CDGT_BACLI	P14014 bacillus 11
24	271.5	10.2	528	1 AMY_BACCI	P08137 bacillus ci
25	262	9.8	494	1 AMY1_SACRI	P21567 saccharomyc
26	259	9.7	368	1 AMY3_HORVU	P04747 hordeum vul
27	259	9.7	427	1 AMY2_HORVU	P04063 hordeum vul
28	259	9.7	429	1 AMY6_HORVU	P04750 hordeum vul
29	257	9.6	428	1 AMY1_ORYSA	P17654 oryza sativ
30	252.5	9.5	438	1 AMY1_HORVU	P00693 hordeum vul
31	247	9.3	441	1 MGTA_THENA	P80099 thermotoga
32	245.5	9.2	719	1 AMYM_BACST	P19531 bacillus st
33	242.5	9.1	443	1 AM2A_ORYSA	P27935 oryza sativ

34	242.5	9.1	445	1 AMC2_ORYSA	P27941 oryza sativ
35	237.5	8.9	713	1 CDG2_PABMA	P31837 paenibacilli
36	236.5	8.9	676	1 AMY1_ECOLI	P25718 escherichia
37	234.5	8.8	581	1 AMY1_SCHPO	O09840 schizosacch
38	233.5	8.8	919	1 AMY_STRLI	O05884 streptococ
39	231.5	8.7	442	1 MGTA_THENA	O06936 thermotoga
40	231.5	8.7	711	1 CDGT_BACST	P31797 bacillus st
41	226	8.5	498	1 AMY3_DICTH	P14839 dictyoglomu
42	218	8.2	478	1 YO29_SCHPO	O10427 schizosacch
43	215.5	8.1	564	1 AMY4_SCHPO	O9Y759 schizosacch
44	211	7.9	704	1 CDGT_BACOH	P27036 bacillus oh
45	211	7.9	1476	1 GFPB_STRMU	P08987 streptococc

ALIGNMENTS

RESULT 1
ID AMY_BACLI STANDARD; PRT; 512 AA.
AC P06278; 084171;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase) (BLA).
GN AMYS OR AMYL.
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1402;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27811;
RX MEDLINE=6611694; PubMed=2418011;
RA Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "Complete nucleotide sequence of a gene coding for heat- and
pH-stable alpha-amylase of Bacillus licheniformis: comparison of the
amino acid sequences of three bacterial liquefying alpha-amylases
deduced from the DNA sequences."
RT J. Biochem. 98:1147-1156(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=66195857; PubMed=3093417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
RA Carmona C., Reguad C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
Bacillus stearothermophilus and Bacillus licheniformis".
RT J. Bacteriol. 166:635-643(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX Shahosseini M., Ziaei A.A., Ghaemi N., Pourbaei A.A.;
RA "An unusual DNA sequence encoded a hyperthermostable alpha-amylase."
RT submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-104 FROM N.A.
RX MEDLINE=94185455; PubMed=6609154;
RA Stephens M.A., Ortlepp S.A., Ollington J.F., McConnell D.J.;
RT "Nucleotide sequence of the 5' region of the Bacillus licheniformis
alpha-amylase gene: comparison with the B. amyloliquefaciens gene".
RT J. Bacteriol. 158:369-372(1984).
RN [5]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=89213924; PubMed=2540150;
RA Lacle B.M., Chambliss G.H., McConnell D.J.;
RT "Bacillus licheniformis alpha-amylase gene, amyL, is subject to
promoter-independent catapolyte repression in Bacillus subtilis".
RT J. Bacteriol. 171:2435-2442(1989).
RN [6]
RP SEQUENCE OF 30-47.
RX MEDLINE=82098050; PubMed=6172418;
RA Kuhn H., Fietzek P.P., Lampen J.O.;
RT "N-terminal amino acid sequence of Bacillus licheniformis

RT alpha-amylase: comparison with Bacillus amyloliquefaciens and
RT Bacillus subtilis enzymes.";
RL J. Bacteriol. 149:372-373(1982).
RN [7]
RP MAPPING OF SUBSTRATE-BINDING SITE.
RX MEDLINE=2199278; PubMed=11997021;
RA Kandra L., Gyemant G., Remyak J., Hovaszki G., Lipcak A.;
RT "Action pattern and subsite mapping of Bacillus licheniformis
RT alpha-amylase (BA) with modified maltotigosaccharide substrates.";
RL FEBS Lett. 518:79-82(2002).
RN [8]
RP MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.
RC STRAIN=ATCC 6598;
RX MEDLINE=90368748; PubMed=2394736;
RA Declerck N., Joyet P., Gallardin C., Maeson J.M.;
RT "Use of amber suppressors to investigate the thermostability of
RT Bacillus licheniformis alpha-amylase. Amino acid replacements at 6
RT histidine residues reveal a critical position at His-133.";
RL J. Biol. Chem. 265:15481-15486(1990).
RN [9]
RP MUTAGENESIS OF ALA-238.
RC STRAIN=ATCC 6598;
RX MEDLINE=96367070; PubMed=8771184;
RA Declerck N., Joyet P., Trosset J.Y., Garnier J., Gallardin C.;
RT "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:
RT multiple amino acid replacements and molecular modelling.";
RL Protein Eng. 8:1029-1037(1995).
RN [10]
RP MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
RP ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLU-300; GLN-359
RP AND GLU-365.
RC STRAIN=ATCC 6598;
RX MEDLINE=20425100; PubMed=10966804;
RA Declerck N., Machius M., Wiegand G., Huber R., Gallardin C.;
RT "Probing structural determinants specifying high thermostability in
RT Bacillus licheniformis alpha-amylase.";
RL J. Mol. Biol. 301:1041-1057(2000).
RN [11]
RP MUTAGENESIS OF GLN-293 AND ASN-294.
RC STRAIN=ATCC 6598;
RX MEDLINE=22622182; PubMed=12736372;
RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R.,
RA Gallardin C.;
RT "Hyperthermostabilization of Bacillus licheniformis alpha-amylase and
RT modulation of its stability over a 50 degrees C temperature range.";
RL Protein Eng. 16:287-293(2003).
RN [12]
RP MUTAGENESIS OF TRP-292 AND VAL-315.
RC STRAIN=ATCC 27811;
RX MEDLINE=22797417; PubMed=12915728;
RA Rivera M.H., Lopez-Munguia A., Soberon X., Saab-Rincon G.;
RT "Alpha-amylase from Bacillus licheniformis mutants near to the
RT catalytic site: effects on hydrolytic and transglycosylation
RT activity.";
RL Protein Eng. 16:505-514(2003).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RC STRAIN=ATCC 27811;
RX MEDLINE=95182462; PubMed=7877175;
RA Machius M., Wiegand G., Huber R.;
RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-
RT amylase at 2.2-A resolution.";
RL J. Mol. Biol. 246:545-559(1995).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=98212915; PubMed=9551551;
RA Machius M., Declerck N., Huber R., Wiegand G.;
RT "Activation of Bacillus licheniformis alpha-amylase through a
RT disorder-->order transition of the substrate-binding site mediated
RT by a calcium-sodium-calcium metal triad.";
RL Structure 6:281-292(1998).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 330-512.

RX MEDLINE=20384196; PubMed=10924103;
RA Brozowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,
RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
RT "Structural analysis of a chimeric bacterial alpha-amylase.
RT High-resolution analysis of native and ligand complexes.";
RL Biochemistry 39:9099-9107(2000).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT
RP H162V/N219F/A238V/Q293S/N294Y.
RC STRAIN=ATCC 6598;
RX MEDLINE=22538505; PubMed=12540849;
RA Machius M., Declerck N., Huber R., Wiegand G.;
RT "Kinetic stabilization of Bacillus licheniformis alpha-amylase through
RT introduction of hydrophobic residues at the surface.";
RL J. Biol. Chem. 278:11546-11553(2003).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- BIOTECHNOLOGY: Used in the food industry for high temperature
CC liquefaction of starch-containing mashes and in the detergent
CC industry to remove starch. Sold under the name termamyl by
CC Novozymes.
CC -1- MISCELLANEOUS: Able to work at relatively high (alkaline) pH
CC values (up to pH 11) and at high temperatures (up to 100 degrees
CC Celsius).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; X03236; CAA26981.1; -;
DR EMBL; M38570; AAA22226.1; -;
DR EMBL; M13256; AAA22240.1; -;
DR EMBL; K01984; AAA22193.1; -;
DR EMBL; AF438149; AA026743.1; -;
DR EMBL; M26412; AAA22237.1; -;
DR EMBL; A17930; CAA01355.1; -;
DR PIR; A91997; ALBSL.
DR PDB; 1BLI; 23-MAR-99.
DR PDB; 1BPL; 17-AUG-96.
DR PDB; 1E3X; 21-JUN-01.
DR PDB; 1E3Z; 24-JUN-03.
DR PDB; 1E40; 24-JUN-03.
DR PDB; 1E43; 21-JUN-01.
DR PDB; 1O80; 03-APR-03.
DR PDB; 1VUS; 12-MAR-97.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase_1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 512 ALPHA-AMYLASE.
FT ACT_SITE 260 260
FT ACT_SITE 264 264
FT ACT_SITE 357 357
FT METAL 133 133
FT METAL 190 190
FT METAL 210 210 CALCIUM 2 AND SODIUM.
FT METAL 212 212 CALCIUM 2 (VIA CARBONYL OXYGEN).
FT METAL 223 223 CALCIUM 2 AND SODIUM.
FT METAL 229 229 CALCIUM 1 AND SODIUM.
FT METAL 231 231 CALCIUM 2.
FT METAL 233 233 CALCIUM 2.

Query Match 99.3%; Score 2648; DB 1; Length 512;
 Best Local Similarity 99.2%; Pred. No. 9.5e-187;
 Matches 479; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ANLNGTLMQFEMWMPDQGMRLQNDASVLAHGGTAWTPAYKGTSGADVGYGAYD 60
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 DB 90 LYDGEFHQGTAVTKYGTGKELGSATKSLHSRDINYGVDVINHKGAADTEVTVEV 149
 QY 121 DPADRNVIAGEHLIKMTWHPFGSGSTYSDPFKMHWHFEDGTWDESRKLNRIYKFGK 180
 DB 150 DPADRNVIAGEHLIKMTWHPFGSGSTYSDPFKMHWHFEDGTWDESRKLNRIYKFGK 209
 QY 181 AMDWEVSNGENGYDYLWADIDYHPDVAARIKMGWYANELQDGFRLDAVGHKFSF 240
 DB 210 AMDWEVSNGENGYDYLWADIDYHPDVAARIKMGWYANELQDGFRLDAVGHKFSF 269
 QY 241 LRDVNVHREKTEGEMFTVAEYMONDGALENYLNTKTFNHSVDPVPLHYGFHAASVQGG 300
 DB 270 LRDVNVHREKTEGEMFTVAEYMONDGALENYLNTKTFNHSVDPVPLHYGFHAASVQGG 329
 QY 301 GYDMRKLNGTVSKHPLKSVTFVNDHDTOPQGSLESTVOTWPFPLAVALITRESGYPO 360
 DB 330 GYDMRKLNGTVSKHPLKSVTFVNDHDTOPQGSLESTVOTWPFPLAVALITRESGYPO 389
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 DB 390 VFYDVMYGTGKDSQREIPALGHKLEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSVA 449
 QY 421 NSGIALITDGPAGAKMTVGRONAGETWHDITGRSEPVYINSEGMGEFHVNGSVISY 480
 DB 450 NSGIALITDGPAGAKMTVGRONAGETWHDITGRSEPVYINSEGMGEFHVNGSVISY 509
 QY 481 VQR 483
 DB 510 VQR 512

RESULT 2
 ID AMY_BACAM STANDARD; PRT; 514 AA.
 AC P00692;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha-amyase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 glucanohydrolase).
 OS Bacillus amylioliquefaciens.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CX NCBI_TaxID=1390;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=IH;
 RX MEDLINE=83108808; PubMed=6185474;
 RA Takkinen K., Petersson R.F., Kalkkinnen N., Palva I., Soederlund H.,
 Kaasarijaenen L.;
 RT "Amino acid sequence of alpha-amyase from Bacillus amylioliquefaciens
 deduced from the nucleotide sequence of the cloned gene.";
 RL J. Biol. Chem. 258:1007-1013 (1983).
 RN [2]
 RP SEQUENCE OF 32-222.
 RX MEDLINE=80241725; PubMed=6156671;
 RA Chung H.S., Friedberg F.;
 RT "Sequence of the N-terminal half of Bacillus amylioliquefaciens alpha-
 amyase.";
 RL Biochem. J. 185:387-395 (1980).
 RN [3]
 RP SEQUENCE OF 1-96 FROM N.A.
 RX MEDLINE=82051296; PubMed=6170539;

RA Palva I., Petersson R.F., Kalkkinnen N., Lehtovaara P., Sarvas M.,
 Soederlund H., Takkinen K., Kaasarijaenen L.;
 RT "Nucleotide sequence of the promoter and NH2-terminal signal peptide
 region of the alpha-amyase gene from Bacillus amylioliquefaciens.";
 RL Gene 15:43-51 (1981).
 RN [4]
 RP SEQUENCE OF 1-39 FROM N.A.
 RX MEDLINE=88137952; PubMed=2830166;
 RA Ruohonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Karaenen S.;
 RT "Efficient secretion of Bacillus amylioliquefaciens alpha-amyase by
 its own signal peptide from Saccharomyces cerevisiae host cells.";
 RL Gene 59:161-170 (1987).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.
 RX MEDLINE=20384196; PubMed=10924103;
 RA Brozowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,
 Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
 RT "Structural analysis of a chimeric bacterial alpha-amyase.
 High-resolution analysis of native and ligand complexes.";
 RL Biochemistry 39:9099-9107 (2000).
 CC -1 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 linkages in oligosaccharides and polysaccharides.
 CC -1 COPFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
 CC -1 SUBUNIT: Monomer.
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 or send an email to license@ebi.ac.uk).
 CC
 CC EMBL: J01542; AAA22191.1; -
 CC EMBL: V00092; CAA23430.1; -
 CC EMBL: A20154; CAA01489.1; -
 CC EMBL: M18424; AAA22192.1; -
 CC PIR: A92389; ALBSN.
 CC PDB: 1E3X; 21-JUN-01.
 CC PDB: 1E3Z; 24-JUN-03.
 CC PDB: 1E40; 24-JUN-03.
 CC PDB: 1E43; 21-JUN-01.
 CC InterPro: IPR005589; Alp_amy1_cat_sub.
 CC InterPro: IPR006047; Alpha_amy1_cat.
 CC InterPro: IPR006046; Glyco_hydro_13.
 CC Pfam: PF00128; alpha-amyase; 1.
 CC PRINTS: PR00110; ALPHAMYLASE.
 CC SMART: SMO0642; Amy; 1.
 CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 KW Signal; 3D-structure.
 FT CHAIN 1 31
 FT ACT_SITE 32 514
 FT ACT_SITE 262 262
 FT ACT_SITE 292 292
 FT ACT_SITE 359 359
 FT METAL 133 133
 FT METAL 190 190
 FT METAL 212 212
 FT METAL 214 214
 FT METAL 225 225
 FT METAL 231 231
 FT METAL 233 233
 FT METAL 235 235
 FT METAL 266 266
 FT METAL 331 331
 FT METAL 438 438
 FT METAL 461 461
 FT CONFLICT 54 54
 FT CONFLICT 64 64
 FT CONFLICT 79 79
 FT CONFLICT 84 84

ALPHA-AMYLASE.
 BY SIMILARITY.
 CALCITUM 1.
 CALCITUM 2 AND SODIUM.
 CALCITUM 2 (VIA CARBOXYL OXYGEN).
 CALCITUM 2 AND SODIUM.
 CALCITUM 1 AND SODIUM.
 CALCITUM 1 AND SODIUM.
 CALCITUM 2.
 CALCITUM 2.
 CALCITUM 1 (VIA CARBOXYL OXYGEN).
 CALCITUM 3 (VIA CARBOXYL OXYGEN).
 CALCITUM 3 (BY SIMILARITY).
 CALCITUM 3 (BY SIMILARITY).
 L -> I (IN REF. 2).
 I -> L (IN REF. 2).
 S -> D (IN REF. 2).
 G -> S (IN REF. 2).

SQ SEQUENCE 514 AA; 58403 MW; 3DE6B3FB5CCDE7E CRC64;
 Query Match 81.9%; Score 2184; DB 1; Length 514;
 Best Local Similarity 80.3%; Pred. No. 9.8e-155;
 Matches 388; Conservative 44; Mismatches 49; Indels 2; Gaps 1;

QY 3 LNTLMQYFEWYMPNDGQHMRLQNDASAYLAHEGTTAWIPPAVKGSQADVGAADLY 62
 DB 32 VNGTLMQYFEWYMPNDGQHMRLQNDASAYLAHEGTTAWIPPAVKGSQADVGAADLY 91
 QY 63 DLGEFHOKGIVRTKYGKGELOSAIKSLHSRDINVGDVVNHKGADATEDVAVEYDP 122
 DB DLGEFHOKGIVRTKYGKGELOSAIKSLHSRDINVGDVVNHKGADATEDVAVEYDP 151
 QY 123 ADNRVVSSEHLIKAMTHFHPGSGSTYSDPKMWHFDGDMDSRKLNTYF--QCK 180
 DB 152 ANRQETSEYQIAWMDFFRPGKNTYSDPKMWHFDGDMDSRKLNTYF--QCK 211
 QY 181 AMDWEVSENGNVDYLYMADIDYDHPVAEIKRWGTYANELQJDFRDLAVGHKFSF 240
 DB 212 AMDWEVSENGNVDYLYMADIDYDHPVAEIKRWGTYANELQJDFRDLAVGHKFSF 271
 QY 241 LRDVNVHREKTKGEMFTVAEYQNDGALFNLYNKTNFHSVDVPLHYQFHAASQGG 300
 DB 272 LRDVNVHREKTKGEMFTVAEYQNDGALFNLYNKTNFHSVDVPLHYQFHAASQGG 331
 QY 301 GYDMRKLLNGTVKHPKLSYTPVNDHDTOPGSLSTVQWTFEPLAVALITRESGYPQ 360
 DB 332 GYDMRKLLNGTVKHPKLSYTPVNDHDTOPGSLSTVQWTFEPLAVALITRESGYPQ 391
 QY 361 VFYGDWYTKGDSQREIPALFKHTEPLIKAKQYAYAGQHDYFDHDI VGTREGDSVA 420
 DB 392 VFYGDWYTKGDSQREIPALFKHTEPLIKAKQYAYAGQHDYFDHDI VGTREGDSVA 451
 QY 421 NSGIALITDPGGAKXMYGRONAGETWMDITGNRSEPVYINSGEHPHNGGSYIY 480
 DB 452 KSGIALITDPGGAKXMYGRONAGETWMDITGNRSEPVYINSGEHPHNGGSYIY 511
 QY 481 VQR 483
 DB 512 VQR 514

RESULT 3
 AMT6_BACS7 STANDARD; PRT; 518 AA.
 ID AMT6_BACS7 STANDARD; PRT; 518 AA.
 AC P1957L;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Glucan 1,4-alpha-maltohexosidase precursor (EC 3.2.1.98) (G6-amyase)
 DE (Maltotetraose-producing amylase) (Exo-maltotetraohydrolase).
 OS Bacillus sp. (strain 707).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1416;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.
 RX MEDLINE=88162814; PubMed=3258152;
 RA Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
 RT "Nucleotide sequence of the maltotetraose-producing amylase gene from
 RT an alkaliphilic Bacillus sp. #707 and structural similarity to
 RT liquefying type alpha-amyases";
 RL Biochem. Biophys. Res. Commun. 151:25-31(1988).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
 CC in amyloseous polysaccharides so as to remove successive
 CC maltotetraose residues from the non-reducing chain ends.
 CC -1- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By
 CC similarity).
 CC -1- PATHWAY: Starch degradation.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL/MI8862; AAA2231.1; --
 DR PIR; A27705; A27705.
 DR HSP; P06278; 1Y0S.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amyase; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR SMART; SM00642; Amy; 1.
 DR KEGG; 04101; Glycosylase; Carbohydrate metabolism; Signal.
 FT SIGNAL 1 33
 FT CHAIN 34 518
 FT ACT_SITE 269 269
 FT ACT_SITE 273 273
 FT ACT_SITE 366 366
 FT METAL 139 139
 FT METAL 196 196
 FT METAL 219 219
 FT METAL 221 221
 FT METAL 232 232
 FT METAL 238 238
 FT METAL 240 240
 FT METAL 242 242
 FT METAL 273 273
 SQ SEQUENCE 518 AA; 59009 MW; 3A961E21612682C4 CRC64;
 Query Match 70.5%; Score 1879; DB 1; Length 518;
 Best Local Similarity 67.8%; Pred. No. 2.3e-130;
 Matches 329; Conservative 67; Mismatches 79; Indels 10; Gaps 4;

QY 4 NGTLMQYFEWYMPNDGQHMRLQNDASAYLAHEGTTAWIPPAVKGSQADVGAADLY 63
 DB 39 NGTLMQYFEWYMPNDGQHMRLQNDASAYLAHEGTTAWIPPAVKGSQADVGAADLY 98
 QY 64 DLGEFHOKGIVRTKYGKGELOSAIKSLHSRDINVGDVVNHKGADATEDVAVEYDP 123
 DB 99 DLGEFHOKGIVRTKYGKGELOSAIKSLHSRDINVGDVVNHKGADATEDVAVEYDP 158
 QY 124 DNRNVISGEHLIKAMTHFHPGSGSTYSDPKMWHFDGDMDSRKL-NRIYKFO--CK 180
 DB 159 DNRNVISGEHLIKAMTHFHPGSGSTYSDPKMWHFDGDMDSRKL-NRIYKFO--CK 218
 QY 181 AMDWEVSENGNVDYLYMADIDYDHPVAEIKRWGTYANELQJDFRDLAVGHKFSF 240
 DB 219 AMDWEVSENGNVDYLYMADIDYDHPVAEIKRWGTYANELQJDFRDLAVGHKFSF 278
 QY 241 LRDVNVHREKTKGEMFTVAEYQNDGALFNLYNKTNFHSVDVPLHYQFHAASQGG 300
 DB 279 LRDVNVHREKTKGEMFTVAEYQNDGALFNLYNKTNFHSVDVPLHYQFHAASQGG 338
 QY 301 GYDMRKLLNGTVKHPKLSYTPVNDHDTOPGSLSTVQWTFEPLAVALITRESGYPQ 360
 DB 339 GYDMRKLLNGTVKHPKLSYTPVNDHDTOPGSLSTVQWTFEPLAVALITRESGYPQ 398
 QY 361 VFYGDWYTKGDSQREIPALFKHTEPLIKAKQYAYAGQHDYFDHDI VGTREGDS 418
 DB 399 VFYGDWYTKGDSQREIPALFKHTEPLIKAKQYAYAGQHDYFDHDI VGTREGDS 453
 QY 419 VANSGLALITDPGGAKXMYGRONAGETWMDITGNRSEPVYINSGEHPHNGGSYIY 478
 DB 454 VANSGLALITDPGGAKXMYGRONAGETWMDITGNRSEPVYINSGEHPHNGGSYIY 513
 QY 479 IYVQR 483
 DB 512 IYVQR 514

Db 514 IWVWK 518

RESULT 4

AMY_BACST STANDARD; PRT; 549 AA.

AC P06279; Q45519; (Created)

DT 01-JAN-1998 (Rel. 06, Last sequence update)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Alpha-amy-lase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).

GN AMYS.

OS Bacillus stearothermophilus.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.

OX NCBI_TaxID=1422;

[1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.

RX MEDLINE=65234394; PubMed=3924897;

RA Nakajima R., Imanaka T., Alba S.;

RT "Nucleotide sequence of the Bacillus stearothermophilus alpha-amy-lase gene.";

RT active sites.";

RL J. Biochem. 98:95-103(1985).

[3]

RP SEQUENCE FROM N.A.

RC STRAIN=NZ-3;

RX MEDLINE=86195857; PubMed=3009417;

RA Gray G.L., Mainzer S.E., Rey M.W., Iamasa M.H., Kindle K.L., Carmona C., Reguadt C.;

RT "Structural genes encoding the thermophilic alpha-amy-lases of Bacillus stearothermophilus and Bacillus licheniformis.";

RL J. Bacteriol. 166:635-643(1986).

[4]

RP SEQUENCE FROM N.A.

RA Suominen I., Kari M., Lautamo J., Knowles J., Mantsaenla P.;

RT "Thermophilic alpha-amy-lase of Bacillus stearothermophilus: cloning, expression, and secretion by Escherichia coli.";

RL (in) Chaloupka J., Krumpal V. (eds.);

RL Extracellular enzymes of microorganisms, pp.129-137, Plenum Press, New York (1987).

[5]

RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.

RC STRAIN=NY-5;

RX MEDLINE=86059211; PubMed=2999073;

RA Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H., Ido T., Yamagata H., Ueda S.;

RT "Efficient synthesis and secretion of a thermophilic alpha-amy-lase by protein-producing Bacillus brevis 47 carrying the Bacillus stearothermophilus amy-lase gene.";

RL J. Bacteriol. 164:1182-1187(1985).

[6]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=21125602; PubMed=11226887;

RA Svud D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;

RT Crystal structure of Bacillus stearothermophilus alpha-amy-lase: possible factors determining the thermostability.";

RL J. Biochem. 129:461-468(2001).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.

CC -1- SUBUNIT: Monomer.

CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

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CC -----

DR EMBL; M11450; AAA2235.2; -

DR EMBL; X02769; CAA26547.1; -

DR EMBL; M57457; AAA2227.1; -

DR EMBL; M13255; AAA2224.1; -

DR PIR; A24436; A24436.

DR PIR; A91999; ALBSF.

DR PDB; 1HVX; 05-ANG-03.

DR InterPro; IPR006589; Alp_amy1_cat_sub.

DR InterPro; IPR006047; Alpha_amy1_cat.

DR InterPro; IPR006046; Glyco_hydro_13.

DR Pfam; PF00128; alpha-amy-lase; 1.

DR PRINTS; PR00110; ALPHAMYLASE.

DR SMART; SM00642; Amy; 1.

KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.

FT CHAIN 1 34

FT SIGNAL 35 549

FT ACT_SITE 268 268

FT ACT_SITE 272 272

FT ACT_SITE 365 365

FT METAL 139 139

FT METAL 196 196

FT METAL 218 218

FT METAL 220 220

FT METAL 231 231

FT METAL 237 237

FT METAL 238 238

FT METAL 239 239

FT METAL 272 272

FT METAL 337 337

FT METAL 339 339

FT METAL 440 440

FT METAL 441 441

FT METAL 464 464

FT CONFLICT 13 13

FT CONFLICT 19 19

FT CONFLICT 23 23

FT CONFLICT 31 31

FT CONFLICT 107 107

FT CONFLICT 167 167

FT CONFLICT 179 179

FT CONFLICT 251 251

FT CONFLICT 260 260

FT CONFLICT 284 284

FT CONFLICT 312 312

FT CONFLICT 338 338

FT CONFLICT 342 342

FT CONFLICT 346 346

FT CONFLICT 376 376

FT CONFLICT 526 527

FT CONFLICT 527 527

FT CONFLICT 535 535

FT CONFLICT 549 549

SEQUENCE 549 AA; 62670 MW; 3A2DD93A955E79D3 CRC64;

Query Match 66.6%; Score 1776.5; DB 1; Length 549;

Best Local Similarity 64.7%; Pred. No. 7.9e-123;

Matches 314; Conservative 66; Mismatches 100; Indels 5; Gaps 2;

Qy 1 ANLNGTLMQYFEWYMPNDGQWRLQNDLSAYLAHGTTAVWIPPAKYGTSGADVGAYD 60

Db 36 APFNGTMMQYFEWYLPDGLTMTKVNANLSSGLTALMLPAPAYGTSGSDVGAYD 95

Qy 61 LYDGEFHQGTGVTTKYTGELQSAIKSLHSRDINYGVDVINHGQADATEDVYAVEV 120

Db 96 LYDGEFHQGTGVTTKYTGELQSAIKSLHSRDINYGVDVINHGQADATEDVYAVEV 155

Qy	121	DBADNRVYSGHHLLKAMTHFHPGGSGYSDCKMKMYHFDGDMBESRLNLYKQ--	178
		156	NSDDNRQOEISGYQIQDAMTKFPFGKGNYSYSSKMYHFDGDGMESRLNLYKRG1
Qy	179	GKAMPMEVSENGENGYDYLWYADIDYHPVAAEIKKMGTYANELODGEFLDAVHKIF	238
		216	GKAMWEVDTEGNNDYLLMYADLDMDHPEVYELKSMGKRYVNTTNIIDGFLDAVHKIF
Qy	239	SFLRDVNVHREKTEKMEFTVAEYWMNDLGALENYLNKTNFNHSDVPDLPHYFOHASTQ	298
		276	SFFPDMLSDVRSQGTGKPLFTVGBYMSYDINKLHNYIMKNTNGTMSFLDAPLHNKFLYASKS
Qy	299	GGGYDMRKLLNGTVVYSKHELSYTFPDNDHTOPGGSLESTVQTFMFLPAYAFILITBESGY	358
		336	GGTFLMRITLMTNTLTKMDQPTLLAVTFVDNHDTEBGALOSWVDFMFLPAYAFILITBOBGY
Qy	359	POVFYGDWYGTGDSGOREIPALKHKEPLILKARKOYAGAOHYPFHNDIYVGTREGDS	418
		396	PCVFIFGDIYGT--POYNIPSLSKSIDPLILARRDYAIGTQHDYLDHSDILIGTRGCVTE
Qy	419	VANSGLAALITDGPGAKMYRGONAGEETHMDITGNREBPVIVINSEGMGEFHVNGSVS	478
		453	KPGSGLAALITDGPGSKMYVYVGKQAHGKVFYDLTGNRSDTYVINSDGMEFVNGGVS
Qy	479	IYVOR	483
		513	VWVPR

RESULT 5	AMY2	SALTY	STANDARD;	PRT;	494 AA.
ID	AMY2	SALTY	STANDARD;	PRT;	494 AA.
AC	P26613;				
DT	01-AUG-1992	(Rel. 23, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Cycloplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan				
DE	glucanohydrolase).				
GN	AMYA OR STM1963.				
OS	<i>Salmonella typhimurium</i> .				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OC	Enterobacteriaceae; <i>Salmonella</i> .				
OX	NCBI_TaxID=602;				
NP	[1]				
NP	SEQUENCE FROM N.A.				
RC	STRAIN=SGM1103;				
RC	MEDLINE=3015717; PubMed=1400215;				
RA	Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;				
RT	"Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";				
RL	J. Bacteriol. 171:6644-6652(1992).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=LT2 / SGSC1412 / ATCC 700720;				
RC	MEDLINE=21534948; PubMed=11677609;				
RA	McLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,				
RA	Courtney L., Potwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,				
RA	Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,				
RA	Ryan B., Sun H., Florea D., Miller W., Stoneking T., Nhan M.,				
RA	Waterston R., Wilson R.K.;				
RT	"Complete genome sequence of <i>Salmonella enterica</i> serovar <i>Typhimurium</i>				
RT	LT2".				
RL	Nature 413:852-856(2001).				
RN	[3]				
RP	SEQUENCE OF 1-6 FROM N.A.				
RC	STRAIN=SGM1103;				
RC	MEDLINE=92407478; PubMed=1527488;				
RA	Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;				
RT	"Subdivision of flagellar region III of the <i>Escherichia coli</i> and				
RT	<i>Salmonella typhimurium</i> chromosomes and identification of two				
RT	additional flagellar genes.";				
RL	J. Gen. Microbiol. 138:1051-1065(1992).				
RN	[4]				
RP	SEQUENCE OF 476-494 FROM N.A.				

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RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Khara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions iira and iirb, including a
RT large non-coding region."
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COPACATOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC -----
DR EMBL, L01643; AAA27110.1; -.
DR EMBL, AE00887; AAL20875.1; -.
DR EMBL, M85241; AAA27079.1; -.
DR EMBL, L13280; AAA71970.1; -.
DR PIR, B45738; B45738.
DR HSP, P06278; IV05.
DR StyGene; SG10011; amyA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR SMART; SM00642; Aamy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Complete proteome.
FT ACT_SITE 235 BY SIMILARITY.
FT ACT_SITE 265 BY SIMILARITY.
FT ACT_SITE 332 BY SIMILARITY.
FT METAL 104 CALCIUM (BY SIMILARITY).
FT METAL 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT CONFLICT 462 462 L -> S (IN REF. 1).
SQ SEQUENCE 494 AA; 56522 MW; 5C1B662FEFDD5B47C CMC64;

Query Match 39.7%; Score 1058; DB 1; Length 494;
Best Local Similarity 42.4%; Pred. No. 3.2e-70;
Matches 208; Conservative 87; Mismatches 180; Indels 16; Gaps 6;

4 NGTLQYEWYEMTPMDGQHWRLQDMSAYLAHGTAWIPPAKYGTSGA-DYVGANDLY 62
3 NPTLLQYFHWYYPGGGKLMSELABRADGLNDIGIMTWLPAPACGASGGYSGVDYDYL 62
63 DLGEFHQKGYRTKYGKGTGELQSAIKSLHSRDINWVGDVVNHKGADATEDYAVEYDP 122
63 DLGEFDQKGYRTATKYGKQGLLTALIDAKKNVIALVLDVNNHMGADKKRIRYQRYNQ 122
123 ADNRKVISGEHLIAWTHFHPPGSGSYSDPKWYHFDGTDMDSRKLRIYK----FQ 178
123 DDRKQIDNITIECGWTRRYTPPAPAGQSYNITWDYHCGSGIDHLENDEDEIFXIVNDYT 182
179 GKAMDWEYSNENGYDYLMADIDYDHDVDAELIKRNGTYANELQDDGFLLDAVKIKF 238
183 GDGNNDQYDDMDGPNFYDLMGENDIFRNHNAVTEELIKYARWMEQTHCDGFRLDVVKIPA 242
239 SFLDDVNVHAEKTKGKMEFTYAEKWDGLAEVLYLKTNNHNSVDFVPLHYQFHAASQ 298
243 WFYKEMIEHVAOVAPEKPLFVIAEYWSHSEVDKLTQTYIDQVDSKTMFLDPAFLQMKHESRQ 302
299 GGGYDMERKLNGTVASKHLKSYVFVNNDTOPQOSLESYQOTWFKPLAVALFITRESGY 358
303 GAEDYDMHIFGTIVLEADPPFAAVLVANHDQPLQALEAPVEPFFKPLAVALILIRENGV 362
359 POFYVGYMGYGT-----KEDSQS-ELPALKHKTEPLKARKQAYAYAGHDYPPHHDIV 410

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Db 363 PSVFPDLYGASVDSNGENGTCTVMDPVI-NQDLRLILARQRAHGIQTLFDPHPNCIA 421
Qy 411 WTRBGSSVANSGLAALITDGPAGAKMYVGRONAGETWDTGNRSEPVINSEKGEF 470
Db 422 FSRSGTBE--NPGCVVVLNSNDDEKTLTLLGDVANKTMDPFGNDRDEYVTVNDQGSATF 479
Qy 471 HVGGSVSIYV 481
Db 480 FCNAGSVSVWV 490

RESULT 6
AMT2_ECOLI STANDARD; PRT; 495 AA.
ID AMT2_ECOLI P26612; P78072;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AMYA OR B1927.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL1;
RX MEDLINE=93015717; PubMed=1400215;
RA Rana M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA";
RL J. Bacteriol. 174:6644-6652 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Zhao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474 (1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Maki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Saito N., Sampaio G., Seki Y., Sivasubraman S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horikuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map";
RL DNA Res. 3:379-392 (1996).
RN [4]
RP SEQUENCE OF 1-5 FROM N.A.
RC STRAIN=JAL1;
RX MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes";
RL J. Gen. Microbiol. 138:1051-1065 (1992).
RN [5]
RP SEQUENCE OF 475-495 FROM N.A.
RC STRAIN=JAL1;
RX MEDLINE=93381452; PubMed=8371104;
RA Rana M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIA and IIB, including a
RT large non-coding region";
RL J. Gen. Microbiol. 139:1401-1407 (1993).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; L01642; AAA23810.1; -.
DR EMBL; AEO00285; AAC74994.1; -.
DR EMBL; D90833; BAA15755.1; -.
DR EMBL; M85240; -; NOT_ANNOTATED_CDS.
DR EMBL; L13279; AAA82575.1; -.
DR PIR; D64956; A45738.
DR HSP; P06278; IVUS.
DR EcoGene; EG11387; amyA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KM Complete proteome.
FT ACT_SITE 235 235 BY SIMILARITY.
FT ACT_SITE 265 265 BY SIMILARITY.
FT ACT_SITE 332 332 BY SIMILARITY.
FT METAL 104 104 CALCIUM (BY SIMILARITY).
FT METAL 239 239 CALCIUM (VIA CARBOXYL OXYGEN) (BY
FT SIMILARITY).
FT CONFLICT 19 20 KL -> SS (IN REF. 1).
FT CONFLICT 109 109 A -> V (IN REF. 1).
FT CONFLICT 149 149 Q -> E (IN REF. 1).
FT CONFLICT 234 234 L -> I (IN REF. 1).
SQ SEQUENCE 495 AA; 56639 MW; 26AF6797DDA54D6 CRC64;
Query Match 39.3%; Score 1047; DB 1; Length 495;
Best local similarity 42.2%; Pred. NO. 2.1e-69;
Matches 208; Conservative 86; Mismatches 179; Indels 20; Gaps 8;
Qy 4 NGTLMQYFWMYMRNDQGMRLQNDASVLAHGTATVTPAYKTSQA-DVCGAARDLY 62
Db 3 NPTLLQCFHYTYPEGKGLWPELBRADGFNDIGINWMLPPAYKASGGYSGVDSYDLF 62
Qy 63 DLGFHDKGVTRPYGKGLQSAIKSLHSRDINVDVYINHGADATEDVTAVEVP 122
Db 63 DLGFHDKGVTRPYGKGLQSAIKSLHSRDINVDVYINHGADATEDVTAVEVP 122
Qy 63 DLGFHDKGVTRPYGKGLQSAIKSLHSRDINVDVYINHGADATEDVTAVEVP 122
Db 63 DLGFHDKGVTRPYGKGLQSAIKSLHSRDINVDVYINHGADATEDVTAVEVP 122
Qy 123 ADNRNRVSGEHLI-KAMTFHFGPGSTYSDFKMHVHFDGTDWDSRLNRYK---- 176
Db 123 DDRTOI--DEILIECBETRYTTPPARAGQYSQFIMDKCSGDIHINPDEGIFKLVND 180
Qy 177 FQKAMPWEVSNENGYDYLMDIDVDHPDVAEIRKGTWANEQLDGFRLDAVKHI 236
Db 181 YTGEGMDQVDDELGNPDYLMGENIDFRNHAVEREIKYRWARWMEQTCGGRFLDAVKHI 240
Qy 237 KESFLRQWNVHVEKQKEMFTVAEYQNDGLNENTLNFHNSVFDVPLHYQPHAS 296
Db 241 PAMFYKMIHVOQVAPKPLIVAEVSHEDKQTYIVDQEGKTMFLDAPLQKKEHAS 300
Qy 297 TQGGYDMRKLNGTVVSKPLKSVTFVDNHDTPQGSLESTVQWTKPRLAYAFILTRRS 356
Db 301 RMGRDYMGTQIFGLTLEADPFAHVTLVANHDTPQLQALAPVAPWPKPLAYALILREN 360
Qy 357 GYPOVYFGDMYGRK----GDSQR--EIPALKKIEPILKARQVAYGQHYFDHNDI 408
Db 361 GVPSVFPDLYGAYHEDVGDVGQGYTPIDMPIE-QDELILARQRAHGIQTLFDPHPNC 419

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Qy 409 VGMTEGDSVANSGLALITDPCGAKMYVRGONAGEWTMDITGNSEFPVINSQWG 468
Db 420 IAFERSGIDEF--PCGVVMSNGDGGDEKTHHNGYNGKTRDFLNGRQERVVDNGEA 477
Qy 469 EFHVNGSVSIVY 481
Db 478 TFCNGSGSVSYWV 490

RESULT 7
AMTB_PAPEO STANDARD; PRT; 1196 AA.
ID AMTB_PAPEO
AC P21543;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Beta/alpha-amyase precursor (includes: Beta-amyase (EC 3.2.1.2);
DE Alpha-amyase (EC 3.2.1.1)).
OS Paenibacillus polymyxa (Bacillus polymyxa).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxId=1406;

RN [1]
RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=87165765; PubMed=2435707;
RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,
RA Tsukagoshi N., Udaoka S.;
RT "Cloning and nucleotide sequence of the gene coding for enzymatically
RT active fragments of the Bacillus polymyxa beta-amyase.";
RL J. Bacteriol. 169:1564-1570(1987).
RN [2]
RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=89123046; PubMed=2464578;
RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
RA Tsukagoshi N., Udaoka S.;
RT "A single gene directs synthesis of a precursor protein with beta-
RT and alpha-amyase activities in Bacillus polymyxa.";
RL J. Bacteriol. 171:375-382(1989).
RN [3]
RP SEQUENCE OF 1-776 FROM N.A.
RC STRAIN=ATCC 8523;
RX MEDLINE=87231094; PubMed=2438660;
RA Rhodes C., Strasser J., Friedberg F.;
RT "Sequence of an active fragment of B. polymyxa beta amyase.";
RL Nucleic Acids Res. 15:3934-3934(1987).
RN [4]
RP DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.
RX MEDLINE=91215008; PubMed=1827035;
RA Uozumi N., Matsuda T., Tsukagoshi N., Udaoka S.;
RT "Structural and functional roles of cysteine residues of Bacillus
RT polymyxa beta-amyase.";
RL Biochemistry 30:4594-4599(1991).
CC -1- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
CC PRODUCE MULTIFORM BETA-AMYLASES AND A 48 kDa ALPHA-AMYLASE AFTER
CC SECRETION.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
CC polysaccharides so as to remove successive maltose units from the
CC non-reducing ends of the chains.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: In the N-terminal section; belongs to family 14 of
CC glycosyl hydrolases.
CC -1- SIMILARITY: In the C-terminal section; belongs to family 13 of
CC glycosyl hydrolases.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
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CC -----
CC EMBL; M15817; AA85446.1; -.
CC EMBL; Y00150; CA868344.1; -.
CC PIR; A29130; A29130.
CC HSSP; P36924; 1B92.
CC InterPro; IPR006589; Alp_ami1_cat_sub.
CC InterPro; IPR006048; Alpha_ami1_C.
CC InterPro; IPR006047; Alpha_ami1_cat.
CC InterPro; IPR005085; CBM_25.
CC InterPro; IPR006046; Glyco_hydro_13.
CC InterPro; IPR001554; Glyco_hydro_14.
CC Pfam; PF00128; alpha-amyase; 1.
CC Pfam; PF02806; alpha-amyase_C; 1.
CC Pfam; PF01373; Glyco_hydro_14; 1.
CC PRINTS; PR00110; ALPHAMYLASE.
CC SMART; SM00642; Amyy; 1.
CC SMART; SM00632; Amyy_C; 1.
CC PROSITE; PS00506; BETA_AMYLASE_1; 1.
CC PROSITE; PS00679; BETA_AMYLASE_2; 1.
CC Multicatalytic enzyme; Hydrolase; Glycosidase; Signal;
CC Polyaccharide degradation; Repeat.
CC SIGNAL 1 35
CC CHAIN 36 1196 BETA/ALPHA-AMYLASE.
CC DOMAIN 36 454 BETA-AMYLASE.
CC REPEAT 435 558
CC REPEAT 565 668
CC DOMAIN 669 1196
CC DISULFID 118 126
CC ACT_SITE 198 198
CC ACT_SITE 394 394
CC MOTIFAN 118 118
CC MOTIFAN 126 126
CC MOTIFAN 116 116
CC MOTIFAN 358 358
CC CONFLICT 1 1
CC CONFLICT 67 67
CC CONFLICT 100 100
CC CONFLICT 154 154
CC CONFLICT 177 177
CC CONFLICT 227 228
CC CONFLICT 330 330
CC CONFLICT 425 425
CC CONFLICT 493 493
CC CONFLICT 532 532
CC CONFLICT 559 559
CC CONFLICT 665 665
CC CONFLICT 681 681
CC CONFLICT 686 686
CC CONFLICT 725 728
CC CONFLICT 736 736
CC CONFLICT 741 741
CC CONFLICT 758 758
CC SEQUENCE 1196 AA; 130893 MW; A41BA6B70F257064 CRC64;

Query Match 12.8%; Score 340; DB 1; Length 1196;
Best Local Similarity 23.1%; Pred. No. 4,2e-17;
Matches 119; Conservative 64; Mismatches 175; Indels 158; Gaps 22;

Qy 12 EWMTPMDGQWRRLQNDASVLAHSGITAVIPRPAVYKTSQ-ADVCGAYDIVDLSGFHK 70
Db 779 KWH-----GGDFQGITINKLDYIKMGFTAWITPVTKSEYAVGHYDFY----- 826
Qy 71 GVTRTYGTGKGLQSAIKSLHSRDINVDVYINHGAGADATEDVAVVEVDADRNRVLS 130
Db 827 -ANDGLGTMDKQGLQELVRKAHDKNIAVMVDVNVNHGDPQ----- 865
Qy 131 GEHLIAMWTHFHPGSGSYSDF-KWNYWHPDGTMDSESRKLNRIYKFGQKAMDEVSNE 189
Db 866 -----PGNGFAKAPFDKADWYHHNGDITDGGYNSNN-----QWRI--E 901
Qy 190 NGWYDYLWADYDIDYDHPDAELIKRWGTYWYANBELQDGRLDVAVVHKIKFSFLRDWVNHVR 249

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Db      902 NG--DVAGLDLNNENPATANLKNWIKMLNKGIDGLRLDTYKHPKGFLLDF----- 954
Qy      250 EKTKEMFTVAEYQONLGLALNNTNFNSVFEDVLYHQFHAATOGGAGYDMRLT-- 307
Db      955 -DQANTFTNGEITFGHPAYVGT--TRYDALDLPMTYTT--KVFHGDSMRKIKD 1008
Qy      308 -----LNGTVVSKHPLKSVTFVDNHDTPQCSLESTVQTFKPLAVAFILTR 355
Db      1009 RYSDRRYRDAQNTGVFLIDNHDK--RFLNDASGKPPANDKMPQL--KALGFTLT-S 1062
Qy      356 SGTPQVFTGMYGTGDSQREIPALKKIEPILKARQVYAGQHYFDHHDVGMTR 415
Db      1063 RGPIIYQTEQSGSGDD--PA-----NRENMFNANHDLQYIAKLIVYRNN 1109
Qy      416 DSVANGSLAALITDGGGAKRMVYGRQNGETHD-----ITGRSEPVYINSGW- 467
Db      1110 HPALQN-----GSGR-----EKWVDSFYSFORSKNGDEALVFINSMN 1148
Qy      468 -----GEF-----HVGGSVSI 479
Db      1149 SQRRTGNFNLNGRTLTNLQNSDSVQINNGLTV 1164

RESULT 8
AMYA_VIGMU STANDARD; PRT; 421 AA.
AC P1785;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alpha-amyase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AMY1.1.
OS Vigna mungo (Rice bean) (black gram).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosides I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OC NCBI_TaxID=3915;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cotyledon;
RX MEDLINE=90332425; PubMed=2377468;
RA Yamauchi D., Minamikawa T.;
RL "Nucleotide sequence of cDNA for alpha-amyase from cotyledons of
RT germinating Vigna mungo seeds.";
RL Nucleic Acids Res. 18:4250-4250(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94120017; PubMed=8290640;
RA Takeuchi H., Yamauchi D., Wada S., Minamikawa T.;
RL "Nucleotide sequence of the alpha-amyase gene from Vigna mungo.";
RL Plant Physiol. 103:1459-1459(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
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CC -----
DR EMBL; X53049; CA37217.1; -
DR EMBL; X73301; CA31734.1; -
DR PIR; S10514; S10514.
DR HSSP; P04063; IAVA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alp_amy1_cat.

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DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAAMYLA.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal.
FT SIGNAL 1 23
FT CHAIN 24 421
FT ACT_SITE 201 201
FT ACT_SITE 309 309
FT METAL 113 113
FT METAL 130 130
FT METAL 133 133
FT METAL 135 135
FT METAL 139 139
FT METAL 149 149
FT METAL 160 160
FT METAL 168 168
FT METAL 170 170
SQ SEQUENCE 421 AA; 4688 MW; 15CA0DBA3DB4656 CRC64;
Query Match 11.7%; Score 311.5; DB 1; Length 421;
Best Local Similarity 27.2%; Pred. No. 1,4e-15;
Matches 126; Conservative 48; Mismatches 159; Indels 131; Gaps 22;
Qy 7 LMQPEWYMNDDQHRRLQNDASAYLAEGITVWIPPAVKGSQADVGAYDYLDTGE 66
Db 26 LFGFNWESSKKQGWYSLNLSIPDLNAGITWVLPSPQSVPPE--GLPGRLLD- 82
Qy 67 FHOQGVTRTKYGTGKELQSAIKSLHSRDINVDVIVNHKGADATEDVAVEDPADRN 126
Db 83 -----ASKYGSKNELKSLIAAFHEKGIKCLADIVINHR-----TAERKD----- 121
Qy 127 RVISGEHLIKAWTHFHPGSGSTYSDFKWHYHFDGT-----DWDSRKLNRITKFGCKA 181
Db 122 -----GRG-IYCIFFE-----GGTPDSRDQW-----GPS 143
Qy 182 W-----DWEVSENGENVYD-----YLMYADIDYDHPDVAIEIRKGTWYANELQDGFRLDAV 233
Db 144 FICRDTAAYSDGTGNDGSGEYDAAPDIDHLNPQVORESEMMNWLKTELGFQGRWDFV 203
Qy 234 KHIFSFILRDVNVNHNVEKTKEMFTVAEYV-----QNDLGLALNNTNFNSVFEDVLYHQFHAATOGGAGYDMRLT 278
Db 204 KGYAPSSISKIYM-----EGT-KRDPFAVEKMDKDSISYGDDGKPPNNQDSHRGALVWVBSAG 258
Qy 279 FNSHVPDVLHYGFPAASTVGAGYDMRLK--NGT--VSKHPLKSVTFVDNHDTPQ 333
Db 259 GAITAFDFTTKGILQAA-VQG-----ELWRLLDPNGKPPGMIGVKEPENAATFIDNHD- 310
Qy 334 SLSTVQVTFKPE-----LNAFILTRESGYPOVFGMYGTGKDSQREIPALKKIEPIL 388
Db 311 --GSTQRLMPFPDPDKWQGYAYILT-HPGTPSIFYDHFWM-----GLKEQIAKLK 358
Qy 389 KARKQVYAGQHYFDHHDVGMTRBGDSVANGSLAALITDGP 432
Db 359 SIR-----LNGINKSTYKYNASBDLYAAKDKIMKVIKGP 396

RESULT 9
AMJA_ORYSA STANDARD; PRT; 440 AA.
AC P27932;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amyase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-
glucan glucanohydrolase).
GN AMY1.2 OR AMY3A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzaceae; Oryza.

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CC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
 RX MEDLINE=91329692; PubMed=1714318;
 RA Sutcliffe T.D., Huang N., Lites J.C., Rodriguez R.L.;
 RT "Characterization of an alpha-amylase multigene cluster in rice.";
 RL Plant Mol. Biol. 16:579-591 (1991).
 CC -1- FUNCTION: Important for breakdown of endosperm starch during
 germination.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.
 CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
 CC in the aleurone cells under the control of the plant hormone
 CC gibberellic acid and in the developing grains at a low level.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 CC -----
 DR EMBL, X56336; CA39776.1; -.
 DR PIR, S14958; S14958.
 DR HSSP, P04063; IAVA.
 DR Gramene; P27932; -.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR SMART; SM00642; Amyy; 1.
 KW Carbohydrate metabolism; Hydrolyase; Glycosidase; Calcium-binding;
 KM Signal; Multigene family.
 FT SIGNAL 1 26
 FT CHAIN 27 440 ALPHA-AMYLASE ISOZYME 3A.
 FT ACT_SITE 207 207 BY SIMILARITY.
 FT ACT_SITE 315 315 BY SIMILARITY.
 FT METAL 119 119 CALCIUM 1 (BY SIMILARITY).
 FT METAL 145 145 CALCIUM 2 (BY SIMILARITY).
 FT METAL 155 155 CALCIUM 3 (BY SIMILARITY).
 FT METAL 166 166 CALCIUM 3 (BY SIMILARITY).
 FT METAL 169 169 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
 FT SIMILARITY).
 FT METAL 170 170 CALCIUM 1 (BY SIMILARITY).
 FT METAL 171 171 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
 FT SIMILARITY).
 FT METAL 174 174 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
 FT SIMILARITY).
 FT METAL 176 176 CALCIUM 1 AND 3 (BY SIMILARITY).
 SQ SEQUENCE 440 AA; 48872 MW; 5E9B78C29A81C2B CRC64;
 Query Match 11.4%; Score 304; DB 1; Length 440;
 Best Local Similarity 27.0%; Pred. No. 5.2e-15;
 Matches 115; Conservative 46; Mismatches 149; Indels 116; Gaps 19;
 QY 7 LMOYFEH-YMNDQHRRLONDSAYLAHNGITAVMIPRAYKGSQADVGYGAYDLYDLG 65
 DB 31 LFGGFNDQSWKQGGWVNMMLDQVGDJASAGVTHVWLPPTHVSPO--GMPGRSLVDLN 88
 QY 66 EFHQKGTVRTYKYGKGLQSAIKLSRDIVYGDVYVNHKGADAEDEVTAVAEVDADR 125
 DB 89 -----ASKYGRKALKSLIAFAHAKGICVADIVNRCADK----- 126
 QY 126 NRVISGHLIKAWTHFHPGSGSYSPFKMWHYFDG-----TDWDSRKLNIYKFGK 180
 DB 127 -----DGRG-VYCIYK-----GGPRGCLDWDGSMIC----- 152

QY 181 AMWVEVSENGN-----YDYIMADIDYDHPVAAEIKRWGTWYANELQDGFBLDAVKHI 236
 DB 153 CDDTQYSDGTGHNDTGADFAAPDIDHNLPLVOREISDWLRRLRDVGFGMLDPAKGY 212
 QY 237 KFSFLRDVWVHVEKTEKMEFTVAEYWONDG-----ALENYANKTFN 280
 DB 213 SAAVARTYVGNAPS-----FVVAETW-NSLSYDGGKPAANDGGRQBELVNVVKVCGP 266
 QY 281 HSYFDVPLHYQFHAASTGGGYDMKRLNGT---VSKAPLKVTFYDNDHTOPGOSLES 337
 DB 267 ATAFDFTTKGILQSA-VQGLWEMRD-KQKAKAGMIGWPEKAVTFVDNHTD-----GS 318
 QY 338 TVQWTFEP-----LAAYFLITRESGYQVYGMVGTGKSDGREIPALKHKIEPIILARK 392
 DB 319 TORWMPSPSKVILIGAYIYL-HPGVCFIYDQVFMN-----LKOENALATRK 368
 QY 393 QYAVGA 398
 DB 369 RINGNA 374
 RESULT 10
 AM3C ORYSA STANDARD; PRT; 437 AA.
 ID AM3C ORYSA
 AC P27932;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha-amylase isozyme 3C precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase).
 GN AMYL 7 OR AMY3B.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
 RX MEDLINE=91329692; PubMed=1714318;
 RA Sutcliffe T.D., Huang N., Lites J.C., Rodriguez R.L.;
 RT "Characterization of an alpha-amylase multigene cluster in rice.";
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 CC germination.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- TISSUE SPECIFICITY: Germinating seeds.
 CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
 CC in the aleurone cells under the control of the plant hormone
 CC gibberellic acid and in the developing grains at a low level.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, X56336; CA39776.1; -.
 DR PIR, S14956; S14956.
 DR HSSP, P04063; IAVA.
 DR Gramene; P27932; -.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.

DR SMART; SM00642; Aamy; 1.
 KM Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 KW Signal; Multigene family.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 437 ALPHA-AMYLASE ISOZYME 3C.
 FT ACT_SITE 205 205 BY SIMILARITY.
 FT ACT_SITE 313 313 BY SIMILARITY.
 FT METAL 117 117 CALCIUM 1 (BY SIMILARITY).
 FT METAL 134 134 CALCIUM 2 (BY SIMILARITY).
 FT METAL 137 137 CALCIUM 2 (BY SIMILARITY).
 FT METAL 139 139 CALCIUM 2 (BY SIMILARITY).
 FT METAL 143 143 CALCIUM 2 (BY SIMILARITY).
 FT METAL 153 153 CALCIUM 3 (BY SIMILARITY).
 FT METAL 164 164 CALCIUM 3 (BY SIMILARITY).
 FT METAL 167 167 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
 FT METAL 168 168 CALCIUM 1 (BY SIMILARITY).
 FT METAL 169 169 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
 FT METAL 172 172 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
 FT METAL 174 174 CALCIUM 1 AND 3 (BY SIMILARITY).
 FT SEQUENCE 437 AA; 48637 MW; B0304250B40CTAB8 CRC64;
 Query Match 11.3%; Score 300; DB 1; Length 437;
 Best Local Similarity 25.8%; Pred. No. 1e-14;
 Matches 109; Conservative 48; Mismatches 146; Indels 120; Gaps 16;
 QY 7 LMQYFWMYMPNDQGHWR-LONDSAYLAHEGITAVMIPPAKGTSGADVGYGAYDLYDG 65
 DB 29 LFQGFNFMESNMKQGWYFLLSHVDYLAATGVTHWMLPP-PSHSAVAPQGYMPGLYDLD 86
 QY 66 EFHOKGTRTKYTKGELQSAIKSLHSRDINVGDVVNHKGADADIEDYAVAVDPADR 125
 DB 87 -----ASKYGTGAELRSLIAFHSHSKICVADIVNH----- 118
 QY 126 NRVISGEHLIKAMTHFHPRGSTYSDPKMWHYPDG-----TDMPESRLKLNRYKQG 179
 DB 119 -----RCADYKDSRGTYICFEGSTPRSLDMDGDMTCSD----- 152
 QY 180 KAMPMEVSENENG-----YDLYMTADIDYDHPDVAEIKRWGTWYANLEQLDGFRLDAVKH 235
 DB 153 ---DTQVSNGRGHRDYGADFGAAPDIDHLNTRVGTSLSDMLNWKSDYGFQGMRLDFPKG 209
 QY 236 IKFSEFLRWVNVHVRKTKEMFTVAEYQN-----DGLALENYLANKTNEN 280
 DB 210 YSATVYAKTYVNT-----DPSFVVAEISNMRYDNGNRPWNODGDELTVMNAQAVGCP 264
 QY 281 HSVFDVPLHYGFHASVTOGGGYDMRKLNGT-----VVSXKPLKSYFVDNHDTPQPSL 335
 DB 265 ASADPFTTKGELQAA-VQG---ELWRMKDGNKAPGMGLPEKAVTFIDNHD----- 314
 QY 336 ESTVQWTFKP-----LAAVFLITRESGYPOVFGDMYGTGKDSOREIPALKHKEPILKA 390
 DB 315 GSTQNSMFPDPDKWQRYAYILT-HRVPICFIYDHVPMW-----LKGISTLAAY 364
 QY 391 RKQ 393
 DB 365 RSR 367
 RESULT 11
 CDGT_BACS8 STANDARD; PRT; 713 AA.
 ID CDGT_BACS8
 AC P17692;
 DT 01-AUG-1990 (Rel. 15, last sequence update)
 DT 01-AUG-1990 (Rel. 15, last sequence update)
 DT 10-OCT-2003 (Rel. 42, last annotation update)
 DE Cyclodextrin-glycosyltransferase precursor (EC 2.4.1.19)
 DE (Cyclodextrin-glycosyltransferase) (CGTase) (Raw-starch-digesting amy1ase).
 OS Bacillus sp. (strain B1018).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1417;
 RN [1].
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-47.
 RX MEDLINE=9014765; PubMed=1689153;
 RA Iktor P., Tsukagoshi N., Uekura S.;
 RT "Nucleotide sequence of the raw-starch-digesting amy1ase gene from Bacillus sp. B1018 and its strong homology to the cyclodextrin RT glucanotransferase genes.";
 RL Biochem. Biophys. Res. Commun. 166:630-636(1990).
 CC -1- FUNCTION: This endo-type adsorbable amy1ase is capable to digest raw starch.
 CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation of a 1,4-alpha-D-glucosidic bond.
 CC -1- COFACTOR: Binds 2 calcium ions per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 CC -----
 DR EMBL; M33302; AAA22329.1; -;
 DR EMBL; D90112; BAA14140.1; -;
 DR PIR; S09196; S09196.
 DR HSSP; P43379; ICDG.
 DR InterPro; IPR006589; Alp_amy1_cat_sub.
 DR InterPro; IPR006048; Alpha_amy1_C.
 DR InterPro; IPR006047; Alpha_amy1_cat.
 DR InterPro; IPR002044; CBD_4.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR InterPro; IPR007110; Ig-Ilike.
 DR InterPro; IPR002909; IPT_TIG.
 DR Pfam; PF00128; alpha-amy1ase; 1.
 DR Pfam; PF02806; alpha-amy1ase_C; 1.
 DR Pfam; PF00686; CBM_20; 1.
 DR Pfam; PF01833; TIG; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR PRODOM; PD001568; CBD_4; 1.
 DR SMART; SM00642; Aamy; 1.
 DR SMART; SM00632; Aamy; C; 1.
 KM Transferase; Glycosyltransferase; Calcium-binding; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 713 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
 FT ACT_SITE 256 256 BY SIMILARITY.
 FT ACT_SITE 284 284 BY SIMILARITY.
 FT ACT_SITE 355 355 BY SIMILARITY.
 FT METAL 54 54 CALCIUM 1 (BY SIMILARITY).
 FT METAL 56 56 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
 FT METAL 59 59 CALCIUM 1 (BY SIMILARITY).
 FT METAL 60 60 CALCIUM 1 (BY SIMILARITY).
 FT METAL 80 80 CALCIUM 1 (BY SIMILARITY).
 FT METAL 166 166 CALCIUM 2 (BY SIMILARITY).
 FT METAL 217 217 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
 FT METAL 226 226 CALCIUM 2 (BY SIMILARITY).
 FT METAL 260 260 CALCIUM 2 (VIA CARBONYL OXYGEN) (BY SIMILARITY).
 FT SEQUENCE 713 AA; 77420 MW; 85FB616DA687B888 CRC64;
 Query Match 11.2%; Score 298; DB 1; Length 713;
 Best Local Similarity 23.8%; Pred. No. 2.6e-14;
 Matches 113; Conservative 86; Mismatches 175; Indels 100; Gaps 20;
 QY 19 GQMRRLQN--DSAYLAHEGITAVMIPP-----AYKGTSGADVGYGAYDLYDGFHOKGT 72
 DB 78 GSDWQGIINKINGQYTLGKMGVTAIWISQPVENIYSINVGWNTAAGHWARDPKK--- 134
 QY 73 VRTKYGKGELOSAIKSLHSRDINVGDVVNHKGADADIEDYAVAVDPADRNRVSGE 132

Db 135 TNPAYGTADPQNIIAAHAKIKIYIDFAPNH-----TSPASDOPSFAMENGLYDNG 188
 Qy 133 HLIAAMTHFHHFGHSTYSDSKMWHYHDPDMDQESRKLNIYFQGGAKMWEVSNENGN 192
 Db 189 TLLGGYT-----NDTQNI.FHNHGGTDFP-----TTENG 217
 Qy 193 YDYMTYADIDYDHPDVAE-----IKRWGTYANIELQDGFRLDAVHIFKSEFLRDPVN 246
 Db 218 YKNI-YLDADLNHNNSISDYVLKDAIKW-----LDLGDIDIRDAVHMFQGGKSMMA 271
 Qy 247 HVREKTEKEMFTVAEY--QNDLQALENYLKNTPNHSVDPVPLHYQFHAATQ----- 298
 Db 272 AVNNY--KPVTFPEMFELGVNEVG-ENHFKANESGMSILD-----FPFAQVRQVFRDNT 324
 Qy 299 GCGDMKRLNGTVVSKHPL-KSVTFVNDHTDQGGQSLSEVQVQWFKPLAFLITSESG 357
 Db 325 DNMYGLKAMEGSAADVAQVDQVTFIDNHMERFPHASNARRLQALAFLLILAR--- 381
 Qy 358 YPOVFYGG-DWY---GTYKGSQREIIPALK-----HKIRPILKARKQVAYGAQHDYFD 404
 Db 382 VPALYYGTEQYMSGTDPDNARIPSPSTTAYQVLOKLAFLKSNPAIAYSGSTQERMT 441
 Qy 405 HHDIWGTREGDSV-----ANSGLAALITDGPQAKMYVGGQNAGET 448
 Db 442 NNDVLIYERKFGSNVAVVAVNRNLNAPASISGLVTSIPQSGYNDVLGGLNGNT 495
 RESULT 12
 CDGT_BACSO STANDARD; PRT; 713 AA.
 ID CDGT_BACSO STANDARD; PRT; 713 AA.
 AC P05618;
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-NOV-1988 (Rel. 09, Last annotation update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cyclomaltoedextrin glucanotransferase precursor (EC 2.4.1.19)
 DE (Cyclodextrin-glycosyltransferase) (CGTase).
 GN CGT.
 OS Bacillus sp. (strain 1011).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1410;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=87308036; PubMed=2957361;
 RA Kimura K., Kataoka S., Ishii Y., Takano T., Yamane K.;
 RT "Nucleotide sequence of the beta-cyclodextrin glucanotransferase gene
 of alkalophilic Bacillus sp. strain 1011 and similarity of its amino
 acid sequence to those of alpha-amylases.";
 RT J. Bacteriol. 169:4399-4402(1987).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RA Harata K., Haga K., Nakamura A., Aoyagi M., Yamane K.;
 RT "X-ray structure of cyclodextrin glucanotransferase from alkalophilic
 Bacillus Sp. 1011. Comparison of two independent molecules at 1.8-A
 resolution.";
 RT Acta Crystallogr. D 52:1136-1145(1996).
 CC -i- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
 of a 1,4-alpha-D-glucosidic bond.
 CC -i- COFACTOR: Binds 2 calcium ions per subunit.
 CC -i- SUBUNIT: Monomer.
 CC -i- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
 IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
 IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
 ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
 ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
 MALTOLOGOSACCHARIDE PRODUCED.
 CC -i- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 Db EMBL; M17366; AA22308.1; -.
 DR PIR; A26678; ALBSG1.
 DR PDB; 1D7F; 17-MAR-00.
 DR PDB; 1DED; 07-APR-00.
 DR PDB; 1I75; 11-APR-01.
 DR PDB; 1PAM; 11-JAN-97.
 DR InterPro; IPR006589; Alp_ami_cat_sub.
 DR InterPro; IPR006048; Alpha_ami1_C.
 DR InterPro; IPR006047; Alpha_ami1_cat.
 DR InterPro; IPR006046; Glyco_hydro_13.
 DR InterPro; IPR007110; Ig-1ike.
 DR InterPro; IPR002909; IPT_TIG.
 DR Pfam; PF00128; alpha-amy1ase; 1.
 DR Pfam; PF02806; alpha-amy1ase_C; 1.
 DR Pfam; PF01833; TIG; 1.
 DR Pfam; PF01833; TIG; 1.
 DR PRINTS; PR00110; ALPHAMYLASE.
 DR PRODOM; PD001568; CBD_4; 1.
 DR SMART; SM00642; Amy; 1.
 DR SMART; SM00632; Amy_C; 1.
 DR Transferase; Glycosyltransferase; Calcium-binding; Signal;
 KW 3D-structure.
 FT SIGNAL 1 27
 FT CHAIN 28 713 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
 FT DOMAIN 28 165 A1.
 FT DOMAIN 166 229 B.
 FT DOMAIN 230 433 A2.
 FT DOMAIN 434 522 C.
 FT DOMAIN 523 609 D.
 FT DOMAIN 610 713 E.
 FT ACT_SITE 256 256
 FT ACT_SITE 284 284
 FT ACT_SITE 355 355
 FT METAL 54 54 CALCIUM 1. (VIA CARBONYL OXYGEN).
 FT METAL 55 55 CALCIUM 1.
 FT METAL 59 59 CALCIUM 1.
 FT METAL 60 60 CALCIUM 1.
 FT METAL 80 80 CALCIUM 1.
 FT METAL 166 166 CALCIUM 2. (VIA CARBONYL OXYGEN).
 FT METAL 217 217 CALCIUM 2. (VIA CARBONYL OXYGEN).
 FT METAL 226 226 CALCIUM 2.
 FT METAL 260 260 CALCIUM 2 (VIA CARBONYL OXYGEN).
 FT DISULFID 70 77
 FT TURN 30 31
 FT TURN 33 34
 FT TURN 33 34
 FT TURN 40 41
 FT STRAND 44 46
 FT TURN 49 51
 FT HELIX 52 52
 FT TURN 57 59
 FT HELIX 63 65
 FT STRAND 66 66
 FT TURN 68 69
 FT TURN 73 74
 FT STRAND 76 76
 FT HELIX 81 89
 FT TURN 90 93
 FT HELIX 94 96
 FT TURN 97 97
 FT STRAND 100 103
 FT STRAND 107 109
 FT STRAND 114 116
 FT TURN 117 118
 FT TURN 119 121
 FT STRAND 124 125
 FT STRAND 129 135
 FT TURN 137 139
 FT HELIX 142 154
 FT TURN 155 156

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FT STRAND 158 163
FT TURN 165 166
FT STRAND 167 170
FT TURN 176 177
FT TURN 179 182
FT STRAND 184 186
FT TURN 187 188
FT STRAND 189 192
FT TURN 195 196
FT TURN 198 199
FT STRAND 202 202
FT STRAND 207 207
FT HELIX 213 218
FT STRAND 220 220
FT TURN 222 223
FT STRAND 224 227
FT TURN 229 230
FT HELIX 232 247
FT TURN 248 249
FT STRAND 252 255
FT TURN 256 257
FT HELIX 258 260
FT HELIX 263 276
FT STRAND 280 283
FT TURN 289 290
FT HELIX 294 302
FT STRAND 306 308
FT HELIX 310 320
FT TURN 321 322
FT HELIX 327 340
FT TURN 342 343
FT HELIX 344 346
FT STRAND 348 349
FT TURN 354 355
FT TURN 362 363
FT HELIX 366 378
FT STRAND 382 386
FT TURN 387 388
FT HELIX 389 391
FT TURN 392 392
FT TURN 398 399
FT HELIX 400 402
FT HELIX 413 421
FT TURN 422 423
FT HELIX 424 427
FT STRAND 429 433
FT STRAND 435 441
FT TURN 445 454
FT STRAND 455 462
FT STRAND 469 471
FT STRAND 475 475
FT STRAND 481 483
FT TURN 486 491
FT STRAND 496 498
FT HELIX 500 502
FT STRAND 503 504
FT STRAND 507 509
FT TURN 511 512
FT STRAND 514 519
FT STRAND 527 532
FT STRAND 535 536
FT TURN 538 539
FT STRAND 541 547
FT STRAND 555 558
FT TURN 559 560
FT STRAND 561 563
FT HELIX 565 567
FT STRAND 568 571
FT STRAND 575 579
FT STRAND 586 593
FT TURN 595 596
FT STRAND 599 599

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FT STRAND 603 608
FT STRAND 613 621
FT TURN 627 628
FT STRAND 630 635
FT STRAND 638 640
FT HELIX 641 643
FT TURN 645 647
FT STRAND 649 649
FT STRAND 653 653
FT TURN 660 661
FT STRAND 663 670

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Query Match 11.0%; Score 294; DB 1; Length 713;

Best Local Similarity 23.0%; Pred. No. 5.2e-14; Matches 127; Conservative 89; Mismatches 173; Indels 164; Gaps 29;

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QY 19 GQHRRLLQ--DSAYLAHGGITAWIIP--AYKGTSGADVGYGAYDLVDSGFHOKGT 72
DB 78 GGDWGGIINKINDGYLGMGITAISQPVENIYSVINSGVNNTAHYGWARDFPK-- 134
QY 73 VRTKYGTEGLOSAISLSHRDINVGDVVINKSGADATEDVAVEVP--ADRNVIS 130
DB 135 TNPAYGTMDPKULIDPAHANIKVILIDFAPNHTSPASSD-----DSFANGELVYD 186
QY 131 GEHLIKAMTHFFHFGSGSTYSDFKMWYHFDGTDWDSRKLRIYKFGKAMPWEYSNEN 190
DB 187 NGNLLGGYT-----NDTONLFHHYGTDFS-----TIEN 215
QY 191 GNYDYIM-VADIDYDHDVAA---EIKRWGTVANELQDGRFLDAVKIKSFLEDMV 245
DB 216 GIYKNLYDLADLNHNNSVDVYLKDAIKMW-----LDLGVGIRVDVKHMPFGMOKSFM 270
QY 246 NHVREKTKEMFTVAEYWDNLGALF-----NYLNTKTNHNSVFDVPLHYGFHASTO- 298
DB 271 ATINNY--KPVFTGEWF--LGVNESPEYHOFANSGMS-----LDPRFAQKARQV 319
QY 299 -----GGYDMRKLLNGTVVSKHPLK-SYTFVDNHD-----TOPG--QSLESTVQWFKP 345
DB 320 FRDNTDMYGLKAMLESSEVDYAQVNDQVTFINHDHERFHTSGDRKLEQ----- 371
QY 346 LAYAFILTRSGYPQVFG--DMY---GTKGDSQREIPALK-----HKIEPILKARK 392
DB 372 -ALAFITLT-SRGVPAIYVGGSEQWMSGNDPDNRARLPSTTTAYVIOKLAFLRKNP 429
QY 393 QYAYGAQHDYFDHHDIVGWTREBGSVA-----NSGLAA 426
DB 430 AIAVGSHTHERWINDVILYERKFGNNVAVVAINRNMTPASITGLVTSLRASINDVLGG 489
QY 427 L-----ITDPPGAKRMVYGRQNAGETWH-----DITGN---RSEP---VVINSEGW 467
DB 490 ILANGTILTVGAGGAASFTLAPGTAVQYTTDATTTIIGNVGPMMAKPGVTITIDGRGF 549
QY 468 GEFHNGSVSIV 480
DB 550 G-----SGKGTIV 557

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RESULT 13

AMY3 WHEAT

ID AMY3 WHEAT STANDARD; PRT; 413 AA.

AC P08117;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-AUG-1988 (Rel. 08, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Alpha-amylase AMY3 precursor (EC 3.2.1.1) (1,4-alpha-D-glucan

glucanohydrolase).

GN AMY1.1 OR ALPHA-AMY3.

OS Triticum aestivum (Wheat).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;

OC Triticaceae; Triticum.

OX NCBI_Taxid=4565;

RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=cv. Chinese Spring;
RA Baulcombe D.C., Huttly A.K., Martienssen R.A., Barker R.F.,
RT Jarvis M.G.;
RL "A novel wheat alpha-amylase gene (alpha-Amy3).";
RM Mol. Gen. Genet. 209:33-40(1987).
CC -1- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurone cells under the control of the plant hormone
CC gibberellin acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC or send an email to license@isb-sib.ch).
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DR EMBL; X05809; CAA29252.1; -.
DR EMBL; M16991; AAA34259.1; -.
DR PIR; S06357; ALMT3.
DR HSSP; P04063; 1AIV.
DR InterPro; IPR006589; A1p_amyl_cat_sub.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KM Germination; Carbohydrate metabolism; Hydrolase; Glycosidase; Seed;
KM Calcium-binding; Signal; Multicene family.
FT SIGNAL 1 24
FT CHAIN 25 413
FT ACT SITE 203 203
FT METAL 115 115
FT METAL 132 132
FT METAL 135 135
FT METAL 137 137
FT METAL 141 141
FT METAL 151 151
FT METAL 162 162
FT METAL 167 167
FT METAL 170 170
FT METAL 172 172
SQ SEQUENCE 413 AA; 172 MM; C262RCALC54FCG4 CRC64;
Query Match 11.0%; Score 292.5; DB 1; Length 413;
Best Local Similarity 25.7%; Pred. No. 3,4e-14;
Matches 121; Conservative 56; Mismatches 155; Indels 139; Gaps 22;

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QY 237 KESFLRDVNVHVAHEKTKEMFVAEYQNDLGALENYLNTKTNPHNSVDPVPLHYQFHAAS 296
DB 209 SAAMAKTYVDN-----SKPAFVVGELYDRDRLQLLAVWVRGVGPATAPDPYTGVLQEA- 262
QY 297 TOGGGGYDMRLKLNGT-----VSKHPLKSVTFVNDHDTQPGQSLBSTVQTFWFR-----L 346
DB 263 VQG---DLGMRSDGKAPGMIGMPEKTYTFIDNNDT-----GSTQRLMPFSPDKWQ 313
QY 347 AYAFILTBESGYQVRYGDMYTGKDSQREIPLV-----KHKIEP-----ILKARQYAV 396
DB 314 GYAVIIL-HPGICPIFYDHFVWK--LKQETLALATVRSNCHIPGSTLDILKA----- 364
QY 397 GAGHDYDHHDIYQWTRREGSSVANSGLAALIDGPGKAKWVYGQNGE 447
DB 365 -----EGDLVYAKIGKVTYKIG-----SKYINIGD 389

RESULT 14
CDGT_BACCI
ID_CDGT_BACCI STANDARD; PRT; 718 AA.
AC P30920;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomalodextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclomalodextrin-glycosyltransferase) (CGTase).
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8;
RA MEDLINE=91103970; PubMed=1368573;
RX Nitschke L., Heeger K., Bender H., Schulz G.E.;
RT "Molecular cloning, nucleotide sequence and expression in Escherichia
RT coli of the beta-cyclodextrin glycosyltransferase gene from Bacillus
RT circulans strain no. 8.";
RL Appl. Microbiol. Biotechnol. 33:542-546(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE=91171298; PubMed=1826034;
RA Klein C., Schulz G.E.;
RT "Structure of cyclodextrin glycosyltransferase refined at 2.0-A
RT resolution.";
RL J. Mol. Biol. 217:737-750(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (3.4 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE=90064533; PubMed=2531228;
RA Hofmann B.E., Bender H., Schulz G.E.;
RT "Three-dimensional structure of cyclodextrin glycosyltransferase from
RT Bacillus circulans at 3.4-A resolution.";
RL J. Mol. Biol. 209:793-800(1989).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE=98226626; PubMed=9558324;
RA Schmidt A.K., Cottaz S., Driguez H., Schulz G.E.;
RT "Structure of cyclodextrin glycosyltransferase complexed with a
RT derivative of its main product beta-cyclodextrin.";
RL Biochemistry 37:5909-5915(1998).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RC STRAIN=8;
RX MEDLINE=98409292; PubMed=9738912;
RA Paregla G., Schmidt A.K., Schulz G.E.;
RT "Substrate binding to a cyclodextrin glycosyltransferase and
RT mutations increasing the gamma-cyclodextrin production.";
RL Eur. J. Biochem. 255:710-717(1998).
CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
CC of a 1,4-alpha-D-glucosidic bond.

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```

FT      TURN      493      498

Query Match      11.0%; Score 292; DB 1; Length 718;
Best Local Similarity 23.6%; Pred. No. 7.3e-14;
Matches 110; Conservative 82; Mismatches 163; Indels 112; Gaps 21;

QY 19 GQHWRLON--DSAVLAHGITAAMIIPA-----YKG-TSQADVGYGYLDYDGE 66
DB 85 GGDWGLINKINDNFSDGLVLTALMISQPVENIFATINYSVTWTAHYGVARDPKKTNP 144
QY 67 FHQKGTVTKYGTKEGLOSAIKLSHRDINYGVDVINHKSGADATEDVTAVEVDP--AD 124
DB 145 Y-----FGTMADFQNLITTAHAKGIKIVIDFAPNHTS-----PAMETDTSFAE 187
QY 125 RNRVYSGEHLIAKMTWHFHPGSGSYSPDKMWHYFDTGWDDESKLRIRYKFGQKAMDW 184
DB 188 NGRLYDNGTLVGGYT-----NDTNGYFHHNGSDFS----- 218
QY 185 EVSNENGVYDYLMYADIDYHPDVAAE-----IKRWGTWYANELQDGFRLDAVKHIF 238
DB 219 --SLENGYYKNL-YDLADFNHNNATIDKYFKDAIKLM-----LDMGVDGIRVDAYKAMPL 270
QY 239 SFLRDVWNVHREKTEGKEMFTVAEYQNDLGALENYLNKTNFNSHVPVPLHYQFHAA--- 295
DB 271 GMDKSWMSI--YVAKPVFTFGEWF---LGSAAADADNTDPAFKSGMSLDFRNSAVRN 325
QY 296 ---STGGGVYMRKLLNGTGVVSKHPLK-SYTFVNNHDTQPGQSLSESTYQWFKPLAFAFI 351
DB 326 VFRDNTSNMTALDSMINSTATDYVQNDQVTFIDNHMDRPKT--SAVNNRRLQALAFI 383
QY 352 LTRBSGYPOVYFG-DMYGTGK---DSOREIPALK-----HKIPILKARKQAYGA 398
DB 384 LT-SRGVPATYYGTEQVLTNGDPDNRAKPSFSKTTAENVISKAPLRKSNALAYGS 442
QY 399 QHDFDHDYGVMTREBDSVA-----NSGLALITDGGGA 435
DB 443 TOGRMINNDVYVERKFKGSVAVAVNRNLSTASITGLSTLPTGS 489

RESULT 15
CDGT_BACSS
ID CDGT_BACSS STANDARD; PRT; 718 AA.
AC P31747;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cyclomalto-dextrin glucanotransferase precursor (EC 2.4.1.19)
DE (Cyclodextrin-glycosyltransferase) (CGTase).
GN CGT.
OS Bacillus sp. (strain 6.6.3).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxId=29335;
RN [1]
RP SEQUENCE FROM N.A.
RA Ahmetzjanov A.A.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Degrades starch to cyclodextrins by formation
of a 1,4-alpha-D-glucosidic bond.
CC -1- COFACTOR: Binds 2 calcium ions per subunit (by similarity).
CC -1- SUBUNIT: Monomer.
CC -1- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
MALTOOLIGOSACCHARIDE PRODUCED.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X66106; CAA46901.1; -.
DR PIR; S21532; ALBSG6.
DR HSSP; P30920; 1CGT.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006048; Alpha_amy1_c.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR007110; 1g-1ike.
DR InterPro; IPR002909; IPT_TIG.
DR Pfam; PR00128; alpha-amy1ase; 1.
DR Pfam; PF02806; alpha-amy1ase_C; 1.
DR Pfam; PF00686; CBW_20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PR00110; ALPHAMYLIASE.
DR ProDom; PD001568; CBD_4; 1.
DR SMART; SM00642; Amyy_1.
DR SMART; SM00632; Amyy_C; 1.
KW transferase; Glycosyltransferase; Calcium-binding; signal.
KW SIGNAL 1 34
FT CHAIN 35 718
FT DOMAIN 35 172
FT DOMAIN 173 236
FT DOMAIN 237 440
FT DOMAIN 441 528
FT DOMAIN 529 614
FT DOMAIN 615 718
FT ACT_SITE 263 263
FT ACT_SITE 291 291
FT ACT_SITE 362 362
FT METAL 61 61
FT METAL 63 63
FT METAL 66 66
FT METAL 67 67
FT METAL 85 85
FT METAL 87 87
FT METAL 173 173
FT METAL 224 224
FT METAL 233 233
FT METAL 267 267
FT DISULFID 77 84
SQ SEQUENCE 718 AA; 78014 MW; 7644096D402707E5 CRC64;

Query Match      10.9%; Score 291.5; DB 1; Length 718;
Best Local Similarity 23.0%; Pred. No. 8e-14;
Matches 118; Conservative 91; Mismatches 180; Indels 123; Gaps 24;

QY 19 GQHWRLON--DSAVLAHGITAAMIIPA-----YKG-TSQADVGYGYLDYDGE 66
DB 85 GGDWGLINKINDNFSDGLVLTALMISQPVENIFATINYSVTWTAHYGVARDPKKTNP 144
QY 67 FHQKGTVTKYGTKEGLOSAIKLSHRDINYGVDVINHKSGADATEDVTAVEVDP--AD 124
DB 145 Y-----FGTMADFQNLITTAHAKGIKIVIDFAPNHTS-----PAMETDTSFAE 187
QY 125 RNRVYSGEHLIAKMTWHFHPGSGSYSPDKMWHYFDTGWDDESKLRIRYKFGQKAMDW 184
DB 188 NGRLYDNGTLVGGYT-----NDTNGYFHHNGSDFS----- 218
QY 185 EVSNENGVYDYLMYADIDYHPDVAAE-----IKRWGTWYANELQDGFRLDAVKHIF 238
DB 219 --SLENGYYKNL-YDLADFNHNNATIDKYFKDAIKLM-----LDMGVDGIRVDAYKAMPL 270
QY 239 SFLRDVWNVHREKTEGKEMFTVAEYQNDLGALENYLNKTNFNSHVPVPLHYQFHAA--- 295
DB 271 GMDKSWMSI--YVAKPVFTFGEWF---LGSAAADADNTDPAFKSGMSLDFRNSAVRN 325

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QY 296 ---STGGGYDMRKLNGTVVSKHPLK-SYTFVNDHDTQGSLESTVQTFKPLAVAFI 351
Db 326 VFRDNTSNMYALDSMINSTATDYNOVDQYTFIDNHMDRFKT--SAVNNRRLEQALAFI 383
QY 352 LTRSEGYPOVFG--DMYGTG---DSQREIPLAK-----HKLEPIUKAKQYAYGA 398
Db 384 LT-SRGVPAIYYGTBOYLITNGDDEPNRAKMSFSKSTTAPNVI SKLAPLRKSNPAIAYGS 442
QY 399 QHDYFDHHDIVGWTREGDSSVA-----NSGLAALITDGPQAKRMVYGRQUNGET 448
Db 443 TQGRMINNDVYIERKFKGSAVAVVAVNNRNLSTPANITGLSTSLPTGSYTDVYLGGLANG-- 500
QY 449 MHDITGNRSEPPVYINSEGEFHVNGGSVSIY 480
Db 501 -NNITSNGS---VNS-----FTLAGATAVM 523

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Search completed: October 7, 2004, 00:13:22
 Job time : 10.4712 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 / Search time 46.3093 Seconds
(without alignments)
3290.816 Million cell updates/sec

Title: US-09-925-576C-8
Perfect score: 2666
Sequence: 1 ANINGTIMQFWEYMPNDQ.....SEGMGFHVNGSVSIYVR 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp archaea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
7: sp mhc:*
8: sp organelle:*
9: sp phage:*
10: sp plant:*
11: sp rodent:*
12: sp virus:*
13: sp vertebrate:*
14: sp unclassified:*
15: sp virus:*
16: sp bacteriaph:*
17: sp archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2025	76.0	513	16 Q81AS4	Q81AS4 bacillus ce
2	2021	75.8	519	2 Q9RCR8	Q9RCR8 cytophaga s
3	2021	75.8	533	2 Q9A0S4	Q9A0S4 bacillus me
4	1991	74.7	513	16 Q81YJ4	Q81YJ4 bacillus an
5	1909	71.6	516	2 Q82839	Q82839 bacillus sp
6	1789.5	67.1	549	2 Q31193	Q31193 bacillus st
7	1784.5	66.9	521	2 P71034	P71034 bacillus sp
8	1784.5	66.8	549	2 Q9KMY6	Q9KMY6 bacillus st
9	1755.5	65.8	613	2 Q59222	Q59222 bacillus sp
10	1723.5	64.6	501	2 Q93148	Q93148 bacillus sp
11	1502.5	56.4	507	16 Q87HG6	Q87HG6 vibrio para
12	1336	50.1	481	16 Q89YF1	Q89YF1 bacteroides
13	1262	47.3	493	2 Q03657	Q03657 bacillus ci
14	1244	46.7	492	16 Q8YU21	Q8YU21 anabaena sp
15	1233	46.2	484	16 Q97Q49	Q97Q49 streptococ
16	1230.5	46.2	484	2 Q50583	Q50583 streptococ

17	1228	46.1	484	16 Q8DPC8	Q8DPC8 streptococ
18	1197.5	44.9	488	16 Q8E596	Q8E596 streptococ
19	1196.5	44.9	488	16 Q8E0M2	Q8E0M2 streptococ
20	1195.5	44.8	486	16 Q8D708	Q8D708 streptococ
21	1182.5	44.4	485	2 Q53786	Q53786 streptococ
22	1156.5	43.4	486	2 Q68875	Q68875 streptococ
23	1108	41.6	491	16 Q9CG59	Q9CG59 lactococcus
24	1091.5	40.9	506	16 Q80916	Q80916 agrobacteri
25	1053	39.5	494	16 Q8Z5S5	Q8Z5S5 salmonella
26	1048	39.3	495	16 Q8RGL8	Q8RGL8 escherichia
27	1047	39.3	495	16 Q8XBB6	Q8XBB6 escherichia
28	1037	38.9	495	16 Q7UBA0	Q7UBA0 shigella fl
29	1035	38.8	495	16 Q83R40	Q83R40 shigella fl
30	1018.5	38.2	529	3 Q877B1	Q877B1 aspergillus
31	485.5	18.2	460	1 Q9P9L0	Q9P9L0 pyrococcus
32	485.5	18.2	460	1 Q08452	Q08452 pyrococcus
33	485.5	18.2	473	17 Q8U319	Q8U319 pyrococcus
34	476.5	17.9	461	1 Q33476	Q33476 pyrococcus
35	469.5	17.6	461	1 Q8NKR5	Q8NKR5 thermococu
36	469	17.6	469	1 Q50200	Q50200 thermococu
37	467.5	17.5	461	1 Q8NKR4	Q8NKR4 thermococu
38	455	17.1	457	1 Q93647	Q93647 thermococu
39	448.5	16.8	432	14 Q8ZTK3	Q8ZTK3 uncultured
40	321	12.0	826	10 Q9CAR6	Q9CAR6 arabidopsis
41	321	12.0	887	10 Q94A41	Q94A41 arabidopsis
42	310	11.6	420	10 Q9ZP43	Q9ZP43 phaseolus v
43	310	11.6	504	1 Q60224	Q60224 natronococ
44	308.5	11.6	906	10 Q8LQK4	Q8LQK4 oryza sativ
45	303.5	11.4	421	10 Q7X9T1	Q7X9T1 phaseolus a

ALIGNMENTS

RESULT 1	ID	Q81AS4	PRELIMINARY;	PRT;	513 AA.
AC	Q81AS4				
DT	01-JUN-2003	(TRENBERL_24, Created)			
DT	01-JUN-2003	(TRENBERL_24, Last sequence update)			
DT	01-OCT-2003	(TRENBERL_25, Last annotation update)			
DE	Glucan 1,4-alpha-maltohexosidase (BC 3.2.1.98).				
GN	BC3482.				
OS	Bacillus cereus (strain ATCC 14579 / DSM 31).				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_TaxID=226900;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=22608415; PubMed=12721630;				
RA	Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,				
RA	Kapratel V., Bhattacharya A., Reznik G., Mikhailova N., Lapidis A.,				
RA	Chu L., Mazur M., Golsman E., Larsen N., D'Souza M., Walunas T.,				
RA	Grechkin Y., Pasch G., Haselkorn R., Fomstein M., Ehrlich S.D.,				
RA	Overbeek R., Kyriades N.,				
RT	"Genome sequence of Bacillus cereus and comparative analysis with				
RT	Bacillus anthracis";				
RL	Nature 423:87-91(2003).				
RL	EMBL; AEO17009; AAPI0417.1; -				
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.				
DR	GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.				
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.				
DR	InterPro; IPR006047; Alpha-amyl_cat.				
DR	InterPro; IPR006589; Alp_amyl_cat_sub.				
DR	Pfam; PF00128; alpha-amylase; 1.				
DR	SMART; SM00642; Amy; 1.				
KW	GLYCOSIDASE; Hydrolase; Complete proteome.				
SQ	SEQUENCE 513 AA; 58306 MW; 05C4611CABFP9P6 CRC64;				
QY	Query Match	76.0%;	Score 2025;	DB 16;	Length 513;
	Best Local Similarity	74.5%;	Pred. No. 2.4e-140;		
	Matches 359;	Conservativity 49;	Mismatches 72;	Indels 2;	Gaps 1;
	4	NGTLMQFWEYMPNDQGMRLQNDSAVLAHGITAVWIPRAYKGTQADVGAYDLYD	63		

```
Db 32 NGTLMQYFEWYAPNDGNHMRRLRTDVENLAEKIGTSVWI PPAYKGTQNDVGYGAYDLXD 91
Qy 64 LGEFHOKGVTYKTKGTGELQSAIKSLHSRDINVGDVVNHKGADATEVTAVEVDA 123
Db 92 LGEBNQGKVTYKTKGTGELQSAIKSLHSRDINVGDVVNHKGADATEVTAVEVDA 151
Qy 124 DRNRVISEGHLIKAMTHFHPGRGSTYSDFKMHWYHFDGTDWDSRKLNRITYKQ--GKA 181
Db 152 NRNVNVEGDIYSMTGTFNPGRGDSYSNFKMKYHHDGTDWDSRKLNRITYKRGIGKA 211
Qy 182 WDWSEVSNNGNYDYLMATADIDYDHPDVAALIKRWGTWYANELQDGRDLAVKHIKESFL 241
Db 212 WDWSEVSNNGNYDYLMATADIDYDHPDVAALIKRWGTWYANELQDGRDLAVKHIKESFL 271
Qy 242 RDMVNHVREKTKGEMFTVAEYQNDLGALENYLAKTNPNHSEVDFVPHYQHAASQGG 301
Db 272 RDMVNHVREKTKGEMFTVAEYQNDLGALENYLAKTNPNHSEVDFVPHYQHAASQGG 331
Qy 302 YDMRKLNGTVVSKHPLKSVTFVNDHDTQPGQSLSTVQTWFKPLAAYAFILTRSGY 361
Db 332 YDMRKLNGTVVSKHPLKSVTFVNDHDTQPGQSLSTVQTWFKPLAAYAFILTRSGY 391
Qy 362 FYGDMYGTGDSQREIPALKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVAN 421
Db 392 FYGDMYGTGDSQREIPALKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSSVAN 451
Qy 422 SGGLAALITDPPGAKRMVYVGRONAGETWHDITGNRSEPVYINSKGEFHYNGGSV 481
Db 452 SGGLAALITDPPGAKRMVYVGRONAGETWHDITGNRSEPVYINSKGEFHYNGGSV 511
Qy 482 QR 483
Db 512 QQ 513
```

```
RESULT 2
Q9RQT8 PRELIMINARY; PRT; 519 AA.
ID 09ROT8
AC 09ROT8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, last annotation update)
DE Raw starch digesting amylase precursor.
OS Cytophaga sp.
OC Bacteria; Bacteroidetes; Sphingobacteriales;
OC Flexibacteriaceae; Cytophaga.
OX NCBI_TaxID=29535;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeang C.L., Chen L.S., Chen M.Y.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067653; AAF0567.1; -.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amyy; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 58 519 POTENTIAL.
SQ SEQUENCE 519 AA; 58337 MW; 3E6B88A4DF98B163 CRC64;
```

```
Query Match 75.8%; Score 2021; DB 2; Length 519;
Best Local Similarity 73.4%; Pred. No. 4.8e-140;
Matches 356; Conservative 60; Mismatches 67; Indels 2; Gaps 1;
Qy 1 ANLNGTLMQYFEWYAPNDGNHMRRLQNDSEYLAEGHTAWIPPAKGTSGQADVGYGAYD 60
```

```
Db 35 AATNGTLMQYFEWYAPNDGQOMRRLRTDAPYLLSVGITAATVTPPAKGTSGQADVGYG 94
Qy 61 LYDGEFHOKGVTYKTKGTGELQSAIKSLHSRDINVGDVVNHKGADATEVTAVEVDA 120
Db 95 LYDGEFHOKGVTYKTKGTGELQSAIKSLHSRDINVGDVVNHKGADATEVTAVEVDA 154
Qy 121 DPADRNRVISEGHLIKAMTHFHPGRGSTYSDFKMHWYHFDGTDWDSRKLNRITYKQ-- 178
Db 155 NPNRNVNVEGDIYSMTGTFNPGRGDSYSNFKMKYHHDGTDWDSRKLNRITYKRGIG 214
Qy 179 GKAMDSEVSNNGNYDYLMATADIDYDHPDVAALIKRWGTWYANELQDGRDLAVKHIK 238
Db 215 GKAMDSEVSNNGNYDYLMATADIDYDHPDVAALIKRWGTWYANELQDGRDLAVKHIK 274
Qy 239 SPLRDMVNHVREKTKGEMFTVAEYQNDLGALENYLAKTNPNHSEVDFVPHYQHAASQ 298
Db 275 SPLRDMVNHVREKTKGEMFTVAEYQNDLGALENYLAKTNPNHSEVDFVPHYQHAASQ 334
Qy 299 GGGYDMRKLNGTVVSKHPLKSVTFVNDHDTQPGQSLSTVQTWFKPLAAYAFILTRSGY 358
Db 335 GGGYDMRKLNGTVVSKHPLKSVTFVNDHDTQPGQSLSTVQTWFKPLAAYAFILTRSGY 394
Qy 359 PÖVFYGDMYGTGDSQREIPALKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSS 418
Db 395 PÖVFYGDMYGTGDSQREIPALKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREGDSS 454
Qy 419 VANSGLAALITDPPGAKRMVYVGRONAGETWHDITGNRSEPVYINSKGEFHYNGGSV 478
Db 455 VANSGLAALITDPPGAKRMVYVGRONAGETWHDITGNRSEPVYINSKGEFHYNGGSV 514
Qy 479 IYVQR 483
Db 515 VWYQQ 519
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RESULT 3
Q9AQS4 PRELIMINARY; PRT; 533 AA.
ID 09AQS4
AC 09AQS4;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, last annotation update)
DE Alpha-amylase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
RA Park K.-H.;
RL "Cloning of maltopentase-producing amylase from Bacillus megaterium
RT KSM B-404."
DR EMBL; AF220440; AAK00598.1; -.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amyy; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;
```

```
Query Match 75.8%; Score 2021; DB 2; Length 533;
Best Local Similarity 74.3%; Pred. No. 4.9e-140;
Matches 358; Conservative 49; Mismatches 73; Indels 2; Gaps 1;
Qy 4 NGTLMQYFEWYAPNDGNHMRRLQNDSEYLAEGHTAWIPPAKGTSGQADVGYGAYDLXD 63
Db 52 NGTLMQYFEWYAPNDGNHMRRLQNDSEYLAEGHTAWIPPAKGTSGQADVGYGAYDLXD 111
Qy 64 LGEFHOKGVTYKTKGTGELQSAIKSLHSRDINVGDVVNHKGADATEVTAVEVDA 123
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Db      112 LGEFNKGIVRTKXGTAOLKSAIDALHKKONIDYGVVNMHKGADYETETVAVEVPS 171
Qy      124 DRRRVISGEHLIKAMTHFHPFGSGSTYSDPKMWHYHFDGTDWDESRKLANIYKQ--GKA 181
      172 NRVNVEVSGDYEISAMTGFNPPGRGDSYSNFKMKYHFDGTDWDEGRKLANIYKRGIGKA 231
Qy      182 WDEVSENNENYDYLMTADIDYDHPVAEIKRWGTYANELQDGRDLAVKHIKESFL 241
      232 WDEVESENENYDYLMTADIDPHDPVANEMKMGTYANELNDGRDLAVKHIDHEYL 291
Db      242 RDVNVHREKTKGEMFTVAEYWMNDLGALENYLNKTFNHSVPDPLHYOFHAASSTOGG 301
      292 RDVNVHREKTKGEMFTVAEYWMNDIOTLNNYLAKVYNGSVFDPALHYNFHYASKNGN 351
Qy      302 YDMRKILNGTVSGKHPKSYTPVDNHDTPQGSLSTVQTFPKPLAFAFLITRESGYPQV 361
      352 YDMRNILKGTGVNHPPLAVTLVNHDSQPGSLSTSVSPFKPLAFAFLITRAEGYPSV 411
Qy      362 FYGDMYTKGDSQREIPALKHKIEPIILKARKOYAYGAOHYFDHDIYGMTREGDSSVAN 421
      412 FYGDIYGTGKNSNVEIPALDKDIPILTARKNAYYGRDYFDHPDVIYGMTREGDSVHAN 471
Db      422 SGLAALITDGPGGAKRMVYVRONAGETWHDITGNRSBPVYINSEGEFHYNGSVSIYV 481
      472 SGLATLISDGPGGAKMMDVGKNNAGEIMYDITGNQTVITINKGWQGFVSGGSVSIYV 531
Qy      482 QR 483
      532 QR 533
Db

```

RESULT 4

Q81YJ4 PRELIMINARY; PRT; 513 AA.

AC Q81YJ4;

DT 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Alpha-amyase.

GN AMYS OR BA3551.

OS Bacillus anthracis (strain Ames).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxId=198094;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22608414; PubMed=12721629;

RA Read T.D., Peterson S.N., Tourasse N., Baillye L.W., Paulsen I.T.,

RA Nelson K.E., Tetteijn H., Fouts D.E., Bisen J.A., Gill S.R.,

RA Holtzaple E.K., Okstad O.A., Helgason E., Ristone J., Wu M.,

RA Kolonay J.F., Beaman M.J., Dodson R.J., Brinkac L.W., Gwinn M.,

RA Deboy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,

RA Nelson W.C., Peterson J.D., Pop M., Khouli H.M., Radue D.,

RA Berton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

RA Berry K.J., Platt R.D., Wolf A.M., Watkins K.L., Niemman W.C.,

RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,

RA Thompson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,

RA Fraser C.M.;

RT "The genome sequence of Bacillus anthracis Ames and comparison to

RT closely related bacteria.";

RL Nature 423:81-86(2003)

RL EMBL; AB017035; AAF27311.1; -.

DR TIGR; BA3551; -.

DR GO; GO:0004556; F:alpha-amyase activity; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006047; Alpha_amy1_cat.

DR InterPro; IPR006589; Alp_amy1_cat_sub.

DR Pfam; PF00128; alpha-amyase; 1.

DR SMART; SM00642; Amy; 1.

KW Complete proteome.

SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

```

      Matches 352; Conservative 51; Mismatches 77; Indels 2; Gaps 1;
Qy      4 NGTLMQFFMYMNDGQHMRLONDSAYLAHGTAVMIPPAVKGTQADVGYGAYLYD 63
      32 NGTLMQFFMYASDRHNMRLTDAENLQKGTITWIPPAVKGTQNDVGYGAYLYD 91
Db      64 LGEFHOKGIVRTKXGKGLQSAIKSLHSDINVGVDVINHKGADATEDVTAVEVPA 123
      92 LGEFNKGIVRTKXGTAOLKSAIEALHKKONIDYGVVNMHKGADYETETVAVEVDRN 151
Qy      124 DRRRVISGEHLIKAMTHFHPFGSGSTYSDPKMWHYHFDGTDWDESRKLANIYKQ--GKA 181
      152 NRVNVEVSGDYEISAMTGFNPPGRGDSYSNFKMKYHFDGTDWDEGRKLANIYKRGIGKA 211
Db      182 WDEVSENNENYDYLMTADIDYDHPVAEIKRWGTYANELQDGRDLAVKHIKESFL 241
      212 WDEVESENENYDYLMTADIDPHDPVANEMKMGTYANELNDGRDLAVKHIDHEYL 271
Qy      242 RDVNVHREKTKGEMFTVAEYWMNDLGALENYLNKTFNHSVPDPLHYOFHAASSTOGG 301
      272 RDVNVHREKTKGEMFTVAEYWMNDIOTLNNYLAKVYNGSVFDPALHYNFHYASKNGN 331
Db      302 YDMRKILNGTVSGKHPKSYTPVDNHDTPQGSLSTVQTFPKPLAFAFLITRESGYPQV 361
      332 YDMRNILKGTGVNHPPLAVTLVNHDSQPGSLSTSVSPFKPLAFAFLITRAEGYPSV 391
Qy      362 FYGDMYTKGDSQREIPALKHKIEPIILKARKOYAYGAOHYFDHDIYGMTREGDSSVAN 421
      392 FYGDIYGTGKNSNVEIPALDKDIPILTARKNAYYGRDYFDHPDVIYGMTREGDSVHAN 451
Db      422 SGLAALITDGPGGAKRMVYVRONAGETWHDITGNRSBPVYINSEGEFHYNGSVSIYV 481
      452 SGLATLISDGPGGAKMMDVGKNNAGEIMYDITGNQTVITINKGWQGFVSGGSVSIYV 511
Qy      482 QR 483
      512 QR 513
Db

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RESULT 5

O82839 PRELIMINARY; PRT; 516 AA.

AC O82839;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Amyase.

OS Bacillus sp.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxId=1409;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=KSM-1378;

RX MEDLINE=98342096; PubMed=9675143;

RA Igataishi K., Hatada Y., Ikawa K., Arai H., Ozawa T., Kobayashi T.,

RA Ozaki K., Ito S.;

RT "Improved thermostability of a Bacillus alpha-amyase by deletion of

RT an arginine-glycine residue is caused by enhanced calcium binding.";

RL Biochem. Biophys. Res. Commun. 248:372-377(1998).

RL EMBL; AB008763; BAA32431.1; -.

DR HSSP; P06278; IVUS.

DR GO; GO:0004556; F:alpha-amyase activity; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006047; Alpha_amy1_cat.

DR InterPro; IPR006589; Alp_amy1_cat_sub.

DR Pfam; PF00128; alpha-amyase; 1.

DR PRINTS; PR00110; ALPHAMYASE.

DR SMART; SM00642; Amy; 1.

SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;

Query Match 74.7%; Score 1991; DB 16; Length 513;

Best Local Similarity 73.0%; Pred. No. 7.5e-138;

Query Match 71.6%; Score 1909; DB 2; Length 516;

Best Local Similarity 69.1%; Pred. No. 8e-132;

	Matches	335;	Conservative	68;	Mismatches	72;	Indels	10;	Gaps	4.
OY		4	NGTLMQYETWMPDQCQHRLQNDSAVIAEHGTAVMIPRAYKTSQADVGAYGLDYL							63
Dd		37	NGTMQYETWMLPNDGNHNR.LRDAAMLKSGITAVMI.PPAWKTSQNDVGAYGLDYL							96
OY		64	LGEFHKGTVRKYGTGKLGASIKLSLRSDINYGDVINHKGADATEDVTAYEVDPA							123
Dd		97	LGEFHKGTVRKYGTGRSOLQGVSLKNNGIQVIGDYVNHHKGADGTENVNAEVARS							156
OY		124	DRNRVISSEHLIKANTHPFGPGSTYSDFKMWHYFDGTDWDESRKL-NRIYKFO--GK							180
Dd		157	NRMQISEGYTIEAWTKEDPEGRGNTSHNFKKRWTHFPDGTDWDQRQLNKTYKFRGTK							216
OY		181	AMDMEVSNNNGYDVLMTADIDYHDPRVAALIKRGTVYANELDLQGERLVAHQIKESF							240
Dd		217	AMDMEVDJENAGYDILMTADIDMDPEVYNELKMGVNYTLNLNDFRIDLVKHIKSYI							276
OY		241	LRDVNVHVREKTGEMFTVAEYWONDLGALENYLNKTFNHSSVPDPVLPHO.FHAASTOGG							300
Dd		277	TRDMVLTHVRNTGKKPMFAVAFPMKNDLAILEYLNKTSMSHSVFDPVLHYNLVANAISGG							336
OY		301	GVDMKLANGTVYSGHPLKSYTPUNDNHTPOQSLESYYQMFKFLAFLITLESSTGPQ							360
Dd		337	YFDKNILNGSVVQGHPIHATVEVDNHDSPQEALSESFVOSMFXPLAYALILTREGYPS							396
OY		361	VFYGDMYG--TKGSOREIPALKKHIEPILAKKOYAAGAODHDEDHDIIVGMTREGDS							418
Dd		397	VFYGDYGIPIHG-----VPSMKSIDPDLQARQVYATGHDYFDHDDIIIGMTREGDS							451
OY		419	VANSGLALLITDGPAGAKRMVYGRONAGETMHDTIGNRSERVYINSBEGGFPHVNGSVS							478
Dd		452	HNSGLAITMSDGPCKNMVYVKHKAQQWRDITGNRS.GVTYTNADGMGNFTVNGAVS							511
OY		479	IYVOR 483							
Dd		512	VWVKQ 516							
RESULT 6										
ID	031193		PRELIMINARY;	PRT;	549 AA.					
AC	031193;									
DT	01-JAN-1998	(TREMBLrel. 05	Created)							
DT	01-JAN-1998	(TREMBLrel. 05,	Last sequence update)							
DT	01-OCT-2003	(TREMBLrel. 25,	Last annotation update)							
De		Alpha amylase.								
GN	AMI.									
OS	Bacillus stearothermophilus.									
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.									
OX	NCBI_TextID=1422;									
RN	[1]	SEQUENCE FROM N.A.								
RP	STRAIN=ATCC 31195;									
RC	da Silva A.C.R., Fernandes E., Pueyo M.T.;									
RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.									
DR	EMBL; AF032864; AAB86961.1; --									
DR	PIR; A54541; A54541.									
DR	HSSP; P06278; IVUS.									
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.									
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.									
DR	InterPro; IPR006047; Alpha.amyl.cat.									
DR	InterPro; IPR006589; Alp.amyl.cat.sub.									
DR	InterPro; IPR006046; Glyco.hydro_13.									
DR	pfam; PF00128; alpha-amylase, 1.									
DR	PRINTS; PR00110; ALPHAMYLASE.									
DR	SMART; SM00642; Amy; 1.									
DQ	SEQUENCE 549 AA; 62651 MW; 2CA689BDACC4D262 CRC64;									

Query Match	67.1%	Score 1789.5;	DB 2;	Length 549;
Best Local Similarity	64.9%	Pred. No. 5.2e-123;		
Matches 315;	Conservative 67;	Mismatches 98;	Indels 5;	Gaps 2;

```

QY 1 ANLNTGLTQYFEMWTWPNBQGWRRRLONDSAYLAHEGTLVMTLPPAYKTSQADVYGAYD 60
Db 36 AEFNNTMQYFEMWYLPDDGTLTMTKVAANEANNLSLSLDTALMTLPPAYKTSRSRSPVGYAVD 95
QY 61 LYDLBEPHQKGVVRKRYGTGKELQSAIKSLHSRDINVDVYVJNHKGADATBEDVAYEV 120
Db 96 LYDLBEPHQKGVVRKRYGTGKAYOLQIQAHAHAQOVYADVVPFDHKGADGTEWDAVEV 155
QY 121 DPADNRNVLISGEHLIKAWTHFHPFGSGTYSDFPKMHWYHFDGTDWDESRKLNRYEFO-- 178
Db 156 NPSDNDQETISGTYQAWTKFDPFBGRKNYTSFFKRNWHPFDGDVMDSEKLSIYFREGI 215
QY 179 GKAMDWEVSNENGNDYLMYADIDVDHPVAEIKRWGTWYANELQLDGFRDVAHKIF 238
Db 216 GKAMDWEVDTEGNGNDYLMYADLDMDHPVEVTELNKMGKMYVNTTIDGFRDVAHKIF 275
QY 239 SFLRWVNVHVRKTEKEMFTVAEYQUNDGALENTLNKRNFNHSVVDVPLHQFHAASIO 298
Db 276 SFPRPMLSVYRSQTKPLFTVGEYMSYDINKLHNYITKNGTMSLEDAPLHNKFYASKS 335
QY 299 GGGYVNRKILNGLNTVVSXKPLKSVTEVVDNHDNDPQGSLESTVQTWPKPLAYAFILTEBSG 358
Db 336 GGAFFMRKILMTNTYTKDQPTLAVTEVDNHDNDEFGQLSQWVPWPKPLAYAFILTRQBSG 395
QY 359 PQVFYGDYGTGSDQREIPLAKHKEIPLTKARQOYAGQADYFDPHNDIVGWTREBDS 418
Db 396 PCVFYGDYGT---PQYNIPLSKSIDPLILNRQYAVATQGDYDHDHSIIGMTRRGVTE 452
QY 419 VANSGLAALLIDGPGAGARMYVGRONAGEBTHDITGNRSEPVYINSEMGEEFHVNGGSYS 478
Db 453 KPGSGLAALLIDGPGGSKMVYQKHAGKVFYDLTGNRSDVTIINSDGEEFKVNGGSYS 512
QY 479 IYVOR 483
Db 513 VWVPR 517

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RESULT 7			
ID	P71034	PRELIMINARY;	PRT; 521 AA.
AC	P71034;		
DT	01-FEB-1997 (TrEMBLrel. 02, Created)		
DT	01-FEB-1997 (TrEMBLrel. 02, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Alpha-amyase precursor.		
OS	Bacillus sp. MK 716.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxId=54116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=MK 716;		
RA	Sidhu G.S., Chakrabarti T.;		
RT	"Molecular cloning and expression of the gene encoding for		
RT	thermostable alpha-amyase of a thermophilic bacterial isolate."		
RL	Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; U75445; AAB18785.1; -.		
DR	HSSP; P06278; IVUS.		
DR	GO; GO:0004556; F:alpha-amyase activity; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	InterPro; IPR006047; Alpha_amy1_cat.		
DR	InterPro; IPR006589; Alp_amy1_cat_sub.		
DR	InterPro; IPR006046; Glyco_hydro_13.		
DR	Pfam; PF00128; alpha-amyase; 1.		
DR	PRINTS; PR00110; ALPHAMYASE.		
DR	SMART; SM00642; Amyy; 1.		
KW	Signal.		
FT	SIGNAL. 1 34	POTENTIAL.	
FT	CHAIN 35 521	ALPHA-AMYASE.	
SQ	SEQUENCE 521 AA; 59311 MW; 56151288596922281 CRC64;		

Query Match	Score	DB 2	Length
Best Local Similarity	66.9%	64.7%	521
Matches 314; Conservative	Pred. No. 1.1e-12;	67; Mismatches 99;	Indels 5; Gaps 2;


```
QY 1 ANINGTLMQYFEMWMPNDGQHRRLONDSAYLAHSGITAVIIPRAYKTSQADYGYAYD 60
D 36 APFNGTMMQYFEMWLPDGLMTKRVANBANNSLSGITLMLPRAVYKTSRSDYGYAYD 95
QY 61 LYDGEFHQKGVTRTKYKGTGELQSAIKSLHSRDINYGVVINKHGADATEDVYAVEV 120
D 96 LYDGEFHQKGVTRTKYKGTGELQSAIKSLHSRDINYGVVINKHGADATEDVYAVEV 155
QY 121 DPADNRNVIAGEHLIKAWTHFHPFGSGTYSDFKMHYHFDGTDWDSRKLRIYKFO-- 178
D 156 NPSDRNOEISGTVOIQAMTKFDFPGRGNTYSSFFKRWYHFDGVWMDSRKLSRIYKRG 215
QY 179 GKAMDVEVSNENGVYDLYMADIDYDHPVAAEIKRWGTWYANLQDGFRLDVKHIF 238
D 216 GKAMDVEVDTENGYDLYMADIDYDHPVAAEIKRWGTWYANLQDGFRLDVKHIF 275
QY 239 SFLADVNVHREKTKEMFTVAEYQNDLGALENYLNKTNFNHVSVPDPLHYOFAASTQ 298
D 276 SFPEDMLSYRSQTKGLFTVGEYMSYDINKLHNYIKTNGTMSLFPAPLHNFYTKSKS 335
QY 299 GGGYDMRKLNGVYSGHPLKSVTFVNDHTQPGQSLESTVQTFKPLAYAFILTRBSGX 358
D 336 GGAFDKRTMTMTLMKQDPTLAVTFVNDHTEPGQALQSWDPMFKPLAYAFILTRBSGX 395
QY 359 POFYGDYGTGDSOREIPALKHIEPILKARKOYAYGAOHYFEDHDIWGTRBDS 418
D 396 PGVFTGYGTGDSOREIPALKHIEPILKARKOYAYGAOHYFEDHDIWGTRBDS 452
QY 419 VANSGLAALITDGPAGKRVYGRONAGETWHDITGNRSEPVVINSBGGEFHNQGSVS 478
D 453 KPGSGLAALITDGPAGKRVYGRONAGETWHDITGNRSEPVVINSBGGEFHNQGSVS 512
QY 479 IYVQR 483
D 513 VWVPR 517
```

RESULT 8

```
Q9KMY6 PRELIMINARY; PRT; 549 AA.
AC Q9KMY6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DS1100;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y17557; CAB93517.1; -.
DR HSP; P06278; IYUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 549 AA; 62582 MW; 8DA3B6D9F9120BCE CRC64;
```

Query Match 66.9%; Score 1784.5; DB 2; Length 549;
Best Local Similarity 64.7%; Pred. No. 1.2e-122;
Matches 314; Conservative 67; Mismatches 99; Indels 5; Gaps 2;

```
QY 1 ANINGTLMQYFEMWMPNDGQHRRLONDSAYLAHSGITAVIIPRAYKTSQADYGYAYD 60
D 36 APFNGTMMQYFEMWLPDGLMTKRVANBANNSLSGITLMLPRAVYKTSRSDYGYAYD 95
QY 61 LYDGEFHQKGVTRTKYKGTGELQSAIKSLHSRDINYGVVINKHGADATEDVYAVEV 120
D 96 LYDGEFHQKGVTRTKYKGTGELQSAIKSLHSRDINYGVVINKHGADATEDVYAVEV 155
QY 121 DPADNRNVIAGEHLIKAWTHFHPFGSGTYSDFKMHYHFDGTDWDSRKLRIYKFO-- 178
D 156 NPSDRNOEISGTVOIQAMTKFDFPGRGNTYSSFFKRWYHFDGVWMDSRKLSRIYKRG 215
QY 179 GKAMDVEVSNENGVYDLYMADIDYDHPVAAEIKRWGTWYANLQDGFRLDVKHIF 238
D 216 GKAMDVEVDTENGYDLYMADIDYDHPVAAEIKRWGTWYANLQDGFRLDVKHIF 275
QY 239 SFLADVNVHREKTKEMFTVAEYQNDLGALENYLNKTNFNHVSVPDPLHYOFAASTQ 298
D 276 SFPEDMLSYRSQTKGLFTVGEYMSYDINKLHNYIKTNGTMSLFPAPLHNFYTKSKS 335
QY 299 GGGYDMRKLNGVYSGHPLKSVTFVNDHTQPGQSLESTVQTFKPLAYAFILTRBSGX 358
D 336 GGAFDKRTMTMTLMKQDPTLAVTFVNDHTEPGQALQSWDPMFKPLAYAFILTRBSGX 395
QY 359 POFYGDYGTGDSOREIPALKHIEPILKARKOYAYGAOHYFEDHDIWGTRBDS 418
D 396 PGVFTGYGTGDSOREIPALKHIEPILKARKOYAYGAOHYFEDHDIWGTRBDS 452
QY 419 VANSGLAALITDGPAGKRVYGRONAGETWHDITGNRSEPVVINSBGGEFHNQGSVS 478
D 453 KPGSGLAALITDGPAGKRVYGRONAGETWHDITGNRSEPVVINSBGGEFHNQGSVS 512
QY 479 IYVQR 483
D 513 VWVPR 517
```

RESULT 9

```
Q59222 PRELIMINARY; PRT; 613 AA.
AC Q59222;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Alpha-amylase (EC 3.2.2.1).
GN Amy.
OS Bacillus sp. TS-23.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=38441;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TS-23;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U22045; AAA63900.1; -.
DR HSP; P06278; IYUS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0008477; F:purine nucleosidase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_amy1_cat.
DR InterPro: IPR006589; Alp_amy1_cat_sub.
DR InterPro: IPR002044; CBD_4.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amylase; 1.
DR Pfam: PF00686; CBM 20; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR ProDom; PD001568; CBD_4; 1.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase.
SQ SEQUENCE 613 AA; 69537 MW; 14684A30FC289558 CRC64;
```

Query Match 65.8%; Score 1755.5; DB 2; Length 613;

Best Local Similarity 64.1%; Pred. No. 1.9e-120;
Matches 311; Conservative 68; Mismatches 101; Indels 5; Gaps 2;

```
QY 1 ANLNGTLMQYFEMWYMPNDGQHWRLQNDSDAYLAHSGITTAWVIPPAYKGTSGADYGVAYD 60
DB 33 APINETMMQYFEMWLPNDGTLMTKVKNEANLSLGLTALMLPRAKGTSGSIVSGAYD 92
QY 61 LYDGEFHQKGTIVRTKGTGKGLQSAIKSLHSPDINVGDVYVNHKGADATEDYTAVEV 120
DB 93 LYDGEFHQKGTIVRTKGTGTYOYIQAIAKAKAGMAYADVAVNHHKAGDTEFVDAVEV 152
QY 121 DPADRNKVISGEHLIKAMTHFHPGSGTYSDFKMWYHPDGDMDPESKRLRIYEQ-- 178
DB 153 DPNRNQGTSTGYQIQAMTKEFDPFGNGNTYSFKMWYHPDGDMDPESKRLRIYERST 212
QY 179 GKAMDVEVSNENYDIYLAADIDYDHPDVAEIKKMGWYANELQDGRFLDAVKHKEF 238
DB 213 GKAMDVEVDTENYNYLMPADLMDHPEVTELKMGWYVNTNIDGFRFLDAVKHKE 272
QY 239 SFPLDWNHVRKTKGEMFVFAEYQNDGALENTYKTNPNHSPVDPVLAHQFHAATQ 298
DB 273 SFPPDLTYVRNQTGNLPAVGEFMSYDVNKLHNTYTKNSGMSLFDAPLHNNFYTASKS 332
QY 299 GGGYDMRKLTNGTVSVKPLKSVTFVNDHTQPGQSLBSTVQTFWFKPLAFAFILTRBSGY 358
DB 333 SGYFDMRYLNTLTKMDQPSLAFTLVNDHTQPGQSLQSWEPWFKPLAFAFILTRBSGY 392
QY 359 POFYGDWGTGKDSGREIPALKKHTEPLTKARKQAYAGQHDYDHHDIYGMTREGDSS 418
DB 393 PCVFGDYGT--PKNIPGLKSKIDPLLIARRDYAGTORDYDHDIDIGMTREGIDT 449
QY 419 VANSGLAALITDGPQAKMYVGRONAGETWHDITGNRSEPVYINSEGMGEFHNQGSVS 478
DB 450 KENSGLAALITDGPQSGSKMYVYKKGAKGVFYDLTGNRSDTYTINADGGEFKNQGSVS 509
QY 479 IYVOR 483
DB 510 IYVAK 514
```

RESULT 10

Q93148 PRELIMINARY; PRT; 501 AA.

AC O93148; 087HG6;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Amylase.

GN AMYK38.

OS Bacillus sp. KSM-K38.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=129736;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=KSM-K38;

RA Hayaishi Y.;

RT "Isolation of a new Bacillus alpha-amylase."

RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB051102; BAB71820.1; -

DR GO; GO:0004556; F:alpha-amylase activity; IEA.

DR InterPro; IPR006047; P:carbohydrate metabolism; IEA.

DR Pfam; PF00128; alpha-amylase; 1.

DR KW Complete proteome.

SQ SEQUENCE 501 AA; 57485 MW; 1240F46739A5CC11 CRC64;

Query Match 64.6%; Score 1723.5; DB 2; Length 501;
Best Local Similarity 62.8%; Pred. No. 3.2e-118;
Matches 302; Conservative 72; Mismatches 104; Indels 3; Gaps 1;

```
QY 3 LNTGTMQYFEMWYMPNDGQHWRLQNDSDAYLAHSGITTAWVIPPAYKGTSGADYGVAYD 62
DB 24 LNTGTMQYFEMWYMPNDGQHWRLQNDSDAYLAHSGITTAWVIPPAYKGTSGADYGVAYD 83
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QY 63 DLGEFHQKGTIVRTKGTGKGLQSAIKSLHSPDINVGDVYVNHKGADATEDYTAVEVDP 122
DB 84 DLGEFHQKGTIVRTKGTGKGLQSAIKSLHSPDINVGDVYVNHKGADATEDYTAVEVDP 143
QY 123 ADNRNRVISGEHLIKAMTHFHPGSGTYSDFKMWYHPDGDMDPESKRLRIYKFGQKAM 182
DB 144 TNRWQDISGAYTIDAWTGFPDSGRNNAYSDPKRMHFNKVDVDQKIQENHITREFANTW 203
QY 183 DMEVSNENYDIYLAADIDYDHPDVAEIKKMGWYANELQDGRFLDAVKHKEFPLR 242
DB 204 NMRVDEENQVNDYLGNSIDPSHEVDELKMGWTFTELDIDGRFLDAVKHKEFPLR 263
QY 243 DWNHVRKTKGEMFVFAEYQNDGALENTYKTNPNHSPVDPVLAHQFHAATQCGGY 302
DB 264 DWNHVRKTKGEMFVFAEYQNDGALENTYKTNPNHSPVDPVLAHQFHAATQCGGY 323
QY 303 DMKRLNGTVSVKPLKSVTFVNDHTQPGQSLBSTVQTFWFKPLAFAFILTRBSGYPOVF 362
DB 324 DMKRLNGTVSVKPLKSVTFVNDHTQPGQSLBSTVQTFWFKPLAFAFILTRBSGYPOVF 383
QY 363 YGDWYGTGKDSGREIPALKKHTEPLTKARKQAYAGQHDYDHHDIYGMTREGDSSVANS 422
DB 384 YGDYGTGPNND--ISAKDMIDELDAKQAYAGQHDYDHHDIYGMTREGDSSVANS 440
QY 423 GLAALITDGPQAKMYVGRONAGETWHDITGNRSEPVYINSEGMGEFHNQGSVSIIYQ 482
DB 441 GLATIMSNGSGSKMYVYKKGAKGVFYDLTGNRSDTYTINADGGEFKNQGSVSIIYV 500
QY 483 R 483
DB 501 Q 501
```

RESULT 11

Q87HG6 PRELIMINARY; PRT; 507 AA.

AC Q87HG6; 087HG6;

DT 01-JUN-2003 (TREMBlrel. 24, Created)

DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)

DE Alpha-amylase.

GN VPA0999.

OS Vibrio parahaemolyticus.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrrio.

OX NCBI_TaxID=670;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RIMD 2210633 / Serotype O3:K6;

RX MEDLINE=22508454; PubMed=12620739;

RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Iijima Y., Nishijima M., Nakano M., Yamashita A., Kubota Y., Kimura S., Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae."

RL Lancet 361:743-749 (2003).

DR EMBL; AP005087; BAC62342.1; -

DR GO; GO:0004556; F:alpha-amylase activity; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006047; Alpha.amyl_cat.

DR Pfam; PF00128; alpha-amylase; 1.

DR KW Complete proteome.

SQ SEQUENCE 507 AA; 58428 MW; 91B549E2BE0700BD CRC64;

Query Match 56.4%; Score 1502.5; DB 16; Length 507;
Best Local Similarity 55.8%; Pred. No. 5.6e-102;
Matches 271; Conservative 81; Mismatches 125; Indels 9; Gaps 7;

```
QY 1 ANLNGTLMQYFEMWYMPNDGQHWRLQNDSDAYLAHSGITTAWVIPPAYKGTSGADYGVAY 59
DB 23 AGQNGTMMQYFEMWYMPNDGQHWRLQNDSDAYLAHSGITTAWVIPPAYKGTSGADYGVAY 82
QY 60 DLYDLGEFHQKGTIVRTKGTGKGLQSAIKSLHSPDINVGDVYVNHKGADATEDYTAVE 119
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Db 83 DMYDLGEPDQGSVRYTKYGTGAQYISALINAHNNINIQYGDVVFNRHGGADGKSMVDTKR 142
Qy 120 VDPDRNRVRVSGEHLIKAMTHFHPGRGSTYSDPKMWHYHFDGTDMPDSRKLNRITYK-- 177
Db 143 VDMNMRN-IEIGDGMIEAWWEPFGRNDKYSNFMWYHFDGVDMDAGKKAIFPKFG 201
Qy 178 QGKAMDEVSNENGYIYAWADIDYDHPDVAAEIKEMGTWYANELQDGFRLDAVAKHIK 237
Db 202 EGKAMDEVSEKSNYDILMADLDMDHPEVKQELKMGEMYIMTGVDFRMDAVAKHIK 261
Qy 238 FSLRLDWNHVRKTKGEMFTVAEYQWQNDGALENYLNKTNFNSVDPVPLHYQFHAAS 297
Db 262 YQYIOWEIMDHLRMTKGEKLFVSGYWMYDVQNLNFTKISGMSLDPALHMFYNAASK 321
Qy 298 QGGGIDMKLNGVSKHPLKSTYFVDNHDTPQGSLSTVQWMPKLAFAFLITRESSG 357
Db 322 SGGYDWMKQJNMGTLMKDNPKVAVTLVENHDTQPLQALSTVDMWFKPLAFAFLITREB 381
Qy 358 YPOVFYGDWMTGK-GDSQREIPLK-HKIEPLIKARQYAGAHDFDHHDIWGTREG 415
Db 382 YPSFYADYGAQYSDGKYNINMAKVPYIEELVTLREYAGKONSYLDMWDVIGWTRG 441
Qy 416 DSVANSGLAALITDGPQAKRMVYGRONAGETWHDITGNRSEPVYINSEGWGEFHYNGG 475
Db 442 DAHPNS-MAYIMSDGPGGTMTYTKRST--RYVDKLGITFEVMTDANCMALFPVNGG 498
Qy 476 SVSIVV 481
Db 499 SVSYVW 504

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RESULT 12

```

ID 089YPI PRELIMINARY; PRT; 481 AA.
AC 089YPI;
DT 01-JUN-2003 (TREMblrel. 24, Created)
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Alpha-amylase precursor.
GN BT4690.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=2250858; PubMed=12663928;
RA Xu J., Björnsell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RA "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.",
RL Science 299:2074-2076(2003).
DR EMBL; AE016946; AAC079795.1; -.
DR GO: GO:0004556; F:alpha-amylase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5EB1A CRC64;

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Query Match 50.1%; Score 1336; DB 16; Length 481;
Best Local Similarity 49.6%; Pred. No. 8.9e-90;
Matches 239; Conservative 84; Mismatches 153; Indels 6; Gaps 2;
Qy 4 NGTLMQFEWMPNDGQWRRLQNDASATLAHGITAWWIPRAYKGTSGADVGYAYLDYD 63
Db 3 NGVMQGFEMWLPNDGKMKQIKEDALHLDIGTAWWIPRAYKADQDGGVATYDLYD 62
Qy 64 LGBFHQKGTVTRTKYGTGKELQSAIKSLHSRDINYGVVIVNHKGGADATEDVTAVEVDP 123

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Db 63 LGBFHQKGTVTRTKYGTGKELKMI DELAKHYIAVYLDVIVNHKAGDFTKFMVVEVDPK 122
Qy 124 DNRNVRVSGEHLIKAMTHFHPGRGSTYSDPKMWHYHFDGTDMPDSRKLNRITYKQ--GKA 181
Db 123 ERTALGEPPEIQGWTGYSFHKRDKSDPKMWHYHSGTGFDQKSGVFOIQSGKA 182
Qy 182 MDWVSNENGNVYIYAWADIDYDHPDVAAEIKEMGTWYANELQDGFRLDAVAKHIKESFL 241
Db 183 MSBGVDSNENGYDPLCNDDLDHPEVSLNKGKVNSEINLDGKRLDAIKMKQGFV 242
Qy 242 RDWVNHVRKTKGEMFTVAEYQWQNDGALENYLNKTNFNSVDPVPLHYQFHAAS 301
Db 243 AQFLDAVSRBNDFYAVGEMNGDLEALDAYIEAVGKKNLFPVPLHYMFOASQEGKD 302
Qy 302 YDMRKLNGVSKHPLKSTYFVDNHDTPQGSLSTVQWMPKLAFAFLITRESSG 361
Db 303 YDLRLDILKDLVBEHHPPLAVITVDNHDTPQGSLSVSEVMPKLAAGLLLMKEGYPCL 362
Qy 362 FYGDMYGTGDSQREIPLK-HKIEPLIKARQYAGAHDFDHHDIWGTREGDSSVAN 421
Db 363 FYGDYIKKEKSPH-----TRIIDLARKRATAYGQIETFDHPSTIGFRTGDBEHNG 418
Qy 422 SGLAALITDGPQAKRMVYGRONAGETWHDITGNRSEPVYINSEGWGEFHYNGGSAVSIYV 481
Db 419 SGVYFLMSNDAGSKIMSLGKHKGEVWHITGSISEITLDEBNGEFSVESRNLAVMV 478
Qy 482 QR 483
Db 479 KK 480

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RESULT 13

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ID 003657 PRELIMINARY; PRT; 493 AA.
AC 003657;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Amylase.
GN AMYE.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RA Marcel T.;
RL Nucleic Acids Res. 0:0-0(0).
DR EMBL; X60779; CAA43194.1; -.
DR PIR; S15713; S15713.
DR HSP; P06278; IVUS.
DR GO: GO:0004556; F:alpha-amylase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 493 AA; 56537 MW; FECCD2F805BB4694 CRC64;

```

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Query Match 47.3%; Score 1262; DB 2; Length 493;
Best Local Similarity 47.6%; Pred. No. 2.5e-84;
Matches 230; Conservative 75; Mismatches 16; Indels 12; Gaps 3;
Qy 4 NGTLMQFEWMPNDGQWRRLQNDASATLAHGITAWWIPRAYKGTSGADVGYAYLDYD 63
Db 4 NHTMQGFEMWLPNDGQWRRLQNDASATLAHGITAWWIPRAYKADQDGGVATYDLYD 63
Qy 64 LGBFHQKGTVTRTKYGTGKELQSAIKSLHSRDINYGVVIVNHKGGADATEDVTAVEVDP 123
Db 64 LGBFHQKGTVTRTKYGTGKELQSAIKSLHSRDINYGVVIVNHKGGADATEDVTAVEVDP 123
Qy 124 DNRNVRVSGEHLIKAMTHFHPGRGSTYSDPKMWHYHFDGTDMPDSRKLNRITYKQ--KA 181

```

```
Db 124 DRTKEISEPFELEGMTKFTFPGSGDQSSSEKNNSEHFGTDADAREKRGVFRINGENKK 183
Qy 182 WMBEVENENGVNDYLMYADIDYDHPVAEIKRWGTVYANELODGFRLDAVKH1KFSFL 241
Db 184 KMBENVDEBGNVDYLMFANIIDYHPPVREBMDWGMGLDITQCGGFRDLAIKH1NHETI 243
Qy 242 RDMVNHVREKTEGKEMFTVAEYMONDICALENYINKTNFNHVSFVDYLAHQFPAASOGGG 301
Db 244 KEFAEMIRKRGODPFIIVEFNNNSINDAGREFLDITVDYDIDFVDSIHKHLSLKGKD 303
Qy 302 YMKRLKLNKTVSKHPKLSVTVDNHDTPGSGLESTVQTWKPLAVALITLRESGYOV 361
Db 304 PDLISKIFDDTLVQTFHTHVAFTVDNHDSPHEALSISWIGDMFKPSAVALITLRLDGYFV 363
Qy 362 FVGDMVGTGK----DSOREIPALKKIEPIILAKRQYVGAQHDYFDHHDVGTREBDS 417
Db 364 FYGDYIGGPGPPVQKKEI-----LDLISARCNKAYGEQEDYFDHANTIGWRRGVE 417
Qy 418 SVANSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSRGWGFPHVNGGSV 477
Db 418 EIESSGCAVINSNGDGEKRMFIEGRHAGEVAVDLTKSCDDQITIEEDGMATFHVCGGV 477
Qy 478 STY 480
Db 478 SVW 480
```

RESULT 14

```
Q8YU21 PRELIMINARY; PRT; 492 AA.
ID Q8YU21
AC Q8YU21
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Alpha-amyase.
GN ALR2190.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxId=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriyuchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.,
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003588; BAB73889.1; -.
DR PIR; AH2079; AH2079.
DR GO; GO:0004556; P:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
KW Complete proteome.
SQ SEQUENCE 492 AA; 57063 MW; 11B5D6EC2F18288 CRC64;
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Query Match 46.7%; Score 1244; DB 16; Length 492;
Best Local Similarity 47.5%; Pred. No. 5.2e-83;

Matches 234; Conservative 84; Mismatches 161; Indels 14; Gaps 6;

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Qy 1 ANLNGTLMQYFEMVMDGQHWRLQNDASVLAHGTITAVMIPYKKG-TSQADVGYAY 59
Db 2 AQNMGTMMQYFHWYIPMDGNLMSKVEASAPELADAGFTAWMLPWAYKGFAGSPDVGYVY 61
Qy 60 DLVDLGFHKGKRTVYGTGKGLQSAIKSLHSRDINVDYVINKGADAEEDYTAAY 119
Db 62 DLVDLGFHKGKRTVYGTGKGLQSAIKSLHSRDINVDYVINKGADAEEDYTAAY 119
```

```
Qy 120 VDPADRRNRVISEHLITAMTHFHPFGSGSTYSOPKMTWYHFDGTDWDESKLAR--LYKF 177
Db 122 FPQDDRILNPKGGLODITTYTHYNEPGRQKYSNEEMWHEFDVYNEVNSGSRSTYLL 181
Qy 178 QGKAMDEVSENENGVNDYLMYADIDYDHPVAEIKRWGTVYANELODGFRLDAVKH1K 237
Db 182 EGRKFPDYLVALEKKNFAYLNGCOLDPQNEVNRGEVYTWGKRCDDTTYKDFRDLAIKHIS 241
Qy 238 FSPLRDMVNHVREKTEGKEMFTVAEYMONDICALENYINKTNFNHVSFVDYLAHQFPAAS 297
Db 242 TWFPPEWIDALERRHAGKDLFMVEGEYVNDINTLLMTYDVARGKGSYFEDVLAHNFQASK 301
Qy 298 QGGSYDMRKLNKTVSKHPKLSVTVDNHDTPGSGLESTVQTWKPLAVALITLRESG 357
Db 302 SGGNVDMRRLIDTGMQRPHTHVAFTVEENHDSPQLALBESVBEWPKPLAVALITLRLDGY 361
Qy 358 YPOVFYGDYGTGK----GDSORE---IPALKKIEPIILAKRQYVGAQHDYFDHHDV 409
Db 362 YPCVTHADYIGAEYEDMGKDNRYNIFMESHRIIDTLAKRQYVGAQHDYFDHHDV 421
Qy 410 GMTREGSSVANSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSRGWGF 469
Db 422 GMTRELGDAD--HPQGMAYIMSDGSEGIKMEVGRKPT--KFDLTHH1KEAVYTNEMGWGE 478
Qy 470 FHNNGGSVSITYQ 482
Db 479 FRCLGGSVSVMVQ 491
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RESULT 15

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Q97049 PRELIMINARY; PRT; 484 AA.
ID Q97049
AC Q97049
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Alpha-amyase.
GN SP1382.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxId=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tetteelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapfel E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae."
RL Science 293:498-506(2001).
DR EMBL; AE007435; AAK75480.1; -.
DR PIR; G95160; G95160.
DR TIGR; SP1382; -.
DR GO; GO:0004556; P:alpha-amyase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amyase; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 484 AA; 55918 MW; 4B90A450A90EFB8C CRC64;
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Query Match 46.2%; Score 1233; DB 16; Length 484;

Best Local Similarity 48.6%; Pred. No. 3.3e-82;
Matches 234; Conservative 72; Mismatches 167; Indels 8; Gaps 4;

```
QY 4 NGTLMQYHEWMPNDGQWRLQNDSDATLAHGTITAWIPRAYKTSQADVGYGAYDLYD 63
Db 3 NQTLMOYFEWYLPFHQGOHTRLAENAPHLAHGISHWMPAPFAKATNEKDVGYGYDLFD 62
QY 64 LGEPHOKGTVTKTKGELQSAIKSLHSRDINVGVDVINHKGAADATEDVTAVEVDP 123
Db 63 LGERNQKGTVTKTKGKEDYLOAIQALKAQGIQPMADVVLNKAADHREAFQVIEVDPV 122
QY 124 DRNRVISEHLIKAWTHFHPGSGTYSDFKHWYHEDGTWDSRKLNRIYKFG--KA 181
Db 123 DRTVELGEPFTINGWTSTFTPDGRODTYNGFHMHWYHFTGTDYDAKRSKSGIYLIQGDNKG 182
QY 182 WDWE--VSNENGNDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDANKHIFS 239
Db 183 WANBELVDNENGNDYLMYADLDGKHPEVIONIYDMADMFMETTVAGFRLDAVKHIDSP 242
QY 240 FLRDMVNHVRREKTKGEMFTVAEYQNDLGALENTLNTNFHNSVFDVPLHYQFHAASDQ 299
Db 243 FMRNFIIDMKKRYGDDFYVGSFMPNDKEANLDYEKTEBHPDLVDVRLHONLPEASQAG 302
QY 300 GGYDMRKLLNGTVVSKHPLKSVTEVDNHDTPGQSLBSTVQTWPKPLAYAFILTRBSGYP 359
Db 303 ANYDLRGIFFTDSLVLKPKDKAVTFVDNHDTPGQALBSTVEWFKPAAYALILRQDGLP 362
QY 360 QVRYGDMYGTGDSQREIPALKHIEPILKARKOYANGAHYFDHHDIVGWTREGDSSV 419
Db 363 CVFYGDYGISGQYAE--DFKEILDRLLAIRKDLAYGEONDYFDHANCIGWVRSGAEN- 419
QY 420 ANSGIALITDGPAGAKMYVGRQAGETWHDITGNREBPVINSGEWGEFHNAGSYSI 479
Db 420 -QSPILAVLISNDQENSKSMFVGQEWNTQTFVDLIGNHQGYTIDEEGYGFPPVASRVSIV 478
QY 480 Y 480
Db 479 W 479
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Search completed: October 7, 2004, 00:18:59
Job time : 48.3093 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2004, 00:12:34 ; Search time 14.9658 Seconds
(without alignments)
1666.155 Million cell updates/sec

Title: US-09-925-576C-8

Perfect score: 2666

Sequence: 1 ANLNGTLMQYFEWYMPNDGQ.....SEGWGEFHVNGSVSIYQR 483

Scoring table: BIOSIM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/6C_COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2666	100.0	483	3	US-09-182-859-2
2	2666	100.0	483	3	US-09-170-670-4
3	2666	100.0	483	3	US-09-193-068-4
4	2666	100.0	483	3	US-09-183-412-4
5	2666	100.0	483	3	US-09-264-097-2
6	2666	100.0	483	4	US-09-291-023A-21
7	2666	100.0	483	4	US-09-290-724-4
8	2666	100.0	483	4	US-09-537-168-4
9	2666	100.0	483	4	US-09-672-459-2
10	2666	100.0	483	4	US-09-545-586-4
11	2666	100.0	483	4	US-09-540-715A-21
12	2666	100.0	483	4	US-10-186-042-2
13	2666	100.0	483	4	US-09-769-864-4
14	2666	100.0	512	1	US-08-720-899-2
15	2666	100.0	512	1	US-08-459-610-2
16	2666	100.0	512	2	US-08-343-804-2
17	2666	100.0	512	2	US-08-687-389-2
18	2666	100.0	512	2	US-08-600-908A-2
19	2666	100.0	512	4	US-08-683-838A-2
20	2666	100.0	512	3	US-09-636-252A-2
21	2666	100.0	631	3	US-08-814-052-8
22	2666	100.0	631	3	US-08-812-829-8
23	2663	99.9	483	1	US-08-468-700-34
24	2663	99.9	483	2	US-08-468-220-32
25	2663	99.9	483	2	US-08-468-698-32
26	2663	99.9	483	2	US-08-704-706A-34
27	2663	99.9	483	3	US-08-890-383-3

28	2663	99.9	483	3	US-08-914-679A-3	Sequence 3, Appli
29	2663	99.9	483	3	US-08-985-659-35	Sequence 35, Appli
30	2663	99.9	483	3	US-08-194-664A-32	Sequence 32, Appli
31	2663	99.9	483	5	PCT-US94-01553A-32	Sequence 32, Appli
32	2663	99.9	483	5	PCT-US95-10426-32	Sequence 32, Appli
33	2663	99.9	483	5	PCT-US95-10426-32	Sequence 32, Appli
34	2663	99.9	487	2	US-08-468-220-37	Sequence 37, Appli
35	2663	99.9	487	2	US-08-468-698-37	Sequence 37, Appli
36	2663	99.9	487	5	PCT-US94-01553A-37	Sequence 37, Appli
37	2663	99.9	487	5	PCT-US95-10426-37	Sequence 37, Appli
38	2663	99.9	512	1	US-07-623-953-3	Sequence 3, Appli
39	2663	99.9	512	1	US-07-623-953-5	Sequence 5, Appli
40	2663	99.9	512	3	US-08-985-659-34	Sequence 34, Appli
41	2657	99.7	483	2	US-08-468-220-36	Sequence 36, Appli
42	2657	99.7	483	2	US-08-468-698-36	Sequence 36, Appli
43	2657	99.7	483	3	US-08-194-664A-36	Sequence 36, Appli
44	2657	99.7	483	5	PCT-US94-01553A-36	Sequence 36, Appli
45	2657	99.7	483	5	PCT-US95-10426-36	Sequence 36, Appli

ALIGNMENTS

```
RESULT 1
US-09-182-859-2
Sequence 2, Application US/09182859
Patent No. 6143708
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borchert, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/09/182.859
CURRENT FILING DATE: 1998-10-29
EARLIER APPLICATION NUMBER: 0515/96
EARLIER FILING DATE: 1996-04-30
EARLIER APPLICATION NUMBER: 0712/96
EARLIER FILING DATE: 1996-06-28
EARLIER APPLICATION NUMBER: 0775/96
EARLIER FILING DATE: 1996-07-11
EARLIER APPLICATION NUMBER: 1263/96
EARLIER FILING DATE: 1996-11-08
NUMBER OF SEQ. ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-182-859-2
Query Match
100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
2 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
3 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
4 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
5 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
6 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
7 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
8 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
9 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
10 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
11 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
12 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
13 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
14 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
15 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
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21 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
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25 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
26 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
27 1 ANLNGTLMQYFEWYMPNDGQHWRLQNDASVLAHGTITAWIPRAYGTSGADVGYGYD 60
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Db 241 LRDVNVHVEKTKGEMFTVAEYWMQNDLGALENYLNKTNFNHNVFVPLHYQFHAASSTGG 300
Qy 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAAYAFILTRSGYPQ 360
Db 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAAYAFILTRSGYPQ 360
Qy 361 VFYGDWYGTGDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREBSSVA 420
Db 361 VFYGDWYGTGDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREBSSVA 420
Qy 421 NSGLAALITDGPAGAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGEFFHVGGSYSIY 480
Db 421 NSGLAALITDGPAGAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGEFFHVGGSYSIY 480
Qy 481 VQR 483
Db 481 VQR 483

RESULT 2
US-09-170-670-4
; Sequence 4, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; EARLIER FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: B. licheniformis
US-09-170-670-4

Query Match 100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 2,9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDASAYLAHSGITAVWIIPYKGTSGQADVGYAYD 60
Db 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDASAYLAHSGITAVWIIPYKGTSGQADVGYAYD 60
Qy 61 LYDLGEFHQKGTIVRTKYGTGKELQSAIKSLHSRDINVGVVJNHKGADATEDVTAVEV 120
Db 61 LYDLGEFHQKGTIVRTKYGTGKELQSAIKSLHSRDINVGVVJNHKGADATEDVTAVEV 120
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Db 121 DPADRNRVISEGHLIKAWTHFHPFGSGTYSDFKWHYHFDGTDWDSRKLNIYKFOGK 180
Qy 181 AMWMEVSNENGVYDLYMADIDYDHPDVAAEIKRWGTWYANLQDGFRLDAVKHIKFSF 240
Db 181 AMWMEVSNENGVYDLYMADIDYDHPDVAAEIKRWGTWYANLQDGFRLDAVKHIKFSF 240
Qy 241 LRDVNVHVEKTKGEMFTVAEYWMQNDLGALENYLNKTNFNHNVFVPLHYQFHAASSTGG 300
Db 241 LRDVNVHVEKTKGEMFTVAEYWMQNDLGALENYLNKTNFNHNVFVPLHYQFHAASSTGG 300
Qy 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAAYAFILTRSGYPQ 360
Db 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAAYAFILTRSGYPQ 360
Qy 361 VFYGDWYGTGDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREBSSVA 420
Db 361 VFYGDWYGTGDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREBSSVA 420

Db 361 VFYGDWYGTGDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREBSSVA 420
Qy 421 NSGLAALITDGPAGAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGEFFHVGGSYSIY 480
Db 421 NSGLAALITDGPAGAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGEFFHVGGSYSIY 480
Qy 481 VQR 483
Db 481 VQR 483

RESULT 3
US-09-193-068-4
; Sequence 4, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjulliff, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: B. licheniformis
US-09-193-068-4

Query Match 100.0%; Score 2666; DB 3; Length 483;
Best Local Similarity 100.0%; Pred. No. 2,9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDASAYLAHSGITAVWIIPYKGTSGQADVGYAYD 60
Db 1 ANLNGTLMQYFEMWMPNDGQHRRLQNDASAYLAHSGITAVWIIPYKGTSGQADVGYAYD 60
Qy 61 LYDLGEFHQKGTIVRTKYGTGKELQSAIKSLHSRDINVGVVJNHKGADATEDVTAVEV 120
Db 61 LYDLGEFHQKGTIVRTKYGTGKELQSAIKSLHSRDINVGVVJNHKGADATEDVTAVEV 120
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Db 121 DPADRNRVISEGHLIKAWTHFHPFGSGTYSDFKWHYHFDGTDWDSRKLNIYKFOGK 180
Qy 181 AMWMEVSNENGVYDLYMADIDYDHPDVAAEIKRWGTWYANLQDGFRLDAVKHIKFSF 240
Db 181 AMWMEVSNENGVYDLYMADIDYDHPDVAAEIKRWGTWYANLQDGFRLDAVKHIKFSF 240
Qy 241 LRDVNVHVEKTKGEMFTVAEYWMQNDLGALENYLNKTNFNHNVFVPLHYQFHAASSTGG 300
Db 241 LRDVNVHVEKTKGEMFTVAEYWMQNDLGALENYLNKTNFNHNVFVPLHYQFHAASSTGG 300
Qy 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAAYAFILTRSGYPQ 360
Db 301 GYDMRKLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAAYAFILTRSGYPQ 360
Qy 361 VFYGDWYGTGDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREBSSVA 420
Db 361 VFYGDWYGTGDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREBSSVA 420
Qy 421 NSGLAALITDGPAGAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGEFFHVGGSYSIY 480
Db 421 NSGLAALITDGPAGAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGEFFHVGGSYSIY 480
Qy 481 VQR 483
Db 481 VQR 483


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RESULT 4
US-09-183-412-4
; Sequence 4, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjærulff, Søren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-183-412-4
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Query Match 100.0%; Score 2666; DB 3; Length 483;

Best Local Similarity 100.0%; Pred. No. 2,9e-240; Mismatches 0; Indels 0; Gaps 0;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ANLNGTLMQYFEWMPNDGQHWRLQNDSAVLAHSGITAWIPRAYKTSQADVGYGAYD 60
QY 61 LYDGEFHQGTVAITKTKGTGELQSAIKLSHSDINVGDVINHKGADATEDVTAVEV 120
DB 61 LYDGEFHQGTVAITKTKGTGELQSAIKLSHSDINVGDVINHKGADATEDVTAVEV 120
QY 121 DPADRNVIISGEHLIKAWTHFHPFGSGTYSDFKMHYHFDGTWDSRKLNRITKQOK 180
DB 121 DPADRNVIISGEHLIKAWTHFHPFGSGTYSDFKMHYHFDGTWDSRKLNRITKQOK 180
QY 121 DPADRNVIISGEHLIKAWTHFHPFGSGTYSDFKMHYHFDGTWDSRKLNRITKQOK 180
DB 121 DPADRNVIISGEHLIKAWTHFHPFGSGTYSDFKMHYHFDGTWDSRKLNRITKQOK 180
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DB 181 AMDWESNENGNVYLYMADIDYDHPVAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
QY 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHSDVPLHYQFHAASQGG 300
DB 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHSDVPLHYQFHAASQGG 300
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DB 301 GYDMRKLLNGTVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAFAFLITRESGYPQ 360
QY 361 VFYGDWYGTGDSQREIPALHKIEPLIKARKQAYAGQHDYFPHHDIWGTRGDSOVA 420
DB 361 VFYGDWYGTGDSQREIPALHKIEPLIKARKQAYAGQHDYFPHHDIWGTRGDSOVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGRSEPVVINEGGEFFVNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGRSEPVVINEGGEFFVNGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483
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RESULT 5

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US-09-264-097-2
; Sequence 2, Application US/09264097
; Patent No. 6287826
; GENERAL INFORMATION:
; APPLICANT: Hendriksen, Hanne Vang
; APPLICANT: Enzymatic Preparation of Glucose Syrup
; TITLE OF INVENTION: From Starch
; FILE REFERENCE: 5278.200-US
; CURRENT APPLICATION NUMBER: US/09/264,097
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: PA 0321/98
; EARLIER FILING DATE: 1998-03-09
; EARLIER APPLICATION NUMBER: 60/079,209
; EARLIER FILING DATE: 1998-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-264-097-2
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Query Match 100.0%; Score 2666; DB 3; Length 483;

Best Local Similarity 100.0%; Pred. No. 2,9e-240; Mismatches 0; Indels 0; Gaps 0;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ANLNGTLMQYFEWMPNDGQHWRLQNDSAVLAHSGITAWIPRAYKTSQADVGYGAYD 60
QY 61 LYDGEFHQGTVAITKTKGTGELQSAIKLSHSDINVGDVINHKGADATEDVTAVEV 120
DB 61 LYDGEFHQGTVAITKTKGTGELQSAIKLSHSDINVGDVINHKGADATEDVTAVEV 120
QY 121 DPADRNVIISGEHLIKAWTHFHPFGSGTYSDFKMHYHFDGTWDSRKLNRITKQOK 180
DB 121 DPADRNVIISGEHLIKAWTHFHPFGSGTYSDFKMHYHFDGTWDSRKLNRITKQOK 180
QY 121 DPADRNVIISGEHLIKAWTHFHPFGSGTYSDFKMHYHFDGTWDSRKLNRITKQOK 180
DB 121 DPADRNVIISGEHLIKAWTHFHPFGSGTYSDFKMHYHFDGTWDSRKLNRITKQOK 180
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DB 181 AMDWESNENGNVYLYMADIDYDHPVAEIKRWGTWYANELQDGFRLDAVGHKFSF 240
QY 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHSDVPLHYQFHAASQGG 300
DB 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHSDVPLHYQFHAASQGG 300
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DB 301 GYDMRKLLNGTVSKHPLKSVTFVDNHDTPQGSLESTVQTFKPLAFAFLITRESGYPQ 360
QY 361 VFYGDWYGTGDSQREIPALHKIEPLIKARKQAYAGQHDYFPHHDIWGTRGDSOVA 420
DB 361 VFYGDWYGTGDSQREIPALHKIEPLIKARKQAYAGQHDYFPHHDIWGTRGDSOVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGRSEPVVINEGGEFFVNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGRSEPVVINEGGEFFVNGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483
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RESULT 6

US-09-291-023A-21

; Sequence 21, Application US/09291023A

; Patent No. 6309871

; GENERAL INFORMATION:

; APPLICANT: Outtrup, Helle

; APPLICANT: Borchert, Torben

; APPLICANT: Nielsen, Bjarne

; APPLICANT: Nielsen, Vibeke

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; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
; FILE OF INVENTION: Encoding Same
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/291,023A
; PRIOR FILING DATE: 1999-04-13
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 21
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus
US-09-291-023A-21
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Query Match      100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSAVLAHGITAWMIPPAKGTSGADVGAYD 60
DB      1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSAVLAHGITAWMIPPAKGTSGADVGAYD 60
QY      61 LYDLGEFHQKGTVRTKGTGKELQSAIKSLHSRDINVGDVVINHKGADATEDVTAVEV 120
DB      61 LYDLGEFHQKGTVRTKGTGKELQSAIKSLHSRDINVGDVVINHKGADATEDVTAVEV 120
QY      121 DPADRNKRVISGEHLIKAWTHFHPGRGSTYSDFKMHWYHFGDTWDESRKLNRIYKFGK 180
DB      121 DPADRNKRVISGEHLIKAWTHFHPGRGSTYSDFKMHWYHFGDTWDESRKLNRIYKFGK 180
QY      122 DPAADNRVVISGEHLIKAWTHFHPGRGSTYSDFKMHWYHFGDTWDESRKLNRIYKFGK 180
DB      122 DPAADNRVVISGEHLIKAWTHFHPGRGSTYSDFKMHWYHFGDTWDESRKLNRIYKFGK 180
QY      181 AMDWEVSENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKHIKFSF 240
DB      181 AMDWEVSENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKHIKFSF 240
QY      241 LRDWNVHREKTKGEMFTVAEYVQNDLGALENVYLNKTNFNHVSFDPVPLHYQFHAASVTOGG 300
DB      241 LRDWNVHREKTKGEMFTVAEYVQNDLGALENVYLNKTNFNHVSFDPVPLHYQFHAASVTOGG 300
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DB      301 GYDMRKLTNGTVSKRPKLSVTFVNDHDTOPQOSLESTVQTFWFPPLAYAFILTRSGVPQ 360
QY      361 VFYGDMYGTGKDSQREIPALKKIEPIIKARKQYAYGAQHDYFDHDI VGTWREGDSSVA 420
DB      361 VFYGDMYGTGKDSQREIPALKKIEPIIKARKQYAYGAQHDYFDHDI VGTWREGDSSVA 420
QY      421 NSGLAALITDGPAGAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
DB      421 NSGLAALITDGPAGAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
QY      481 VQR 483
DB      481 VQR 483
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RESULT 7
US-09-290-734-4
; Sequence 4, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Tordzen Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylaae And -Amylaae Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
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; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: B. licheniformis
US-09-290-734-4
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Query Match      100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSAVLAHGITAWMIPPAKGTSGADVGAYD 60
DB      1 ANLNGTLMQYFEMWMPNDGQHRRLQNDSAVLAHGITAWMIPPAKGTSGADVGAYD 60
QY      61 LYDLGEFHQKGTVRTKGTGKELQSAIKSLHSRDINVGDVVINHKGADATEDVTAVEV 120
DB      61 LYDLGEFHQKGTVRTKGTGKELQSAIKSLHSRDINVGDVVINHKGADATEDVTAVEV 120
QY      121 DPADRNKRVISGEHLIKAWTHFHPGRGSTYSDFKMHWYHFGDTWDESRKLNRIYKFGK 180
DB      121 DPADRNKRVISGEHLIKAWTHFHPGRGSTYSDFKMHWYHFGDTWDESRKLNRIYKFGK 180
QY      181 AMDWEVSENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKHIKFSF 240
DB      181 AMDWEVSENGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQDGFRLDAVKHIKFSF 240
QY      241 LRDWNVHREKTKGEMFTVAEYVQNDLGALENVYLNKTNFNHVSFDPVPLHYQFHAASVTOGG 300
DB      241 LRDWNVHREKTKGEMFTVAEYVQNDLGALENVYLNKTNFNHVSFDPVPLHYQFHAASVTOGG 300
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DB      301 GYDMRKLTNGTVSKRPKLSVTFVNDHDTOPQOSLESTVQTFWFPPLAYAFILTRSGVPQ 360
QY      361 VFYGDMYGTGKDSQREIPALKKIEPIIKARKQYAYGAQHDYFDHDI VGTWREGDSSVA 420
DB      361 VFYGDMYGTGKDSQREIPALKKIEPIIKARKQYAYGAQHDYFDHDI VGTWREGDSSVA 420
QY      421 NSGLAALITDGPAGAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
DB      421 NSGLAALITDGPAGAKRMVYGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
QY      481 VQR 483
DB      481 VQR 483
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RESULT 8
US-09-537-168-4
; Sequence 4, Application US/09537168
; Patent No. 6410295
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulf, Soren
; TITLE OF INVENTION: Alpha-Amylaae Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/09/537,168
; CURRENT FILING DATE: 2000-03-29
; EARLIER APPLICATION NUMBER: PA 1999 00437
; EARLIER FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: 60/127,427
; EARLIER FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
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US-09-537-168-4

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANLNGTLMQYFEWMPNDGQHRRLQNDSDAVLAHGTTAVIIPRAYKTSQADVGYGAYD 60
DB 1 ANLNGTLMQYFEWMPNDGQHRRLQNDSDAVLAHGTTAVIIPRAYKTSQADVGYGAYD 60
QY 61 LYDGEFHQKGTAVTKYGTGELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
DB 61 LYDGEFHQKGTAVTKYGTGELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
QY 121 DPADRNVI GSEHLIKAMTHFHPGRGSTYSDFKMHWHPDGTMDSRKLNRIYKFGQK 180
DB 121 DPADRNVI GSEHLIKAMTHFHPGRGSTYSDFKMHWHPDGTMDSRKLNRIYKFGQK 180
QY 181 AMDWEVENENGNVYLYMADIDYDHPVAAEIKKMGTYANELQDGFRLDAVXHKIKFSF 240
DB 181 AMDWEVENENGNVYLYMADIDYDHPVAAEIKKMGTYANELQDGFRLDAVXHKIKFSF 240
QY 241 LRDMVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFNHSPVDPVPLHYQFHAASQTGG 300
DB 241 LRDMVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFNHSPVDPVPLHYQFHAASQTGG 300
QY 301 GYDMRKLLNGTVASKHPLKSTFVDNHDTPQGSLESTVQTFMFKPLAYAFILITRESGPQ 360
DB 301 GYDMRKLLNGTVASKHPLKSTFVDNHDTPQGSLESTVQTFMFKPLAYAFILITRESGPQ 360
QY 361 VFYGDWMTGKDSQREIIPALGHKIEPILKARKQAYAGQHDYFPHHDI VGTREGDSSVA 420
DB 361 VFYGDWMTGKDSQREIIPALGHKIEPILKARKQAYAGQHDYFPHHDI VGTREGDSSVA 420
QY 421 NSGLAALITDGPQGA KMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
DB 421 NSGLAALITDGPQGA KMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483
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RESULT 9

US-09-672-459-2
; Sequence 2, Application US/09672459
; Patent No. 6436888
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Biegaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/09/672.459
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-672-459-2

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANLNGTLMQYFEWMPNDGQHRRLQNDSDAVLAHGTTAVIIPRAYKTSQADVGYGAYD 60
DB 1 ANLNGTLMQYFEWMPNDGQHRRLQNDSDAVLAHGTTAVIIPRAYKTSQADVGYGAYD 60
QY 61 LYDGEFHQKGTAVTKYGTGELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
DB 61 LYDGEFHQKGTAVTKYGTGELQSAIKSLHSRDINVGDVVNHKGADATEDVTAVEV 120
QY 121 DPADRNVI GSEHLIKAMTHFHPGRGSTYSDFKMHWHPDGTMDSRKLNRIYKFGQK 180
DB 121 DPADRNVI GSEHLIKAMTHFHPGRGSTYSDFKMHWHPDGTMDSRKLNRIYKFGQK 180
QY 181 AMDWEVENENGNVYLYMADIDYDHPVAAEIKKMGTYANELQDGFRLDAVXHKIKFSF 240
DB 181 AMDWEVENENGNVYLYMADIDYDHPVAAEIKKMGTYANELQDGFRLDAVXHKIKFSF 240
QY 241 LRDMVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFNHSPVDPVPLHYQFHAASQTGG 300
DB 241 LRDMVNHVREKTKGEMFTVAEYQNDLGALENYLNKTNFNHSPVDPVPLHYQFHAASQTGG 300
QY 301 GYDMRKLLNGTVASKHPLKSTFVDNHDTPQGSLESTVQTFMFKPLAYAFILITRESGPQ 360
DB 301 GYDMRKLLNGTVASKHPLKSTFVDNHDTPQGSLESTVQTFMFKPLAYAFILITRESGPQ 360
QY 361 VFYGDWMTGKDSQREIIPALGHKIEPILKARKQAYAGQHDYFPHHDI VGTREGDSSVA 420
DB 361 VFYGDWMTGKDSQREIIPALGHKIEPILKARKQAYAGQHDYFPHHDI VGTREGDSSVA 420
QY 421 NSGLAALITDGPQGA KMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
DB 421 NSGLAALITDGPQGA KMYVGRQNAGETWHDITGNRSEPVVINSBGWGEFHVNGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483
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RESULT 10

US-09-545-586-4
; Sequence 4, Application US/09545586
; Patent No. 6528298
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Biegaard-Frantzen Henrik
; APPLICANT: Oultrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6528298e1 -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/545.586
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US/09/290.734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: B. licheniformis
US-09-545-586-4

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANLNGTLMQYFEWMPNDGQHRRLQNDSDAVLAHGTTAVIIPRAYKTSQADVGYGAYD 60
DB 1 ANLNGTLMQYFEWMPNDGQHRRLQNDSDAVLAHGTTAVIIPRAYKTSQADVGYGAYD 60
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Db      1 ANINGTLMQYFEWYMPNDGQHMRLQNDSAVLAHEGITAIVIPAYKGTSGQADVGYAYD 60
Qy      61 LYDGEFHQGTATKTKGTGELQSAIKSLHSRDINVGUVVINHGADATEDVTAVEV 120
Db      61 LYDGEFHQGTATKTKGTGELQSAIKSLHSRDINVGUVVINHGADATEDVTAVEV 120
Qy      121 DPADRNRVVISGEHLIKAMTHFFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNRITYFGQK 180
Db      121 DPADRNRVVISGEHLIKAMTHFFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNRITYFGQK 180
Qy      181 AMDVSVNSNGNNDYIMYADIDYDHPVAAEIKRMGTWYANELQDGFRLDAVKHIFSF 240
Db      181 AMDVSVNSNGNNDYIMYADIDYDHPVAAEIKRMGTWYANELQDGFRLDAVKHIFSF 240
Qy      241 LRDVNVHREKTKGEMFTVAEYWMQNDLGALENTLNKTNFHSVFDVPLHYQFHAASQGG 300
Db      241 LRDVNVHREKTKGEMFTVAEYWMQNDLGALENTLNKTNFHSVFDVPLHYQFHAASQGG 300
Qy      301 GYDMRKLNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAAYAFILTRSGYPQ 360
Db      301 GYDMRKLNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAAYAFILTRSGYPQ 360
Qy      361 VFYGDMTGTGDSQREIPALKKHIEPLIKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA 420
Db      361 VFYGDMTGTGDSQREIPALKKHIEPLIKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA 420
Qy      421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSBGMEFHVNGSSVSIY 480
Db      421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSBGMEFHVNGSSVSIY 480
Qy      481 VOR 483
Db      481 VOR 483

RESULT 11
US-09-540-715A-21
; Sequence 21, Application US/09540715A
; Patent No. 6623948
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjørne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A
; FILE REFERENCE: 5821, 010-US
; CURRENT APPLICATION NUMBER: US/09/540, 715A
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/291, 023
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent version 3.0
; SEQ ID NO 21
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus
US-09-540-715A-21

Query Match      100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      121 DPADRNRVVISGEHLIKAMTHFFHPGRGSTYSDPKMWHYHFDGTDWDSRKLNRITYFGQK 180
Qy      181 AMDVSVNSNGNNDYIMYADIDYDHPVAAEIKRMGTWYANELQDGFRLDAVKHIFSF 240
Db      181 AMDVSVNSNGNNDYIMYADIDYDHPVAAEIKRMGTWYANELQDGFRLDAVKHIFSF 240
Qy      241 LRDVNVHREKTKGEMFTVAEYWMQNDLGALENTLNKTNFHSVFDVPLHYQFHAASQGG 300
Db      241 LRDVNVHREKTKGEMFTVAEYWMQNDLGALENTLNKTNFHSVFDVPLHYQFHAASQGG 300
Qy      301 GYDMRKLNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAAYAFILTRSGYPQ 360
Db      301 GYDMRKLNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTFKPLAAYAFILTRSGYPQ 360
Qy      361 VFYGDMTGTGDSQREIPALKKHIEPLIKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA 420
Db      361 VFYGDMTGTGDSQREIPALKKHIEPLIKARKQYAYGAQHDYFDHHDIVGWTREGDSSVA 420
Qy      421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSBGMEFHVNGSSVSIY 480
Db      421 NSGLAALITDGPQAKRMVYGRQNAGETWHDITGNRSEPVVINSBGMEFHVNGSSVSIY 480
Qy      481 VOR 483
Db      481 VOR 483

RESULT 12
US-10-186-042-2
; Sequence 2, Application US/10186042
; Patent No. 6642044
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgaard-Frantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796, 204-US
; CURRENT APPLICATION NUMBER: US/10/186, 042
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/572, 459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182, 859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-186-042-2

Query Match      100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 121 DPAORNRVISEHILIKAMTHHFGPGSTYSDFKMHYHFGDGTOWDSRKLNRITYKFGK 180
Qy 181 AMDVSNENGNNDYLYMADIDYHPVAAEIKKMGWYANELDQGRFLDAVGHKIFSF 240
Db 181 AMDVSNENGNNDYLYMADIDYHPVAAEIKKMGWYANELDQGRFLDAVGHKIFSF 240
Qy 241 LRDVNVHVRKTEKEMFTVAEYWMQNDLGALENYLNKTNPNHNSVDPVPLHYQFHAASQGG 300
Db 241 LRDVNVHVRKTEKEMFTVAEYWMQNDLGALENYLNKTNPNHNSVDPVPLHYQFHAASQGG 300
Qy 301 GYDMRKLLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAYAFILITRESGPQ 360
Db 301 GYDMRKLLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAYAFILITRESGPQ 360
Qy 361 VFYGDWYGTGDSQREIPLAKHKIEPLIKARKQYAYAGQHDYFPHHDI VGMTRGDSVA 420
Db 361 VFYGDWYGTGDSQREIPLAKHKIEPLIKARKQYAYAGQHDYFPHHDI VGMTRGDSVA 420
Qy 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVYINSENGEFPVNGSVISY 480
Db 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVYINSENGEFPVNGSVISY 480
Qy 481 VQR 483
Db 481 VQR 483

RESULT 13
US-09-769-864-4
; Sequence 4, Application US/09769864
; Patent No. 6673589
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-769-864-4

Query Match 100.0%; Score 2666; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.9e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ANLNGTLMQYFEWMPNDGQHMRLONDSAYLAHGIATWVIPPAYKSTQADVGAYD 60
Db 1 ANLNGTLMQYFEWMPNDGQHMRLONDSAYLAHGIATWVIPPAYKSTQADVGAYD 60
Qy 61 LYDGEFHQKQVTKYTKGKELQSAIKLSHRDINVGAVVINKGADATEDVTAVEV 120
Db 61 LYDGEFHQKQVTKYTKGKELQSAIKLSHRDINVGAVVINKGADATEDVTAVEV 120
Qy 121 DPADNRNRYISEGHLIKAWTHFHPGPGSTYSDFKMHYHFGDGTOWDSRKLNRITYKFGK 180
Db 121 DPADNRNRYISEGHLIKAWTHFHPGPGSTYSDFKMHYHFGDGTOWDSRKLNRITYKFGK 180
Qy 181 AMDVSNENGNNDYLYMADIDYHPVAAEIKKMGWYANELDQGRFLDAVGHKIFSF 240
Db 181 AMDVSNENGNNDYLYMADIDYHPVAAEIKKMGWYANELDQGRFLDAVGHKIFSF 240

Qy 241 LRDVNVHVRKTEKEMFTVAEYWMQNDLGALENYLNKTNPNHNSVDPVPLHYQFHAASQGG 300
Db 241 LRDVNVHVRKTEKEMFTVAEYWMQNDLGALENYLNKTNPNHNSVDPVPLHYQFHAASQGG 300
Qy 301 GYDMRKLLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAYAFILITRESGPQ 360
Db 301 GYDMRKLLNGTVVSKHPLKSVTFVNDHDTOPGQSLSTVQTFKPLAYAFILITRESGPQ 360
Qy 361 VFYGDWYGTGDSQREIPLAKHKIEPLIKARKQYAYAGQHDYFPHHDI VGMTRGDSVA 420
Db 361 VFYGDWYGTGDSQREIPLAKHKIEPLIKARKQYAYAGQHDYFPHHDI VGMTRGDSVA 420
Qy 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVYINSENGEFPVNGSVISY 480
Db 421 NSGLAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVYINSENGEFPVNGSVISY 480
Qy 481 VQR 483
Db 481 VQR 483

RESULT 14
US-08-720-899-2
; Sequence 2, Application US/08720899
; Patent No. 5753460
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5753460 No. 5753460disk of No. 5753460th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,899
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowrey Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-720-899-2

Query Match 100.0%; Score 2666; DB 1; Length 512;
Best Local Similarity 100.0%; Pred. No. 3.2e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ANLNGTLMQYFEWMPNDGQHMRLONDSAYLAHGIATWVIPPAYKSTQADVGAYD 60

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Db 30 ANLNGTLMQFEMWMPNDGQHRRLQNDSAVYLAHGTITAWIPPAKYKTSQADVGCAYD 89
QY 61 LYDLGEFHQKGTVRTKTKYGTGKGLQSAIKSLHSRDINVGDVVINKGADATEDVTAVEV 120
Db 90 LYDLGEFHQKGTVRTKTKYGTGKGLQSAIKSLHSRDINVGDVVINKGADATEDVTAVEV 149
QY 121 DPADNRNVIISGEHLIKAWTHFHPGRGSTYSDPKMWHYFDGTWDBSRKLNRIYKFGOK 180
Db 150 DPADNRNVIISGEHLIKAWTHFHPGRGSTYSDPKMWHYFDGTWDBSRKLNRIYKFGOK 209
QY 181 AMDWEVSNEKNGDYDLYMTADIDYDHPDVAAEIKRWGTWYANLQDGFRLDAVKHKFSF 240
Db 210 AMDWEVSNEKNGDYDLYMTADIDYDHPDVAAEIKRWGTWYANLQDGFRLDAVKHKFSF 269
QY 241 LRDVNVHVRKTKGKEMFTVAEYQNDLGALENYLNTKTNFNSVFPVPLHYQFHAASSTGG 300
Db 270 LRDVNVHVRKTKGKEMFTVAEYQNDLGALENYLNTKTNFNSVFPVPLHYQFHAASSTGG 329
QY 301 GYDMRKLNGTVSKHPLKSVTFVDNHDTPQGSLSTVQTMFKPLAVALFILTRESGYPO 360
Db 330 GYDMRKLNGTVSKHPLKSVTFVDNHDTPQGSLSTVQTMFKPLAVALFILTRESGYPO 389
QY 361 VFYGMWGTGKDSQREIPALKHKEIPILKARKQYAYGAQHDYFDHHDIVGWTREGSSVA 420
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QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSRPVYINSBGWGFHNVGGSVSIY 480
Db 450 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSRPVYINSBGWGFHNVGGSVSIY 509
QY 481 VQR 483
Db 510 VQR 512

RESULT 15
US-08-459-610-2
; Sequence 2, Application US/08459610
; Patent No. 5801043
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: No. 58010430 No. 5801043disk of No. 5801043th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,610
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowmey Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054,214-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-610-2

Query Match 100.0%; Score 2666; DB 1; Length 512;
Best Local Similarity 100.0%; Pred. No. 3,2e-240;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQFEMWMPNDGQHRRLQNDSAVYLAHGTITAWIPPAKYKTSQADVGCAYD 60
Db 30 ANLNGTLMQFEMWMPNDGQHRRLQNDSAVYLAHGTITAWIPPAKYKTSQADVGCAYD 89
QY 61 LYDLGEFHQKGTVRTKTKYGTGKGLQSAIKSLHSRDINVGDVVINKGADATEDVTAVEV 120
Db 90 LYDLGEFHQKGTVRTKTKYGTGKGLQSAIKSLHSRDINVGDVVINKGADATEDVTAVEV 149
QY 121 DPADNRNVIISGEHLIKAWTHFHPGRGSTYSDPKMWHYFDGTWDBSRKLNRIYKFGOK 180
Db 150 DPADNRNVIISGEHLIKAWTHFHPGRGSTYSDPKMWHYFDGTWDBSRKLNRIYKFGOK 209
QY 181 AMDWEVSNEKNGDYDLYMTADIDYDHPDVAAEIKRWGTWYANLQDGFRLDAVKHKFSF 240
Db 210 AMDWEVSNEKNGDYDLYMTADIDYDHPDVAAEIKRWGTWYANLQDGFRLDAVKHKFSF 269
QY 241 LRDVNVHVRKTKGKEMFTVAEYQNDLGALENYLNTKTNFNSVFPVPLHYQFHAASSTGG 300
Db 270 LRDVNVHVRKTKGKEMFTVAEYQNDLGALENYLNTKTNFNSVFPVPLHYQFHAASSTGG 329
QY 301 GYDMRKLNGTVSKHPLKSVTFVDNHDTPQGSLSTVQTMFKPLAVALFILTRESGYPO 360
Db 330 GYDMRKLNGTVSKHPLKSVTFVDNHDTPQGSLSTVQTMFKPLAVALFILTRESGYPO 389
QY 361 VFYGMWGTGKDSQREIPALKHKEIPILKARKQYAYGAQHDYFDHHDIVGWTREGSSVA 420
Db 390 VFYGMWGTGKDSQREIPALKHKEIPILKARKQYAYGAQHDYFDHHDIVGWTREGSSVA 449
QY 421 NSGLAALITDGPAGAKRMVYGRONAGETWHDITGNRSRPVYINSBGWGFHNVGGSVSIY 480
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QY 481 VQR 483
Db 510 VQR 512

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Search completed: October 7, 2004, 00:47:10
Job time : 16.9658 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2004, 00:19:14 ; Search time 53.2274 Seconds

(without alignments)
2920.093 Million cell updates/sec

Title: US-09-925-576C-8

Perfect score: 2666
Sequence: 1 ANNGTLMQYFEWYMPDGO.....SEGNGERHNGSVSYVQR 483Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2666	100.0	483	9	US-09-854-346-8
3	2666	100.0	483	9	US-09-918-543-8
4	2666	100.0	483	9	US-09-918-543-30
5	2666	100.0	483	10	US-09-925-576C-8
6	2666	100.0	483	12	US-10-665-667-4
7	2666	100.0	483	12	US-10-644-187-2
8	2666	100.0	483	12	US-10-327-837-2
9	2666	100.0	483	14	US-10-146-327-4
10	2666	100.0	483	14	US-10-186-042-2
11	2666	100.0	483	16	US-10-359-161-6
12	2666	100.0	483	16	US-10-477-725-8
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15	2654	99.5	512	14	US-10-081-872-114

16	2654	99.5	512	14	US-10-105-733-8	Sequence 8, Appli
17	2654	99.5	512	14	US-10-081-739A-8	Sequence 8, Appli
18	2654	99.5	512	15	US-10-385-305-114	Sequence 114, App
19	2582	96.8	481	14	US-10-146-327-2	Sequence 2, Appli
20	2338	87.7	483	14	US-10-184-771-13	Sequence 13, Appli
21	2184	81.9	483	9	US-09-854-346-10	Sequence 10, Appli
22	2184	81.9	483	9	US-09-918-543-10	Sequence 10, Appli
23	2184	81.9	483	10	US-09-925-576C-10	Sequence 6, Appli
24	2184	81.9	483	16	US-10-146-327-6	Sequence 10, Appli
25	2184	81.9	483	14	US-10-477-725-10	Sequence 10, Appli
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33	1999	75.0	513	15	US-10-081-872-146	Sequence 146, App
34	1979	74.2	513	15	US-10-385-305-146	Sequence 166, App
35	1979	74.2	513	15	US-10-081-872-166	Sequence 166, App
36	1961	73.6	478	14	US-10-081-872-166	Sequence 166, App
37	1961	73.6	478	15	US-10-385-305-166	Sequence 166, App
38	1950	73.1	485	9	US-09-769-864-2	Sequence 2, Appli
39	1950	73.1	485	9	US-09-769-864-8	Sequence 8, Appli
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44	1950	73.1	485	10	US-09-925-576C-4	Sequence 4, Appli
45	1950	73.1	485	12	US-10-665-667-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-769-864-4
Sequence 4, Application US/09769864
Patent No. US20010039253A1
GENERAL INFORMATION:
APPLICANT: Borchert, Torben V.
APPLICANT: Svendsen, Allan
APPLICANT: Andersen, Carsten
APPLICANT: Nielsen, Bjørne
APPLICANT: Nielsen, Torben U.
APPLICANT: Kjærulff, Søren
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 5368.200-US
CURRENT APPLICATION NUMBER: US/09/769,864
CURRENT FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/183,412
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-09-769-864-4

Query Match 100.0%; Score 2666; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-239; Indels 0; Gaps 0;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      481 VQR 483
Db      481 VQR 483
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RESULT 2
US-09-854-346-8
; Sequence 8, Application US/09854346
; Patent No. US20020068352A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020068352A1ozymes A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Jorgensen, Christel Thea
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
; FILE REFERENCE: 6140.200-US
; CURRENT APPLICATION NUMBER: US/09/854,346
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 483
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; ORGANISM: Bacillus licheniformis
US-09-854-346-8
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Query Match      100.0%; Score 2666; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-239;
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Qy      481 VQR 483
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RESULT 3
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; Sequence 8, Application US/09918543
; Patent No. US20020155574A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020155574A1ozymes A/S
; APPLICANT: Kjaerulff, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Fuglsang, Claus Crone
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062.200-US
; CURRENT APPLICATION NUMBER: US/09/918,543
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-09-918-543-8
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Query Match      100.0%; Score 2666; DB 9; Length 483;
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Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 30, Application US/09918543
; Patent No. US2002015574A1
; GENERAL INFORMATION:
; APPLICANT: No. US2002015574A1ozymes A/S
; APPLICANT: Thisted, Thomas
; APPLICANT: Kjaerulff, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Fuglsang, Claus Crone
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062.200-US
; CURRENT APPLICATION NUMBER: US/09/918,543
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 30
; LENGTH: 483
; TYPE: PR1
; ORGANISM: Bacillus licheniformis
US-09-918-543-30

Query Match 100.0%; Score 2666; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 LYDGEFHQKGTVTKYGTGGELOSATKSLHSRDINYGVDVINHKGAADTEVTAVEV 120
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Db 181 AMDWEVSNGENGYDLYMADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVGHKIFSF 240
QY 241 LRDVNVNVRREKTGEMFTVAEYMONDGALENYLNKTNFNHSDVDVPLHYOFHAASFOGG 300
Db 241 LRDVNVNVRREKTGEMFTVAEYMONDGALENYLNKTNFNHSDVDVPLHYOFHAASFOGG 300
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Db 421 NSGIAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSEGWGEFFVNGSVSIY 480
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Db 481 VOR 483

RESULT 5
US-09-925-576C-8
; Sequence 8, Application US/09925576C

; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004.204-US
; CURRENT APPLICATION NUMBER: US/09/925,576C
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 483
; TYPE: PR1
; ORGANISM: Bacillus licheniformis
US-09-925-576C-8

Query Match 100.0%; Score 2666; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 LYDGEFHQKGTVTKYGTGGELOSATKSLHSRDINYGVDVINHKGAADTEVTAVEV 120
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Db 121 DPADRNRVISEGHLIKAMTFHFPPGRGSTYSDPFKMHVYHFDGTDWDSRKLNR1YKFGQK 180
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Db 181 AMDWEVSNGENGYDLYMADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVGHKIFSF 240
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Db 241 LRDVNVNVRREKTGEMFTVAEYMONDGALENYLNKTNFNHSDVDVPLHYOFHAASFOGG 300
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Db 361 VFYGDWYGTGDSQREIPALKHKIEPILKAKQYAYGAQHDYFDHDI VGTWREGDSSVA 420
QY 421 NSGIAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSEGWGEFFVNGSVSIY 480
Db 421 NSGIAALITDGPAGAKMYVGRONAGETWHDITGNRSEPVVINSEGWGEFFVNGSVSIY 480
QY 481 VOR 483
Db 481 VOR 483

RESULT 6
US-10-665-667-4
; Sequence 4, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19

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/ PRIOR APPLICATION NUMBER: US/09/769,864
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 09/183,412
/ PRIOR FILING DATE: 1998-10-30
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 483
/ TYPE: PRF
/ ORGANISM: Bacillus licheniformis
US-10-665-667-4
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Query Match      100.0%; Score 2666; DB 12; Length 483;
Best Local Similarity 100.0%; Pred. No. 8,2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 DPADRNRVISGEHLIKAWTHFFHPPGRGSTYSDPKMWHYFDGTDWDESKLNRIYKFGOK 180
DB 121 DPADRNRVISGEHLIKAWTHFFHPPGRGSTYSDPKMWHYFDGTDWDESKLNRIYKFGOK 180
QY 181 AMDWEVSNENGVYDLYMADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKIKFSF 240
DB 181 AMDWEVSNENGVYDLYMADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKIKFSF 240
QY 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHSDVFPVPLHYQFHAASSTOGG 300
DB 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHSDVFPVPLHYQFHAASSTOGG 300
QY 301 GYDMRKILNGTVVSKPLKSVTFVDNHDTPQGSLESTVQTFKPLAFAFILTRESGYPO 360
DB 301 GYDMRKILNGTVVSKPLKSVTFVDNHDTPQGSLESTVQTFKPLAFAFILTRESGYPO 360
QY 361 VFYGMVGTGDSQREIPALKEIEPIILKARQYAYGAQHDYFPHHDIIVGWTREDSVA 420
DB 361 VFYGMVGTGDSQREIPALKEIEPIILKARQYAYGAQHDYFPHHDIIVGWTREDSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVYINSGWGEFHYNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVYINSGWGEFHYNGGSVSIY 480
QY 481 VOR 483
DB 481 VOR 483
```

```
RESULT 7
US-10-644-187-2
/ Sequence 2, Application US/10644187
/ Publication No. US20040048351A1
/ GENERAL INFORMATION:
/ APPLICANT: Svendsen, Allan
/ APPLICANT: Borchert, Torben
/ APPLICANT: Bisgard-Frantzen, Henrik
/ TITLE OF INVENTION: Alpha-Amylase Mutants
/ FILE REFERENCE: 4796.204-US
/ CURRENT APPLICATION NUMBER: US/10/644,187
/ PRIOR APPLICATION NUMBER: 09/182,859
/ PRIOR FILING DATE: 1998-10-29
/ PRIOR APPLICATION NUMBER: 0515/96
/ PRIOR FILING DATE: 1996-04-30
/ PRIOR APPLICATION NUMBER: 0712/96
/ PRIOR FILING DATE: 1996-06-28
/ PRIOR APPLICATION NUMBER: 0775/96
/ PRIOR FILING DATE: 1996-07-11
```

```
/ PRIOR APPLICATION NUMBER: 1263/96
/ PRIOR FILING DATE: 1996-11-08
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 483
/ TYPE: PRF
/ ORGANISM: Bacillus licheniformis
US-10-644-187-2
```

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Query Match      100.0%; Score 2666; DB 12; Length 483;
Best Local Similarity 100.0%; Pred. No. 8,2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 1 ANINGTLMQYFEMWMPNDGQHWRLQNDASAYLAHSGITAWIPPAKGTSGADVGAYD 60
DB 1 ANINGTLMQYFEMWMPNDGQHWRLQNDASAYLAHSGITAWIPPAKGTSGADVGAYD 60
QY 61 LYDLGEFHQKGTVRTKTKGELQSAIKSLHSDINVYGDVYINHGADATEDVTAVEV 120
DB 61 LYDLGEFHQKGTVRTKTKGELQSAIKSLHSDINVYGDVYINHGADATEDVTAVEV 120
QY 121 DPADRNRVISGEHLIKAWTHFFHPPGRGSTYSDPKMWHYFDGTDWDESKLNRIYKFGOK 180
DB 121 DPADRNRVISGEHLIKAWTHFFHPPGRGSTYSDPKMWHYFDGTDWDESKLNRIYKFGOK 180
QY 121 DPADRNRVISGEHLIKAWTHFFHPPGRGSTYSDPKMWHYFDGTDWDESKLNRIYKFGOK 180
DB 121 DPADRNRVISGEHLIKAWTHFFHPPGRGSTYSDPKMWHYFDGTDWDESKLNRIYKFGOK 180
QY 181 AMDWEVSNENGVYDLYMADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKIKFSF 240
DB 181 AMDWEVSNENGVYDLYMADIDYDHPDVAEIKRWGTWYANELQDGFRLDAVKIKFSF 240
QY 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHSDVFPVPLHYQFHAASSTOGG 300
DB 241 LRDVNVHVRKTKGEMFTVAEYQNDLGALENYLNKTNFNHSDVFPVPLHYQFHAASSTOGG 300
QY 301 GYDMRKILNGTVVSKPLKSVTFVDNHDTPQGSLESTVQTFKPLAFAFILTRESGYPO 360
DB 301 GYDMRKILNGTVVSKPLKSVTFVDNHDTPQGSLESTVQTFKPLAFAFILTRESGYPO 360
QY 361 VFYGMVGTGDSQREIPALKEIEPIILKARQYAYGAQHDYFPHHDIIVGWTREDSVA 420
DB 361 VFYGMVGTGDSQREIPALKEIEPIILKARQYAYGAQHDYFPHHDIIVGWTREDSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVYINSGWGEFHYNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVYINSGWGEFHYNGGSVSIY 480
QY 481 VOR 483
DB 481 VOR 483
```

```
RESULT 8
US-10-327-837-4
/ Sequence 4, Application US/10327837
/ Publication No. US20030211958A1
/ GENERAL INFORMATION:
/ APPLICANT: Svendsen, Allan
/ APPLICANT: Borchert, Torben Vedel
/ APPLICANT: Bisgard-Frantzen, Henrik
/ APPLICANT: Oustrup, Helle
/ APPLICANT: Nielsen, Bjarne Ronfeldt
/ APPLICANT: Nielsen, Vibeke Skovgaard
/ TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
/ FILE REFERENCE: 5276.400-US
/ CURRENT APPLICATION NUMBER: US/10/327,837
/ PRIOR APPLICATION NUMBER: 2002-12-23
/ PRIOR APPLICATION NUMBER: US/09/290,734
/ PRIOR FILING DATE: 1999-04-13
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 4
/ LENGTH: 483
```

TYPE: PRT
ORGANISM: B. licheniformis
US-10-327-837-4

Query Match 100.0%; Score 2666; DB 12; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ANLNGTLMQYFEWMPNDGQHWRLQNDSAVLAHGHTTAVWIPRAYKGTQADVGYGAYD 60
DB 1 ANLNGTLMQYFEWMPNDGQHWRLQNDSAVLAHGHTTAVWIPRAYKGTQADVGYGAYD 60
QY 61 LYDGEFHQKGTARTKKTGTGELQSAIKSLHSRDINYGVDVINHKGAADTEVTAVEV 120
DB 61 LYDGEFHQKGTARTKKTGTGELQSAIKSLHSRDINYGVDVINHKGAADTEVTAVEV 120
QY 121 DPADRNVISGEHLIKAWTHFHPGRGSTYSDFKMHHYHFDGTDWDSRKLRIYKFOGK 180
DB 121 DPADRNVISGEHLIKAWTHFHPGRGSTYSDFKMHHYHFDGTDWDSRKLRIYKFOGK 180
QY 181 AMDVESENENGYDLYMAYADIDYDHPVAAEIKKMGTYANELQDGFRLDAVGHKFSF 240
DB 181 AMDVESENENGYDLYMAYADIDYDHPVAAEIKKMGTYANELQDGFRLDAVGHKFSF 240
QY 241 LRDVNNHVRKTKGEMFTVAEYQNDGALENYLNKTNFNHSDVDPVPLHYQFHAASTOGG 300
DB 241 LRDVNNHVRKTKGEMFTVAEYQNDGALENYLNKTNFNHSDVDPVPLHYQFHAASTOGG 300
QY 301 GYDMRKLNGTVSKHPLKSVTFVNDHDTOPGQSLSTVQTFWFKPLAYAFILTRBSGYPQ 360
DB 301 GYDMRKLNGTVSKHPLKSVTFVNDHDTOPGQSLSTVQTFWFKPLAYAFILTRBSGYPQ 360
QY 361 VFYQDMYGTGDSQREIPLAKHKIEPIILKARKQYAYGAQHDYFPHHDI VGTREGDSSVA 420
DB 361 VFYQDMYGTGDSQREIPLAKHKIEPIILKARKQYAYGAQHDYFPHHDI VGTREGDSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFHVNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFHVNGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483
```

RESULT 9

US-10-146-327-4
Sequence 4, Application US/10146327
Publication No. US20030044954A1
GENERAL INFORMATION:
APPLICANT: Andersen, Carsten
APPLICANT: Jorgensen, Christel T.
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Svendsen, Allan
APPLICANT: Kjaerulff, Soren
TITLE OF INVENTION: Alpha-Amylase Variants
FILE REFERENCE: 5886.200-US
CURRENT APPLICATION NUMBER: US/10/146,327
PRIORITY FILING DATE: 2002-05-15
PRIORITY APPLICATION NUMBER: US/09/537,168
PRIORITY FILING DATE: 2000-03-29
PRIORITY APPLICATION NUMBER: PA 1999 00437
PRIORITY FILING DATE: 1999-03-30
PRIORITY APPLICATION NUMBER: 60/127,427
PRIORITY FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-146-327-4

Query Match 100.0%; Score 2666; DB 14; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ANLNGTLMQYFEWMPNDGQHWRLQNDSAVLAHGHTTAVWIPRAYKGTQADVGYGAYD 60
DB 1 ANLNGTLMQYFEWMPNDGQHWRLQNDSAVLAHGHTTAVWIPRAYKGTQADVGYGAYD 60
QY 61 LYDGEFHQKGTARTKKTGTGELQSAIKSLHSRDINYGVDVINHKGAADTEVTAVEV 120
DB 61 LYDGEFHQKGTARTKKTGTGELQSAIKSLHSRDINYGVDVINHKGAADTEVTAVEV 120
QY 121 DPADRNVISGEHLIKAWTHFHPGRGSTYSDFKMHHYHFDGTDWDSRKLRIYKFOGK 180
DB 121 DPADRNVISGEHLIKAWTHFHPGRGSTYSDFKMHHYHFDGTDWDSRKLRIYKFOGK 180
QY 181 AMDVESENENGYDLYMAYADIDYDHPVAAEIKKMGTYANELQDGFRLDAVGHKFSF 240
DB 181 AMDVESENENGYDLYMAYADIDYDHPVAAEIKKMGTYANELQDGFRLDAVGHKFSF 240
QY 241 LRDVNNHVRKTKGEMFTVAEYQNDGALENYLNKTNFNHSDVDPVPLHYQFHAASTOGG 300
DB 241 LRDVNNHVRKTKGEMFTVAEYQNDGALENYLNKTNFNHSDVDPVPLHYQFHAASTOGG 300
QY 301 GYDMRKLNGTVSKHPLKSVTFVNDHDTOPGQSLSTVQTFWFKPLAYAFILTRBSGYPQ 360
DB 301 GYDMRKLNGTVSKHPLKSVTFVNDHDTOPGQSLSTVQTFWFKPLAYAFILTRBSGYPQ 360
QY 361 VFYQDMYGTGDSQREIPLAKHKIEPIILKARKQYAYGAQHDYFPHHDI VGTREGDSSVA 420
DB 361 VFYQDMYGTGDSQREIPLAKHKIEPIILKARKQYAYGAQHDYFPHHDI VGTREGDSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFHVNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSBGGEFHVNGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483
```

RESULT 10

US-10-186-042-2
Sequence 2, Application US/10186042
Publication No. US20030171236A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Borcherdt, Torben
APPLICANT: Bisgaard-Frantzen, Henrik
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 4796.204-US
CURRENT APPLICATION NUMBER: US/10/186,042
PRIORITY FILING DATE: 2002-06-28
PRIORITY APPLICATION NUMBER: US/09/672,459
PRIORITY FILING DATE: 2000-09-28
PRIORITY APPLICATION NUMBER: 09/182,859
PRIORITY FILING DATE: 1998-10-29
PRIORITY APPLICATION NUMBER: 0515/96
PRIORITY FILING DATE: 1996-04-30
PRIORITY APPLICATION NUMBER: 0712/96
PRIORITY FILING DATE: 1996-06-28
PRIORITY APPLICATION NUMBER: 0775/96
PRIORITY FILING DATE: 1996-07-11
PRIORITY APPLICATION NUMBER: 1263/96
PRIORITY FILING DATE: 1996-11-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 483
TYPE: PRT
ORGANISM: Bacillus licheniformis
US-10-186-042-2

Query Match 100.0%; Score 2666; DB 14; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWMPNDGQHMRLONDSAYLAHEGTTAWIPPAKYGTSQADVGYAYD 60
DB 1 ANLNGTLMQYFEMWMPNDGQHMRLONDSAYLAHEGTTAWIPPAKYGTSQADVGYAYD 60
QY 61 LYDGEFHQKGTATKTKGTGKELQSAIKSLHSRDINYGDUVINNHKGADATEDVTAVEV 120
DB 61 LYDGEFHQKGTATKTKGTGKELQSAIKSLHSRDINYGDUVINNHKGADATEDVTAVEV 120
QY 121 DPADRNRVISEGHLIKAMTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180
DB 121 DPADRNRVISEGHLIKAMTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180
QY 181 AMDWEVSNEGNDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIKFSF 240
DB 181 AMDWEVSNEGNDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIKFSF 240
QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHVSFVDPVPLHYOFHAASSTOGG 300
DB 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHVSFVDPVPLHYOFHAASSTOGG 300
QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTMFKPLAYAFILTRREGSYPO 360
DB 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTMFKPLAYAFILTRREGSYPO 360
QY 361 VFYGDWYGTGKDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREBSSVA 420
DB 361 VFYGDWYGTGKDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREBSSVA 420
QY 421 NSGLAALITDGPQAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGEFHHVNGSVISY 480
DB 421 NSGLAALITDGPQAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGEFHHVNGSVISY 480
QY 481 VOR 483
DB 481 VOR 483

RESULT 11
US-10-399-161-6
; Sequence 6, Application US/10399161
; Publication No. US20040091994A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: Alpha-amylose variant with altered properties
; FILE REFERENCE: 10115.204-WO
; CURRENT APPLICATION NUMBER: US/10/399,161
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-399-161-6

Query Match 100.0%; Score 2666; DB 16; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWMPNDGQHMRLONDSAYLAHEGTTAWIPPAKYGTSQADVGYAYD 60
DB 1 ANLNGTLMQYFEMWMPNDGQHMRLONDSAYLAHEGTTAWIPPAKYGTSQADVGYAYD 60
QY 61 LYDGEFHQKGTATKTKGTGKELQSAIKSLHSRDINYGDUVINNHKGADATEDVTAVEV 120
DB 61 LYDGEFHQKGTATKTKGTGKELQSAIKSLHSRDINYGDUVINNHKGADATEDVTAVEV 120
QY 121 DPADRNRVISEGHLIKAMTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180
DB 121 DPADRNRVISEGHLIKAMTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180

DB 121 DPADRNRVISEGHLIKAMTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180
QY 181 AMDWEVSNEGNDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIKFSF 240
DB 181 AMDWEVSNEGNDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIKFSF 240
QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHVSFVDPVPLHYOFHAASSTOGG 300
DB 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHVSFVDPVPLHYOFHAASSTOGG 300
QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTMFKPLAYAFILTRREGSYPO 360
DB 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLSTVQTMFKPLAYAFILTRREGSYPO 360
QY 361 VFYGDWYGTGKDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREBSSVA 420
DB 361 VFYGDWYGTGKDSQREIPALKKHIEPILKARKQYAYGAQHDYFDHHDIVGWTREBSSVA 420
QY 421 NSGLAALITDGPQAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGEFHHVNGSVISY 480
DB 421 NSGLAALITDGPQAGAKMYVGRONAGETWHDITGNRSEPVVINSBGWGEFHHVNGSVISY 480
QY 481 VOR 483
DB 481 VOR 483

RESULT 12
US-10-477-725-8
; Sequence 8, Application US/10477725
; Publication No. US20040096952A1
; GENERAL INFORMATION:
; APPLICANT: NOVOZYMES A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Thisted, Thomas
; TITLE OF INVENTION: Alpha-amylose variant with altered properties
; FILE REFERENCE: 10182.204-US
; CURRENT APPLICATION NUMBER: US/10/477,725
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-477-725-8

Query Match 100.0%; Score 2666; DB 16; Length 483;
Best Local Similarity 100.0%; Pred. No. 8.2e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ANLNGTLMQYFEMWMPNDGQHMRLONDSAYLAHEGTTAWIPPAKYGTSQADVGYAYD 60
DB 1 ANLNGTLMQYFEMWMPNDGQHMRLONDSAYLAHEGTTAWIPPAKYGTSQADVGYAYD 60
QY 61 LYDGEFHQKGTATKTKGTGKELQSAIKSLHSRDINYGDUVINNHKGADATEDVTAVEV 120
DB 61 LYDGEFHQKGTATKTKGTGKELQSAIKSLHSRDINYGDUVINNHKGADATEDVTAVEV 120
QY 121 DPADRNRVISEGHLIKAMTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180
DB 121 DPADRNRVISEGHLIKAMTHFHPGRGSTYSDFKMHWYHFDGTDWDESRKLNRIYKFGOK 180
QY 181 AMDWEVSNEGNDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIKFSF 240
DB 181 AMDWEVSNEGNDYLMYADIDYDHPVAAEIKRWGTWYANELQDGFRLDAVKHIKFSF 240
QY 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHVSFVDPVPLHYOFHAASSTOGG 300
DB 241 LRDVNVHREKTKGEMFTVAEYQNDLGALENYLNKTNFNHVSFVDPVPLHYOFHAASSTOGG 300

QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPGQSLBSTVQTWFKPLAYAFILTRSGYPQ 360
DB 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPGQSLBSTVQTWFKPLAYAFILTRSGYPQ 360
QY 361 VFYDMYGTGDSQREIPALKHKEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 420
DB 361 VFYDMYGTGDSQREIPALKHKEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 420
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEWGEFHVNGGSVSIY 480
DB 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEWGEFHVNGGSVSIY 480
QY 481 VQR 483
DB 481 VQR 483

RESULT 13
US-10-184-771-2
; Sequence 2, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 512
; TYPE: PRP
; ORGANISM: B. licheniformis
US-10-184-771-2

Query Match 100.0%; Score 2666; DB 14; Length 512;
Best Local Similarity 100.0%; Pred. No. 8.9e-239;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANLNGTLMQYFEWMPNDGQWRLQNDASVLAHSGITAWIPRAYGTSQADVGAYD 60
DB 30 ANLNGTLMQYFEWMPNDGQWRLQNDASVLAHSGITAWIPRAYGTSQADVGAYD 89
QY 61 LYDGEFHQKGTVRTKTKGTGELQSAIKSLHSRDINYGVDVINHKGGADATEDVTAVEV 120
DB 90 LYDGEFHQKGTVRTKTKGTGELQSAIKSLHSRDINYGVDVINHKGGADATEDVTAVEV 149
QY 121 DPADRNVIISGEHLIKAMTHFHPGRGSTYSDPFKMHYHFDGTWDSRKLRIYKQK 180
DB 150 DPADRNVIISGEHLIKAMTHFHPGRGSTYSDPFKMHYHFDGTWDSRKLRIYKQK 209
QY 181 AMDWEVSENGNDYLYMADIDYDHPVAAEIKKMGTYANELQDGRFLDAVGHKFSF 240
DB 210 AMDWEVSENGNDYLYMADIDYDHPVAAEIKKMGTYANELQDGRFLDAVGHKFSF 269
QY 241 LRDVNVNREKTKGEMFTVAEYMONDGALENTYLNKTNFNSVDPVPLHYOFHAASQOG 300
DB 270 LRDVNVNREKTKGEMFTVAEYMONDGALENTYLNKTNFNSVDPVPLHYOFHAASQOG 329
QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPGQSLBSTVQTWFKPLAYAFILTRSGYPQ 360
DB 330 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPGQSLBSTVQTWFKPLAYAFILTRSGYPQ 389
QY 361 VFYDMYGTGDSQREIPALKHKEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 420
DB 390 VFYDMYGTGDSQREIPALKHKEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 449

QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEWGEFHVNGGSVSIY 480
DB 450 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEWGEFHVNGGSVSIY 509
QY 481 VQR 483
DB 510 VQR 512

RESULT 14
US-10-199-922-2
; Sequence 2, Application US/10199922
; Publication No. US2003022346A1
; GENERAL INFORMATION:
; APPLICANT: Gist-brocades B.V.
; TITLE OF INVENTION: Alpha-amylase mutants
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Gist-brocades B.V.
; STREET: Wateringseweg 1
; CITY: Delft
; COUNTRY: The Netherlands
; ZIP: 2611 XT
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/199,922
; FILING DATE: 18-Jul-2002
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 512 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-199-922-2

Query Match 99.8%; Score 2663; DB 14; Length 512;
Best Local Similarity 99.8%; Pred. No. 1.7e-238;
Matches 482; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 ANLNGTLMQYFEWMPNDGQWRLQNDASVLAHSGITAWIPRAYGTSQADVGAYD 60
DB 30 ANLNGTLMQYFEWMPNDGQWRLQNDASVLAHSGITAWIPRAYGTSQADVGAYD 89
QY 61 LYDGEFHQKGTVRTKTKGTGELQSAIKSLHSRDINYGVDVINHKGGADATEDVTAVEV 120
DB 90 LYDGEFHQKGTVRTKTKGTGELQSAIKSLHSRDINYGVDVINHKGGADATEDVTAVEV 149
QY 121 DPADRNVIISGEHLIKAMTHFHPGRGSTYSDPFKMHYHFDGTWDSRKLRIYKQK 180
DB 150 DPADRNVIISGEHLIKAMTHFHPGRGSTYSDPFKMHYHFDGTWDSRKLRIYKQK 209
QY 181 AMDWEVSENGNDYLYMADIDYDHPVAAEIKKMGTYANELQDGRFLDAVGHKFSF 240
DB 210 AMDWEVSENGNDYLYMADIDYDHPVAAEIKKMGTYANELQDGRFLDAVGHKFSF 269
QY 241 LRDVNVNREKTKGEMFTVAEYMONDGALENTYLNKTNFNSVDPVPLHYOFHAASQOG 300
DB 270 LRDVNVNREKTKGEMFTVAEYMONDGALENTYLNKTNFNSVDPVPLHYOFHAASQOG 329
QY 301 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPGQSLBSTVQTWFKPLAYAFILTRSGYPQ 360
DB 330 GYDMRKLLNGTVVSKHPLKSVTFVDNHDTPGQSLBSTVQTWFKPLAYAFILTRSGYPQ 389
QY 361 VFYDMYGTGDSQREIPALKHKEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 420
DB 390 VFYDMYGTGDSQREIPALKHKEPILKARKQYAYGAQHDYFPHHDIVGWTREGDSSVA 449
QY 421 NSGLAALITDGPAGAKMYVGRQNAGETWHDITGNRSEPVVINSGEWGEFHVNGGSVSIY 480

```

Db      450 NSGIALITDPGAKRMVYGRONAGETWHDITGNSEPVVINSGEFHVNGGSVSIY 509
QY      481 VOR 483
Db      510 VOR 512
    
```

```

Db      450 NSGIALITDPGAKRMVYGRONAGETWHDITGNSEPVVINSGEFHVNGGSVSIY 509
QY      481 VOR 483
Db      510 VOR 512
    
```

Search completed: October 7, 2004, 00:57:29
Job time : 55.2274 secs

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RESULT 15
US-10-081-872-114
; Sequence 114, Application US/10081872
; Publication No. US20030125534A1
; GENERAL INFORMATION:
; APPLICANT: Callen, Walter
; APPLICANT: Richardson, Toby
; APPLICANT: Frey, Gerhard
; APPLICANT: Short, Jay M.
; APPLICANT: Mathur, Eric J.
; APPLICANT: Gray, Kevin A.
; APPLICANT: Kerveno, Janne S.
; APPLICANT: Slupeka, Malgorzata
; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; FILE REFERENCE: 09010-108001
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US/10/081, 872
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/270, 496
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 60/291,122
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 321
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Environmental
US-10-081-872-114
    
```

```

Query Match      99.5%; Score 2654; DB 14; Length 512;
Best Local Similarity 99.4%; Pred. No. 1.2e-237;
Matches 480; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
    
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```

QY      1 ANINGTMOYFEMWMPNDGQHWRLONDSAYLAHEGITAWIPRAYKTSQADVGYAYD 60
Db      30 ANINGTLMQYFEMWMPNDGQHWRLONDSAYLAHEGITAWIPRAYKTSQADVGYAYD 89
QY      61 LYDLGEFHQGTVATKTKYGTGKELQSAIKSLHSRDINYGDVINHKGADATEDVTAVEV 120
Db      90 LYDLGEFHQGTVATKTKYGTGKELQSAIKSLHSRDINYGDVINHKGADATEDVTAVEV 149
QY      121 DPADRNKVIIGEHILIKAWTHFHPGRGSTYSDEFKMWYHFDGTDWDSRKLNRITYKFQOK 180
Db      150 DPADRNKVIIGEHILIKAWTHFHPGRGSTYSDEFKMWYHFDGTDWDSRKLNRITYKFQOK 209
QY      181 AMDMEVSNENGNVDYLMYADIDYDHPVAAEIKRMGTWVANELQDGFRLDAVKHIKESF 240
Db      210 AMDMEVSNENGNVDYLMYADIDYDHPVAAEIKRMGTWVANELQDGFRLDAVKHIKESF 269
QY      241 LRDMVNHVRKTKGEMFTVAEYQNDLGALENTLNKTNFNHSEVDVPLHYQFHAASTOGG 300
Db      270 LRDMVNHVRKTKGEMFTVAEYQNDLGALENTLNKTNFNHSEVDVPLHYQFHAASTOGG 329
QY      301 GYDMRKILNKTIVYSKPLKASVTYVDNHDTPQGSLBSTVQTWFKPLAYAFILTRSGYPQ 360
Db      330 GYDMRKILNKTIVYSKPLKASVTYVDNHDTPQGSLBSTVQTWFKPLAYAFILTRSGYPQ 389
QY      361 VFYGDWYGTGDSOREIPLAKHKEIPLTKARKOYAYGAOHYFDHHDIVGWTREGDSVA 420
Db      390 VFYGDWYGTGDSOREIPLAKHKEIPLTKARKOYAYGAOHYFDHHDIVGWTREGDSVA 449
QY      421 NSGIALITDPGAKRMVYGRONAGETWHDITGNSEPVVINSGEFHVNGGSVSIY 480
    
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:45:37 ; Search time 58.3101 Seconds
(without alignments)
2340.424 Million cell updates/sec

Title: US-09-925-576C-10
Perfect score: 2638
Sequence: 1 VNGTLNQYFPMYTPNDGQHW.....SDGWGEFHVNDGSIVYOK 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2638	100.0	483	2 AAR72448	Aar72448 Bacillus
2	2638	100.0	483	2 AAW31405	Aaw31405 Bacillus
3	2638	100.0	483	4 AAY97546	Aay97546 B. amy101
4	2638	100.0	483	5 ABB06937	Abb06937 B. amy101
5	2638	100.0	483	5 AAU12153	Aau12153 Bacillus
6	2638	100.0	483	5 AAB47854	Aab47854 Bacillus
7	2638	100.0	483	5 ABB76590	Abb76590 Termany1-
8	2638	100.0	483	6 ABB60488	Abb60488 Bacillus
9	2638	100.0	514	2 AAY29853	Aay29853 Bacillus
10	2638	100.0	514	3 AAB12433	Aab12433 Bacillus
11	2638	100.0	520	6 ABB60497	Abb60497 Bacillus
12	2638	100.0	520	2 AAW39743	Aaw39743 B. amy101
13	2638	100.0	520	2 AAY01584	Aay01584 An alpha-
14	2638	100.0	520	4 AAG65878	Aag65878 B. amy101
15	2635	99.9	514	3 AAB12431	Aab12431 Bacillus
16	2633	99.8	514	3 AAB12430	Aab12430 Bacillus
17	2629	99.7	514	3 AAB12432	Aab12432 Bacillus
18	2626	99.5	514	3 AAB12429	Aab12429 Bacillus
19	2625	99.5	514	2 AAR10379	Aar10379 Wild type
20	2624	99.5	480	2 AAR78268	Aar78268 Bacillus
21	2624	99.5	480	2 AAW14499	Aaw14499 Bacillus
22	2624	99.5	480	2 AAY15419	Aay15419 Bacillus
23	2624	99.5	480	2 AAY07385	Aay07385 Wild type
24	2624	99.5	480	3 AAY9606	Aay9606 Bacillus
25	2617	99.2	514	2 AAR10378	Aar10378 Mutant al

ALIGNMENTS

26	2600	98.6	480	3 AAY99771	Aay99771 Bacillus
27	2598	98.5	483	6 ABB60493	Abb60493 Bacillus
28	2570	97.4	485	6 ABB60494	Abb60494 Bacillus
29	2438	92.4	483	6 ABB60492	Abb60492 Bacillus
30	2341	88.7	483	6 ABB60495	Abb60495 Bacillus
31	2290	86.8	481	6 ABB60491	Abb60491 Bacillus
32	2255	85.5	481	6 ABB60490	Abb60490 Bacillus
33	2225	84.3	481	6 ABB60489	Abb60489 Bacillus
34	2213	83.9	483	2 AAW57979	Aaw57979 Alpha-amy
35	2213	83.9	512	4 AAU07552	Aau07552 Bacillus
36	2211	83.8	483	2 AAW57975	Aaw57975 Alpha-amy
37	2211	83.8	512	4 AAU07556	Aau07556 Bacillus
38	2210	83.8	483	2 AAW57976	Aaw57976 Alpha-amy
39	2210	83.8	483	2 AAW57978	Aaw57978 Alpha-amy
40	2210	83.8	512	4 AAU07554	Aau07554 Bacillus
41	2208	83.7	483	2 AAW08207	Aaw08207 B.licheni
42	2208	83.7	483	2 AAW57971	Aaw57971 Alpha-amy
43	2208	83.7	483	2 AAW57981	Aaw57981 Alpha-amy
44	2208	83.7	483	2 AAW57973	Aaw57973 Alpha-amy
45	2208	83.7	512	4 AAU07551	Aau07551 Bacillus

RESULT 1
ID AAR72448 standard; protein; 483 AA.
AC AAR72448;
XX
XX
DT 25-MAR-2003 (revised)
DT 01-DEC-1995 (first entry)
XX
XX
DE Bacillus amy101quefaciens alpha amylase (mature protein).
XX
XX
KW Alpha amylase; variant; enzyme; detergent; additive; dishwashing;
KW washing; Bacillus licheniformis; Bacillus amy101quefaciens;
KW Bacillus stearotheophilus; dyeing; bleaching; scouring; textile;
KW thermolabile.
XX
XX
OS Bacillus amy101quefaciens.
PN
XX
PI WO9510603-A1.
XX
XX
PD 20-APR-1995.
XX
XX
PF 05-OCT-1994; 94WO-DK00370.
XX
XX
PR 08-OCT-1993; 93DK-00001133.
PR 02-FEB-1994; 94DK-00000140.
XX
XX
PA (NOVO) NOVO-NORDISK AS.
PI
PI Borchert TV, Bisgard-Frantzen H, Svendsen A, Thellersen M;
PI Van Der Zee P;
XX
XX
DR WPI; 1995-161790/21.
DR N-PSDB; AAO88067.
XX
XX
PT New Bacillus derived alpha-amylase variants - having amino acid
PT modifications to improve washing and/or dishwashing performance.
XX
XX
PS Claim 34; Page 11-12; 105pp; English.
XX
XX
CC Variant alpha amylase enzymes which have improved washing and/or as
CC detergent additives. The enzymes have one or more amino acid residues
CC added, deleted or substituted. The variants can also be used for textile
CC desizing prior to scouring, bleaching and dyeing. The variants have
CC improved thermostability, acid/alkaline stability, low temperature
CC optimum; pH optimum; higher hydrolysis velocity and improved tolerance to
CC other composition constituents, e.g. oxidation agents. (Updated on 25-MAR
CC -2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 483 AA:
 SQ Query Match 100.0%; Score 2638; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6,1e-219;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSGSDNGYGPYDLX 60
 DB 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSGSDNGYGPYDLX 60
 QY 61 DLGEFOQKGTVRKTKGTSELDALGSLHSRNVOYGVVNLNKKAGADATEVTVAVEVNP 120
 DB 61 DLGEFOQKGTVRKTKGTSELDALGSLHSRNVOYGVVNLNKKAGADATEVTVAVEVNP 120
 QY 121 ANRNOETSEYQIKAWTDPRFPGRGNTYSDPFKMHYHFDGADWDSRKISRIFFKRGSGK 180
 DB 121 ANRNOETSEYQIKAWTDPRFPGRGNTYSDPFKMHYHFDGADWDSRKISRIFFKRGSGK 180
 QY 181 AMDWEVSSNGNYDYLMADVDYDHPDVAETKKGIWYANIELSDGFRIDAARKIKESF 240
 DB 181 AMDWEVSSNGNYDYLMADVDYDHPDVAETKKGIWYANIELSDGFRIDAARKIKESF 240
 QY 241 LRDWVOAVQATGKEMFTVAEYQWNNAGKLENYLNKTSFNOSVFPDPLHFNLOAASSGCG 300
 DB 241 LRDWVOAVQATGKEMFTVAEYQWNNAGKLENYLNKTSFNOSVFPDPLHFNLOAASSGCG 300
 QY 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTOPGOSLESTVQTMFKPLAVALTLTBESGYPQ 360
 DB 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTOPGOSLESTVQTMFKPLAVALTLTBESGYPQ 360
 QY 361 VFYGMVGTGKTSPEKISLKDNIETPLKARKEVAYGQHDYIDHPDVIQWTRGDSAA 420
 DB 361 VFYGMVGTGKTSPEKISLKDNIETPLKARKEVAYGQHDYIDHPDVIQWTRGDSAA 420
 QY 421 KSGLAALITDGPQSGSKRYAGIKNAGETWYDITGNRSDTVKIGSDGWFHNDGSVSIY 480
 DB 421 KSGLAALITDGPQSGSKRYAGIKNAGETWYDITGNRSDTVKIGSDGWFHNDGSVSIY 480
 QY 481 VQK 483
 DB 481 VQK 483

RESULT 2
 AAM31405
 ID AAM31405 standard; protein; 483 AA.
 AC AAM31405;
 XX 11-MAY-1998 (first entry)
 DE Bacillus amyloliquefaciens Termamy1-like alpha-amylase.
 KW Termamy1, alpha-amylase; enzyme engineering; protein engineering; starch;
 KW liquefaction; saccharification; sweetener; textile desizing;
 KW detergent additive; ss.
 OS Bacillus amyloliquefaciens.
 PN M09741213-A1.
 PD 06-NOV-1997.
 PF 30-APR-1997; 97MO-DK000197.
 PR 30-APR-1996; 96DK-00000515.
 PR 28-JUN-1996; 96DK-00000712.
 PR 11-JUL-1996; 96DK-00000775.
 PR 08-NOV-1996; 96DK-00001263.
 PA (NOVO) NOVO-NORDISK AS.
 XX

PI Svendsen A, Borchert TV, Bisgard-Frantzen H;
 DR WPI; 1997-549718/50.
 DR N-PSDB; AAV02472.
 PT Termamy1-like alpha-amylase variants with improved properties - e.g.
 PT increased stability at low pH and low calcium, useful as detergent
 PT additives and in industrial starch processing e.g. liquefaction.
 PS Disclosure; Page 84; 101pp; English.

XX This protein comprises the Termamy1-like alpha-amylase of Bacillus
 CC amyloliquefaciens. The invention relates to novel variants of Termamy1-
 CC like alpha-amylases that have alpha-amylase activity and exhibit an
 CC alteration in at least one property selected from: substrate specificity;
 CC binding or cleavage pattern; thermal stability; pH/activity or
 CC pH/stability profile; stability towards oxidation; Ca2+ dependency and
 CC specific activity. The variant has one or more mutations from those
 CC listed in the specification in relation to Bacillus licheniformis
 CC Termamy1 (see AAM31404). Also claimed are constructs comprising DNA
 CC encoding the variant (see AAV02471-73), and recombinant expression
 CC vectors and transformed cells containing the DNA. The Termamy1-like alpha
 CC -amylase variant is useful as a detergent additive and can also be used
 CC in industrial starch processing e.g. liquefaction (claimed) or
 CC saccharification to produce sweeteners, and in textile desizing (claimed)

XX Sequence 483 AA:
 SQ Query Match 100.0%; Score 2638; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6,1e-219;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSGSDNGYGPYDLX 60
 DB 1 VNGTLMQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSGSDNGYGPYDLX 60
 QY 61 DLGEFOQKGTVRKTKGTSELDALGSLHSRNVOYGVVNLNKKAGADATEVTVAVEVNP 120
 DB 61 DLGEFOQKGTVRKTKGTSELDALGSLHSRNVOYGVVNLNKKAGADATEVTVAVEVNP 120
 QY 121 ANRNOETSEYQIKAWTDPRFPGRGNTYSDPFKMHYHFDGADWDSRKISRIFFKRGSGK 180
 DB 121 ANRNOETSEYQIKAWTDPRFPGRGNTYSDPFKMHYHFDGADWDSRKISRIFFKRGSGK 180
 QY 181 AMDWEVSSNGNYDYLMADVDYDHPDVAETKKGIWYANIELSDGFRIDAARKIKESF 240
 DB 181 AMDWEVSSNGNYDYLMADVDYDHPDVAETKKGIWYANIELSDGFRIDAARKIKESF 240
 QY 241 LRDWVOAVQATGKEMFTVAEYQWNNAGKLENYLNKTSFNOSVFPDPLHFNLOAASSGCG 300
 DB 241 LRDWVOAVQATGKEMFTVAEYQWNNAGKLENYLNKTSFNOSVFPDPLHFNLOAASSGCG 300
 QY 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTOPGOSLESTVQTMFKPLAVALTLTBESGYPQ 360
 DB 301 GYDMRRLDGTIVSSHPEKAVTFVENHDTOPGOSLESTVQTMFKPLAVALTLTBESGYPQ 360
 QY 361 VFYGMVGTGKTSPEKISLKDNIETPLKARKEVAYGQHDYIDHPDVIQWTRGDSAA 420
 DB 361 VFYGMVGTGKTSPEKISLKDNIETPLKARKEVAYGQHDYIDHPDVIQWTRGDSAA 420
 QY 421 KSGLAALITDGPQSGSKRYAGIKNAGETWYDITGNRSDTVKIGSDGWFHNDGSVSIY 480
 DB 421 KSGLAALITDGPQSGSKRYAGIKNAGETWYDITGNRSDTVKIGSDGWFHNDGSVSIY 480
 QY 481 VQK 483
 DB 481 VQK 483

RESULT 3
 AAY97546
 ID AAY97546 standard; protein; 483 AA.
 XX

AC AAY97546;
 XX
 DT 12-FEB-2001 (first entry)
 XX
 DE B. amyloliquefaciens termamy1-like alpha amylase.
 XX
 KW Termamy1-like alpha-amylase; variant; starch liquefaction; fuel;
 KW detergent composition; laundry cleaning composition; ethanol production;
 KW dish washing cleaning composition; hard surface cleaning composition;
 KW industrial ethanol production; textile desizing.
 XX
 OS Bacillus amyloliquefaciens.
 XX
 PN WO200060059-A2.
 XX
 PD 12-OCT-2000.
 XX
 PF 28-MAR-2000; 2000WO-DK000148.
 XX
 PR 30-MAR-1999; 99DK-00000437.
 XX
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Andersen C, Jorgensen CT, Bisgard-Frantzen H, Svendsen A;
 PI Kjaerulff S;
 XX
 DR WPI: 2001-015656/02.
 DR N-PSDB; AAA37850.
 XX
 PT New variants of parent Termamy1-like alpha-amylase, useful in starch
 PT liquefaction, in detergent compositions and in ethanol production,
 PT exhibit altered cleavage pattern relative to the parent.
 XX
 PS Claim 9; Page 64-67; 78pp; English.
 XX
 CC This sequence represents a termamy1-like alpha amylase. The invention
 CC relates to a variant (I) of parent Termamy1-like alpha-amylase comprising
 CC alteration at one or more of the positions W13, G48, T49, S50, Q51, A52,
 CC D53, V54, G57, G107, G108, A111, S168 and M197. The alterations in (I)
 CC are independently an insertion of an amino acid downstream of the amino
 CC acid which occupies the position of an amino acid substitution of the amino
 CC acid which occupies the position with a different amino acid. The variant
 CC has alpha-amylase activity. (I) or compositions containing it are useful
 CC in starch liquefaction, in detergent composition such as laundry, dish
 CC washing and hard surface cleaning compositions, ethanol production such
 CC as fuel, drinking and industrial ethanol production, desizing of
 CC textiles, fabrics or garments. (I) exhibits a reduced capability of
 CC cleaving a substrate close to the branching point, and further exhibits
 CC improved substrate specificity and/or improved specific activity relative
 CC to the parent alpha-amylase
 CC
 XX
 SQ Sequence 483 AA;
 Query Match 100.0%; Score 2638; DB 4; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6,1e-219;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VNGTLMQYFWEYTPNDGQHWKRLQNDAEHLSDIGTAVWIPPAKGLSOSDNGYGPYDLY 60
 DB 1 VNGTLMQYFWEYTPNDGQHWKRLQNDAEHLSDIGTAVWIPPAKGLSOSDNGYGPYDLY 60
 QY 61 DLGFGQOKGTRTKYTKGTSSELODAIGSHSRNVGYDVLNHRQAGDATEDVAVNVP 120
 DB 61 DLGFGQOKGTRTKYTKGTSSELODAIGSHSRNVGYDVLNHRQAGDATEDVAVNVP 120
 QY 121 ANRQETSESEYQIAWTDFFRPGKNTYSDPKMWHYHFDGADWDSRKISIFRFGSGK 180
 DB 121 ANRQETSESEYQIAWTDFFRPGKNTYSDPKMWHYHFDGADWDSRKISIFRFGSGK 180
 QY 181 AMDWEVSSENGNYIYLMYADVDYDHPDVAATKMGWIYANELSLDGRIDAACHIKFSF 240
 DB 181 AMDWEVSSENGNYIYLMYADVDYDHPDVAATKMGWIYANELSLDGRIDAACHIKFSF 240
 QY 181 AMDWEVSSENGNYIYLMYADVDYDHPDVAATKMGWIYANELSLDGRIDAACHIKFSF 240
 DB 181 AMDWEVSSENGNYIYLMYADVDYDHPDVAATKMGWIYANELSLDGRIDAACHIKFSF 240

QY 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNTKTSFNQSVFDEVLHFNLOQAASSQGG 300
 DB 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNTKTSFNQSVFDEVLHFNLOQAASSQGG 300
 QY 301 GYDMRRLDGTGVVSRHDEKAVTFVENHDTPGQSLSESTVQTFKPLAVALTLRESGPQ 360
 DB 301 GYDMRRLDGTGVVSRHDEKAVTFVENHDTPGQSLSESTVQTFKPLAVALTLRESGPQ 360
 QY 361 VFYGDWYGTGTGTPKEIPSLKDNIEPLTKARKEVAVGPQHDYIDHPVIGMTRESDSAA 420
 DB 361 VFYGDWYGTGTGTPKEIPSLKDNIEPLTKARKEVAVGPQHDYIDHPVIGMTRESDSAA 420
 QY 421 KSGIALALITDGPQSGSKMVAAGLKNAGETWYDITGNRSDTYKISDGMGEFHVNDGSYSIY 480
 DB 421 KSGIALALITDGPQSGSKMVAAGLKNAGETWYDITGNRSDTYKISDGMGEFHVNDGSYSIY 480
 QY 481 VQK 483
 DB 481 VQK 483
 RESULT 4
 ABB06937
 ID ABB06937 standard; protein; 483 AA.
 XX
 AC ABB06937;
 XX
 DT 19-JUN-2002 (first entry)
 XX
 DE B. amyloliquefaciens termamy1-like alpha-amylase protein SEQ ID NO:10.
 XX
 KW Bacillus; termamy1-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
 KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
 KW washing; sweetener; ethanol; starch.
 XX
 OS Bacillus amyloliquefaciens.
 XX
 PN WO200166712-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 07-MAR-2001; 2001WO-DK000144.
 XX
 PR 08-MAR-2000; 2000DK-00000376.
 PR 15-MAR-2000; 2000US-0189857P.
 PR 23-FEB-2001; 2001DK-00000303.
 PR 26-FEB-2001; 2001US-0271382P.
 XX
 PA (NOVO) NOVOTYMS AS.
 XX
 PI Andersen C, Borchert TV, Nielsen BR;
 XX
 DR WPI: 2002-239612/29.
 DR N-PSDB; ABL50568.
 XX
 PT Novel variant of parent termamy1-like alpha-amylase useful as a component
 PT in washing and dishwashing compositions, for textile desizing, for starch
 PT liquefaction, and for producing sweeteners and ethanol from starch.
 XX
 PS Claim 8; Page 145-146; 153pp; English.
 XX
 CC The present invention describes a variant of a parent termamy1-like alpha
 CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
 CC positions of a group of 31 possible amino acid positions. The alteration
 CC in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,
 CC Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
 CC Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
 CC Asn445, Lys446, Glu449, Arg458, Asp471, or Asn484. (I) can be used for
 CC washing and/or dishwashing, textile desizing, and starch liquefaction.
 CC (I) is useful as a component in hard surface cleaning detergent
 CC composition, and for producing sweeteners and ethanol from starch. (I)
 CC has altered solubility, preferably increased solubility, in particular
 CC under washing, dish washing or hard surface cleaning conditions. The

CC present sequence represents a *Bacillus amyloliquefaciens* termamyl-like
CC alpha-amyase which is used in the exemplification of the present
CC invention
CC
SQ Sequence 483 AA;

Query Match 100.0%; Score 2638; DB 5; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.1e-219;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 VNGTLNQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSDNGYGPYLY 60
DB 1 VNGTLNQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSDNGYGPYLY 60
QY 61 DLGEFOOKGTVRTKGTGKSELQDAIGLSHRNVQYGVVLNKKAGADATEDVAVENP 120
DB 61 DLGEFOOKGTVRTKGTGKSELQDAIGLSHRNVQYGVVLNKKAGADATEDVAVENP 120
QY 121 ANRNOETSEERYQIKAWTDFRFGKNTYSDPFKWHVHPDGADWDESRKISRIFKRGSGK 180
DB 121 ANRNOETSEERYQIKAWTDFRFGKNTYSDPFKWHVHPDGADWDESRKISRIFKRGSGK 180
QY 181 AMDWEVSSSENGNYDYLMTADVDPDVAETKKGIWYANELSDGFRIDAAGHIFSF 240
DB 181 AMDWEVSSSENGNYDYLMTADVDPDVAETKKGIWYANELSDGFRIDAAGHIFSF 240
QY 241 LRDWVOAVROATGKEMFTVAEYQNNAGKLENYLNKTSFNOSVDFVPLHFNLOAASOGG 300
DB 241 LRDWVOAVROATGKEMFTVAEYQNNAGKLENYLNKTSFNOSVDFVPLHFNLOAASOGG 300
QY 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLSESTVQWFKPLAFAFILTRESGPQ 360
DB 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLSESTVQWFKPLAFAFILTRESGPQ 360
QY 361 VFYGDWYGTGKTSPEKIPSLKDNIEPIILKARKEVAYGPOHDYIDHPVYIGWTRGDSAA 420
DB 361 VFYGDWYGTGKTSPEKIPSLKDNIEPIILKARKEVAYGPOHDYIDHPVYIGWTRGDSAA 420
QY 421 KSGLAALITDGPQSGKRWYAGLKNAGETWYDITGNRSPTVYKISGDGGEFHVNDGSVSY 480
DB 421 KSGLAALITDGPQSGKRWYAGLKNAGETWYDITGNRSPTVYKISGDGGEFHVNDGSVSY 480
QY 481 VOK 483
DB 481 VOK 483
```

RESULT 5
AAU12153
ID AAU12153 standard; protein; 483 AA.

```
XX AC AAU12153;
XX DT 09-APR-2002 (first entry)
XX DE Bacillus TERMAMYL-like alpha-amyase BAN.
XX KW TERMAMYL; alpha-amyase; detergent; dishwashing; textile desizing;
XX KW starch liquefaction; ethanol production; hard surface cleaner; sweetener;
XX KW amylopectin; limit dextrin; NOVAMYL; BAN.
XX OS Bacillus amyloliquefaciens.
XX FN WO20018107-A2.
XX PD 22-NOV-2001.
XX PR 10-MAY-2001; 2001WO-DK00323.
XX ER 12-MAY-2000; 2000DK-00000779.
XX PA (NOVO) NOVOZYMES AS.
XX
```

PI Svendsen A, Jorgensen CT, Nielsen BR;
XX WPI; 2002-106123/14.
DR N-PSDB; AAS20026.
XX

PT New variant of parent Termamyl-like alpha-amyase for use as a component
PT in washing and dishwashing compositions, for textile desizing, for starch
PT liquefaction, and for producing sweeteners and ethanol from starch.
XX
PS Claim 5; Fig 1; 84pp; English.

The invention relates to a variant of parent TERMAMYL-like alpha-amyase
comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
or at position 234, where the variant has alpha-amyase activity and each
position corresponds to a position of a parent Termamyl-like alpha-
amyase sequence having a *Bacillus licheniformis* alpha-amyase sequence
of 483 amino acids, given in specification. The variant alpha-amyase, a
detergent additive comprising the variant or a detergent composition
comprising the variant, is useful for washing and/or dishwashing or
textile desizing. The alpha-amyase is useful for starch liquefaction or
ethanol production and as a component in a hard surface cleaning
detergent composition, and for producing sweeteners from starch. The
variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage
activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic
branch linkage cleavage activity of amylopectin or a limit dextrin
prepared by TERMAMYL (RTM) or NOVAMYL (RTM). The present sequence is a
natural variant of the TERMAMYL alpha-amyase, BAN

SQ Sequence 483 AA;

Query Match 100.0%; Score 2638; DB 5; Length 483;
Best Local Similarity 100.0%; Pred. No. 6.1e-219;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 VNGTLNQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSDNGYGPYLY 60
DB 1 VNGTLNQYFEMWTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSDNGYGPYLY 60
QY 61 DLGEFOOKGTVRTKGTGKSELQDAIGLSHRNVQYGVVLNKKAGADATEDVAVENP 120
DB 61 DLGEFOOKGTVRTKGTGKSELQDAIGLSHRNVQYGVVLNKKAGADATEDVAVENP 120
QY 121 ANRNOETSEERYQIKAWTDFRFGKNTYSDPFKWHVHPDGADWDESRKISRIFKRGSGK 180
DB 121 ANRNOETSEERYQIKAWTDFRFGKNTYSDPFKWHVHPDGADWDESRKISRIFKRGSGK 180
QY 181 AMDWEVSSSENGNYDYLMTADVDPDVAETKKGIWYANELSDGFRIDAAGHIFSF 240
DB 181 AMDWEVSSSENGNYDYLMTADVDPDVAETKKGIWYANELSDGFRIDAAGHIFSF 240
QY 241 LRDWVOAVROATGKEMFTVAEYQNNAGKLENYLNKTSFNOSVDFVPLHFNLOAASOGG 300
DB 241 LRDWVOAVROATGKEMFTVAEYQNNAGKLENYLNKTSFNOSVDFVPLHFNLOAASOGG 300
QY 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLSESTVQWFKPLAFAFILTRESGPQ 360
DB 301 GYDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLSESTVQWFKPLAFAFILTRESGPQ 360
QY 361 VFYGDWYGTGKTSPEKIPSLKDNIEPIILKARKEVAYGPOHDYIDHPVYIGWTRGDSAA 420
DB 361 VFYGDWYGTGKTSPEKIPSLKDNIEPIILKARKEVAYGPOHDYIDHPVYIGWTRGDSAA 420
QY 421 KSGLAALITDGPQSGKRWYAGLKNAGETWYDITGNRSPTVYKISGDGGEFHVNDGSVSY 480
DB 421 KSGLAALITDGPQSGKRWYAGLKNAGETWYDITGNRSPTVYKISGDGGEFHVNDGSVSY 480
QY 481 VOK 483
DB 481 VOK 483
```

RESULT 6
AAB47854

ID AAB47854 standard; protein; 483 AA.
 XX AAB47854;
 AC 02-APR-2002 (first entry)
 DT 02-APR-2002 (first entry)
 XX
 DE Bacillus alpha amylase BAN.
 XX
 KM Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;
 KM starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
 KM bakery; cereal bar; ice cream; coffee whitener; salad dressing;
 KM cured meat; fermented meat; spice.
 XX
 OS Bacillus amyloliquefaciens.
 PN W0200196537-A2.
 PD 20-DEC-2001.
 XX
 PF 13-JUN-2001; 2001WO-DK000404.
 XX
 PR 14-JUN-2000; 2000DK-00000917.
 PR 20-JUN-2000; 2000US-0212852P.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Nielsen BR, Weibye M;
 DR WPI; 2002-098064/13.
 DR N-PSDB; AAI72215.
 XX
 PT New modified alpha-amylase derived from the genus Bacillus and/or is a
 PT Termamyl-like alpha-amylase, which has been pre-oxidized for producing
 PT maltodextrin or glucose syrup.
 XX
 PS Claim 5; Page 39-41; 47pp; English.
 XX
 XX The sequences given in AAB47850-56 show modified alpha-amylases derived
 CC from the genus Bacillus. These alpha amylases are Termamyl-like alpha-
 CC amylase and they have been pre-oxidized. The alpha amylase is useful for
 CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
 CC oxidized alpha-amylase until a product with a DE between 5-45 has been
 CC provided and/or until a product with a molecular weight of between 5-30
 CC kDa has been provided. The product comprises a maltodextrin with a DE of
 CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The
 CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
 CC where the glucose syrup is useful as an ingredient in food, feed or
 CC pharmaceuticals. Glucose syrup is useful in confectionery such as
 CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
 CC dairy and ice cream such as coffee whiteners, conventional foods such as
 CC salad dressings, and food ingredients and preparations such as cured
 CC meat, fermented meat, spices and seasoning encapsulated flavours
 XX
 SQ Sequence 483 AA:
 Query Match 100.0%; Score 2638; DB 5; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6.1e-219;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 181 AMDWEVSENGNYDYLMTADVDDYDHPDVVAETKKMGIVANELSLDGRIDAAGHIKPSF 240
 QY 241 LRDWVQAVRQATGKEMPTVAEYQWNNAGKLENTLNTKTSFNQSVDPVVLHFNLOAASSQGG 300
 DB 241 LRDWVQAVRQATGKEMPTVAEYQWNNAGKLENTLNTKTSFNQSVDPVVLHFNLOAASSQGG 300
 QY 301 GYDMRRLDGTAVSRHPEKAVTFVENHDTPQGSLESTVQTPFPLVAFILTFRESGYPQ 360
 DB 301 GYDMRRLDGTAVSRHPEKAVTFVENHDTPQGSLESTVQTPFPLVAFILTFRESGYPQ 360
 QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPLTKARKEVAYGPQHDYIDHPDVGMTREBGDSAA 420
 DB 361 VFYGDWYGTGTSPEKIPSLKDNIEPLTKARKEVAYGPQHDYIDHPDVGMTREBGDSAA 420
 QY 421 KSGLAALITDGPQGSKRMVAGLKNAGETWYDITGNRSDTYKIGSDGGEFHVNDGSYSIY 480
 DB 421 KSGLAALITDGPQGSKRMVAGLKNAGETWYDITGNRSDTYKIGSDGGEFHVNDGSYSIY 480
 QY 481 VQK 483
 DB 481 VQK 483
 RESULT 7
 ID ABB76590 standard; protein; 483 AA.
 XX ABB76590
 AC ABB76590;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Termamyl-like-alpha-amylase #5.
 XX
 KM Termamyl; alpha amylase; starch liquefaction; ethanol production;
 KM textile desizing; detergent; enzyme.
 XX
 OS Bacillus amyloliquefaciens.
 XX
 PN W0200210355-A2.
 PD 07-FEB-2002.
 XX
 PF 12-JUL-2001; 2001WO-DK000488.
 XX
 PR 01-AUG-2000; 2000DK-00001160.
 PR 12-SEP-2000; 2000DK-00001354.
 PR 10-NOV-2000; 2000DK-00001687.
 PR 26-APR-2001; 2001DK-00000655.
 XX
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Thisted T, Kjaerulff S, Andersen C, Fugisang CC;
 DR WPI; 2002-280633/32.
 DR N-PSDB; ABL96211.
 XX
 PT Variant of parent Termamyl-like alpha amylase, useful in detergent
 PT compositions, for starch liquefaction, ethanol production, washing and/or
 PT dish washing, and textile desizing.
 XX
 PS Claim 4; Fig 3; 90pp; English.
 XX
 CC This invention relates to variants of a parent Termamyl-like alpha-
 CC amylase. These are used for starch liquefaction, ethanol production,
 CC detergent, and textile desizing. The amylases have altered stability,
 CC particularly at high temperatures from 70-120pH and low pH in the
 CC range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-
 CC amylase
 XX
 SQ Sequence 483 AA;
 Query Match 100.0%; Score 2638; DB 5; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6.1e-219;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 VNGTLMQYFMYTPNPGQHKRLQNDAEHLSDIGITRAWTPPYKGLSGSDNGYGYDLY 60
    |||
Db 1 VNGTLMQYFMYTPNPGQHKRLQNDAEHLSDIGITRAWTPPYKGLSGSDNGYGYDLY 60
QY 61 DLGEFOQKGTVRTKYGTSKSELQDAISLHSRNQYGVVYLNHKGADATEDTVAEYVP 120
    |||
Db 61 DLGEFOQKGTVRTKYGTSKSELQDAISLHSRNQYGVVYLNHKGADATEDTVAEYVP 120
QY 121 ANRNOETSEERYQIKAWTDRFPGRGNTYSDPFKWHYHFDGADWDSRKISRIFKRGEGK 180
    |||
Db 121 ANRNOETSEERYQIKAWTDRFPGRGNTYSDPFKWHYHFDGADWDSRKISRIFKRGEGK 180
QY 181 AMDMEVSSSENGNDYLMYADVDDYDHPDVAEYKKGIMYANELSLDGFRIDAAKIKTSF 240
    |||
Db 181 AMDMEVSSSENGNDYLMYADVDDYDHPDVAEYKKGIMYANELSLDGFRIDAAKIKTSF 240
QY 241 LRDMVQAVRQATGKEMFTVAEYQWONNAGKLENYLNKTSFNQSVFDPVPLHFNLOAASQGG 300
    |||
Db 241 LRDMVQAVRQATGKEMFTVAEYQWONNAGKLENYLNKTSFNQSVFDPVPLHFNLOAASQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPQCSLESTVQWFKPLAAYFILTRESGYPQ 360
    |||
Db 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPQCSLESTVQWFKPLAAYFILTRESGYPQ 360
QY 361 VFYGDWYGTGKTSPEKIEPSLKDNIIEPILKARKEVAYGPHDYIDHPDVIGMTREGDSAA 420
    |||
Db 361 VFYGDWYGTGKTSPEKIEPSLKDNIIEPILKARKEVAYGPHDYIDHPDVIGMTREGDSAA 420
QY 421 KSGLAALITDGPQSGSKRMVAGLKNAGETWYDITGNRSPTYKIGSDGWEFFHVDGVSITY 480
    |||
Db 421 KSGLAALITDGPQSGSKRMVAGLKNAGETWYDITGNRSPTYKIGSDGWEFFHVDGVSITY 480
QY 481 VOK 483
    |||
Db 481 VOK 483

```

RESULT 8
ABP60488
ID ABP60488 standard; protein; 483 AA.
AC ABP60488;
XX
XX 10-MAY-2003 (first entry)
DT
XX
DE Bacillus amyloliquefaciens alpha-amylase SEQ ID NO 4.
Db
KM Bacillus amyloliquefaciens; alpha-amylase; washing; cleaning; textile;
KW dishwashing machine; starch-based capsule; EC 3.2.1.1; enzyme.
XX
XX Bacillus amyloliquefaciens.
OS
XX WO2003014358-A2.
PN
XX 20-FEB-2003.
PD
XX 27-JUL-2002; 2002WO-EP008391.
PF
XX 07-AUG-2001; 2001DE-01038753.
PR
XX (HENK) HENKEL KGAA.
PA
XX Kottwitz B, Breves R, Maurer K;
PI
XX WPI: 2003-278480/27.
DR N-PSDB; ABZ59264.
XX
XX Washing and cleaning composition, useful for laundry and hard surface
PT cleaning, contains hybrid amylase derived from two Bacillus enzymes.
XX
PS Claim 4; Fig 2; 118pp; German.

XX The invention relates to a washing and cleaning composition (A) containing an amylolytic hybrid protein (I) containing sequences from the alpha-amylases (EC 3.2.1.1) of Bacillus amyloliquefaciens and B. licheniformis. (A) are used for cleaning textiles (by hand or machine) or hard surfaces (metal, glass, plastics etc.), especially in dishwashing machines. (I) can also be used to release other components of the compositions from starch-based capsules. The present sequence is that of the Bacillus amyloliquefaciens alpha-amylase of the invention

XX
SQ Sequence 483 AA;
Query Match 100.0%; Score 2638; DB 6; Length 483;
Best Local Similarity 100.0%; Pred. No. 6; 1e-219;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 VNGTLMQYFMYTPNPGQHKRLQNDAEHLSDIGITRAWTPPYKGLSGSDNGYGYDLY 60
    |||
Db 1 VNGTLMQYFMYTPNPGQHKRLQNDAEHLSDIGITRAWTPPYKGLSGSDNGYGYDLY 60
QY 61 DLGEFOQKGTVRTKYGTSKSELQDAISLHSRNQYGVVYLNHKGADATEDTVAEYVP 120
    |||
Db 61 DLGEFOQKGTVRTKYGTSKSELQDAISLHSRNQYGVVYLNHKGADATEDTVAEYVP 120
QY 121 ANRNOETSEERYQIKAWTDRFPGRGNTYSDPFKWHYHFDGADWDSRKISRIFKRGEGK 180
    |||
Db 121 ANRNOETSEERYQIKAWTDRFPGRGNTYSDPFKWHYHFDGADWDSRKISRIFKRGEGK 180
QY 181 AMDMEVSSSENGNDYLMYADVDDYDHPDVAEYKKGIMYANELSLDGFRIDAAKIKTSF 240
    |||
Db 181 AMDMEVSSSENGNDYLMYADVDDYDHPDVAEYKKGIMYANELSLDGFRIDAAKIKTSF 240
QY 241 LRDMVQAVRQATGKEMFTVAEYQWONNAGKLENYLNKTSFNQSVFDPVPLHFNLOAASQGG 300
    |||
Db 241 LRDMVQAVRQATGKEMFTVAEYQWONNAGKLENYLNKTSFNQSVFDPVPLHFNLOAASQGG 300
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPQCSLESTVQWFKPLAAYFILTRESGYPQ 360
    |||
Db 301 GYDMRRLDGTIVSRHPEKAVTFVENHDTQPQCSLESTVQWFKPLAAYFILTRESGYPQ 360
QY 361 VFYGDWYGTGKTSPEKIEPSLKDNIIEPILKARKEVAYGPHDYIDHPDVIGMTREGDSAA 420
    |||
Db 361 VFYGDWYGTGKTSPEKIEPSLKDNIIEPILKARKEVAYGPHDYIDHPDVIGMTREGDSAA 420
QY 421 KSGLAALITDGPQSGSKRMVAGLKNAGETWYDITGNRSPTYKIGSDGWEFFHVDGVSITY 480
    |||
Db 421 KSGLAALITDGPQSGSKRMVAGLKNAGETWYDITGNRSPTYKIGSDGWEFFHVDGVSITY 480
QY 481 VOK 483
    |||
Db 481 VOK 483

```

RESULT 9
AAZ29853
ID AAZ29853 standard; protein; 514 AA.
XX
XX AAZ29853;
AC
XX 18-NOV-1999 (first entry)
DT
XX
DE Bacillus amyloliquefaciens Termamyl-1-like alpha-amylase.
Db
KM Alpha-amylase; Termamyl-1-like alpha-amylase; glucose syrup; starch.
KW
XX Bacillus amyloliquefaciens.
OS
XX Key
FH Peptide 1..31
FT /label= signal
FT Protein 32..514
XX /label= Termamyl-1-like_alpha-amylase

PN WO9946399-A1.
 XX 16-SEP-1999.
 PD 08-MAR-1999; 99WO-DK000114.
 XX 09-MAR-1998; 98DK-00000321.
 PR (NOVO) NOVO-NORDISK AS.
 XX Norman BE, Hendriksen HV;
 PI WPI; 1999-551422/46.
 XX DR N-PSDB; AAZ21079.
 PT Preparation of a glucose syrup, using a Termamyl-like alpha-amylase.
 PS Disclosure; Page 32-34; 36pp; English.
 XX
 CC A method has been developed for the preparation of a glucose syrup using
 CC a Termamyl-like alpha-amylase containing a substitution at Val(54). The
 CC glucose syrup obtained by the process is useful as an ingredient in food
 CC products. The Termamyl-like alpha-amylase facilitates the preparation of
 CC glucose syrups suitable for the food industry, previously only possible
 CC using acid hydrolysis. The present sequence represents *Bacillus*
 CC *amyloliquefaciens* Termamyl-like alpha-amylase
 CC
 XX Sequence 514 AA;

Query Match 100.0%; Score 2638; DB 2; Length 514;
 Best Local Similarity 100.0%; Pred. No. 6,7e-219;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLQYFEMWYTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSQSDNGYGPYDLY 60
 DB 32 VNGTLQYFEMWYTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSQSDNGYGPYDLY 91
 QY 61 DLGFEQKGTGRTKYGKSELODAIGSLHSRNQVYGDVVLNHRKAGADATEDVTAVEVNP 120
 DB 92 DLGFEQKGTGRTKYGKSELODAIGSLHSRNQVYGDVVLNHRKAGADATEDVTAVEVNP 151
 QY 121 ANRQETSEEVQIKAWTDFRFGKNTYSDPKMWHYFDGADMDSEKISRIFFRGEKG 180
 DB 152 ANRQETSEEVQIKAWTDFRFGKNTYSDPKMWHYFDGADMDSEKISRIFFRGEKG 211
 QY 181 AMDVESSSENGNYLYMAYDVYDHPVVAETKKMGWYANELSLDGRIDAAGHIKFSF 240
 DB 212 AMDVESSSENGNYLYMAYDVYDHPVVAETKKMGWYANELSLDGRIDAAGHIKFSF 271
 QY 241 LRDVQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDPVPLHFNLOAASSQGG 300
 DB 272 LRDVQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDPVPLHFNLOAASSQGG 331
 QY 301 GYDMRRLDGTIVSRHPEKAVTVEVNDHTOPGQSLSTVQTFPKPLAFAFLITRESGYPQ 360
 DB 332 GYDMRRLDGTIVSRHPEKAVTVEVNDHTOPGQSLSTVQTFPKPLAFAFLITRESGYPQ 391
 QY 361 VFYDMVTGKTGTSPEKIPSLKONTEPIIKARKEYAYGFQHDYIDHPDVIQGTREGSSAA 420
 DB 392 VFYDMVTGKTGTSPEKIPSLKONTEPIIKARKEYAYGFQHDYIDHPDVIQGTREGSSAA 451
 QY 421 KSGIAALITDGPQSKWYAGLKNAGETWYDITNRSPTVYIGSDGMEFFHVNQGSYIY 480
 DB 452 KSGIAALITDGPQSKWYAGLKNAGETWYDITNRSPTVYIGSDGMEFFHVNQGSYIY 511
 QY 481 VQK 483
 DB 512 VQK 514

RESULT 10
 AAB12433
 ID AAB12433 standard; protein; 514 AA.

XX AAB12433;
 AC 19-OCT-2000 (first entry)
 DT
 XX
 DE *Bacillus amyloliquefaciens* amylase protein SEQ ID NO:9.
 XX
 KW *Bacillus amyloliquefaciens*; alpha-amylase; thermostable; bread.
 XX
 OS *Bacillus amyloliquefaciens*.
 XX JP2000135093-A.
 XX
 PD 16-MAY-2000.
 XX
 PF 20-AUG-1999; 99JP-00234813.
 XX
 PR 24-AUG-1998; 98JP-00237839.
 XX
 PA (DAIW) DAIWA KASEI KK.
 XX WPI; 2000-403584/35.
 XX
 DR Novel thermostable alpha-amylase, useful for improving the preparation of
 XX bread, comprises alpha-amylase activity with less than 80% activity after
 PT treatment at 65degreesC for 30 min.
 PS Claim 1; Page 18-19; 22pp; Japanese.
 XX
 CC The present invention describes a thermostable alpha-amylase (1)
 CC comprising the sequence given in AAB12433 (A) or deletions, replacements
 CC or insertions of one or more amino acids) in the sequence and alpha-
 CC amylase activity with less than 80% activity after treatment at 65 plus
 CC degrees Celsius for 30 minutes. Also described are: (1) DNA encoding (1)
 CC ; (2) DNA containing one of 4 nucleotide sequences comprising 1545 base
 CC pairs (see AAB60576 to AAB60579); (3) expression vectors containing the
 CC above mentioned DNA; (4) host cells containing the above mentioned
 CC expression vectors; (5) preparation of a polypeptide having alpha-amylase
 CC activity by culture of the recombinant host cells; and (6) preparation of
 CC bread including a process to add (1) to the dough. (1) is useful in the
 CC preparation of bread. (1) improves the soft volume of the bread and
 CC prevents it aging
 CC
 XX Sequence 514 AA;

Query Match 100.0%; Score 2638; DB 3; Length 514;
 Best Local Similarity 100.0%; Pred. No. 6,7e-219;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLQYFEMWYTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSQSDNGYGPYDLY 60
 DB 32 VNGTLQYFEMWYTPNDGQHWKRLQNDAEHLSDIGITAWIPRAYKGLSQSDNGYGPYDLY 91
 QY 61 DLGFEQKGTGRTKYGKSELODAIGSLHSRNQVYGDVVLNHRKAGADATEDVTAVEVNP 120
 DB 92 DLGFEQKGTGRTKYGKSELODAIGSLHSRNQVYGDVVLNHRKAGADATEDVTAVEVNP 151
 QY 121 ANRQETSEEVQIKAWTDFRFGKNTYSDPKMWHYFDGADMDSEKISRIFFRGEKG 180
 DB 152 ANRQETSEEVQIKAWTDFRFGKNTYSDPKMWHYFDGADMDSEKISRIFFRGEKG 211
 QY 181 AMDVESSSENGNYLYMAYDVYDHPVVAETKKMGWYANELSLDGRIDAAGHIKFSF 240
 DB 212 AMDVESSSENGNYLYMAYDVYDHPVVAETKKMGWYANELSLDGRIDAAGHIKFSF 271
 QY 241 LRDVQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDPVPLHFNLOAASSQGG 300
 DB 272 LRDVQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDPVPLHFNLOAASSQGG 331
 QY 301 GYDMRRLDGTIVSRHPEKAVTVEVNDHTOPGQSLSTVQTFPKPLAFAFLITRESGYPQ 360
 DB 332 GYDMRRLDGTIVSRHPEKAVTVEVNDHTOPGQSLSTVQTFPKPLAFAFLITRESGYPQ 391

QY 361 VFYGDMYGTGKTSPEKIPSLKONIEPILKARKKEYAYGPOHDYIDHPDVIGWTRBGSSAA 420
| | | | |
Db 392 VFYGDMYGTGKTSPEKIPSLKONIEPILKARKKEYAYGPOHDYIDHPDVIGWTRBGSSAA 451
| | | | |
QY 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGMEGFHVNDGSVSIY 480
| | | | |
Db 452 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGMEGFHVNDGSVSIY 511
| | | | |
QY 481 VQK 483
| | | | |
Db 512 VQK 514
| | | | |
RESULT 11
ABP60497 standard; protein; 514 AA.
ID ABP60497;
AC ABP60497;
XX
DT 10-MAY-2003 (first entry)
XX
DE Bacillus amylioliquefaciens alpha-amylase.
XX
KW Bacillus amylioliquefaciens; alpha-amylase; washing; cleaning; textile;
KM dishwashing machine; starch-based capsule; EC 3.2.1.1; enzyme.
XX
OS Bacillus amylioliquefaciens.
XX
FH Key Location/Qualifiers
FT Peptide 1..31
FT /label= signal_peptide
FT Protein 32..514
FT /label= mature_protein
XX
PN WO2003014358-A2.
XX
PD 20-FEB-2003.
XX
PF 27-JUL-2002; 2002WO-EP008391.
XX
PR 07-AUG-2001; 2001DE-01038753.
XX
PA (HENK) HENKEL KGAA.
XX
PI Kottwitz B, Breves R, Maurer K;
XX
DR WPI; 2003-278480/27.
XX
PT Washing and cleaning composition, useful for laundry and hard surface
PT cleaning, contains hybrid amylase derived from two Bacillus enzymes.
XX
PS Disclosure; Fig 2; 11pp; German.
XX
CC The invention relates to a washing and cleaning composition (A)
CC containing an amyolytic hybrid protein (I) containing sequences from the
CC alpha-amylases (EC 3.2.1.1) of Bacillus amylioliquefaciens and B.
CC licheniformis. (A) are used for cleaning textiles (by hand or machine) or
CC hard surfaces (metal, glass, plastics etc.), especially in dishwashing
CC machines. (I) can also be used to release other components of the
CC compositions from starch-based capsules. The present sequence is that of
CC the full length Bacillus amylioliquefaciens alpha-amylase protein
XX
SQ Sequence 514 AA;
| | | | |
Query Match 100.0%; Score 2638; DB 6; Length 514;
Best Local Similarity 100.0%; Pred. No. 6,7e-219;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
| | | | |
QY 1 VNGTLMQYFFMYTPNDQHWKRLONDAEHLSDIGITRAVWIPAYKGLSGSDNGYGPYDLY 60
| | | | |
Db 32 VNGTLMQYFFMYTPNDQHWKRLONDAEHLSDIGITRAVWIPAYKGLSGSDNGYGPYDLY 91
| | | | |
QY 61 DLGSEFOQKGTVRKTKYGTSELDQAISLHSRNQVYGDVVLNKKAGADATEVTAVERN 120
| | | | |

Db 92 DLGSEFOQKGTVRKTKYGTSELDQAISLHSRNQVYGDVVLNKKAGADATEVTAVERN 151
| | | | |
QY 121 ANRQETSEBYQIKAWTDFRPPRGNTYSDFKWHYHFDGADWDESKISRIKFRGEK 180
| | | | |
Db 152 ANRQETSEBYQIKAWTDFRPPRGNTYSDFKWHYHFDGADWDESKISRIKFRGEK 211
| | | | |
QY 181 AMDWEVSSENGNYDLYAVDADVDHPDVVAETKKWGIWYANELSLGCFRIDAKKHIFSF 240
| | | | |
Db 212 AMDWEVSSENGNYDLYAVDADVDHPDVVAETKKWGIWYANELSLGCFRIDAKKHIFSF 271
| | | | |
QY 241 LRDVQAVRQATGKEMFTVAEYQONNAGKLENTKTSFNQSVFDPVLFHFNQAASSQGG 300
| | | | |
Db 272 LRDVQAVRQATGKEMFTVAEYQONNAGKLENTKTSFNQSVFDPVLFHFNQAASSQGG 331
| | | | |
QY 301 GYDMRRLDGTIVSRHPEKAVTFVENHDPQPGSLSTVQTWKPALAYPILTRSGYRQ 360
| | | | |
Db 332 GYDMRRLDGTIVSRHPEKAVTFVENHDPQPGSLSTVQTWKPALAYPILTRSGYRQ 391
| | | | |
QY 361 VFYGDMYGTGKTSPEKIPSLKONIEPILKARKKEYAYGPOHDYIDHPDVIGWTRBGSSAA 420
| | | | |
Db 392 VFYGDMYGTGKTSPEKIPSLKONIEPILKARKKEYAYGPOHDYIDHPDVIGWTRBGSSAA 451
| | | | |
QY 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGMEGFHVNDGSVSIY 480
| | | | |
Db 452 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGMEGFHVNDGSVSIY 511
| | | | |
QY 481 VQK 483
| | | | |
Db 512 VQK 514
| | | | |

RESULT 12
AAM39743 standard; protein; 520 AA.
ID AAM39743
XX
AC AAM39743;
XX
DT 20-MAY-1998 (first entry)
XX
DE B. amylioliquefaciens alpha amylase protein.
XX
KW Alpha-amylase; calcium binding; starch liquefaction; detergent;
KM baking aid; textile industry.
XX
OS Bacillus amylioliquefaciens.
XX
PN WO9743424-A1.
XX
PD 20-NOV-1997.
XX
PF 06-MAY-1997; 97WO-US007609.
XX
PR 14-MAY-1996; 96US-00645971.
XX
PA (GENV) GENENCOR INT INC.
XX
PI Bott RR, Shaw A;
XX
DR WPI; 1998-008893/01.
XX
PT New modified alpha-amylase enzymes - having altered calcium binding
PT properties to alter e.g. high or low pH activity, thermostability or
PT oxidative stability.
XX
PS Disclosure; Fig 5A; 31pp; English.
XX
CC This sequence represents an alpha-amylase isolated from Bacillus
CC amylioliquefaciens. This sequence is used in the analysis of novel alpha-
CC amylases comprising of an A domain, a C domain and a calcium binding site
CC associated withing of an A domain and the C domain. Ligand residues in the A
CC and/or C domains allow the modification of the alpha-amylase which alter
CC the characteristics of the calcium binding site and thereby alter

performance. This modified enzyme can be used for e.g. starch liquefaction, in laundry or dishwashing detergent compositions, as baking aids or in textile desizing. The alpha-amylase variants can have increased activity at low pH and high temperatures, increased high pH and oxidative stability and improved stability in the absence or low concentrations of calcium ion

XX Sequence 520 AA;

Query Match 100.0%; Score 2638; DB 2; Length 520;
Best Local Similarity 100.0%; Pred. No. 6,8e-219;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 VNGTLMQYFEMWTPNDGQHWKRLONDAEHLSDIGITAVWIPPAKYGISQSDNGGYPDLY 60
DB 38 VNGTLMQYFEMWTPNDGQHWKRLONDAEHLSDIGITAVWIPPAKYGISQSDNGGYPDLY 97
QY 61 DLGEFOQKGVTRTKYGTGKSELQDAIGSLHSRNVOYGVVNLHAKAGADATEDVAVEVNP 120
DB 98 DLGEFOQKGVTRTKYGTGKSELQDAIGSLHSRNVOYGVVNLHAKAGADATEDVAVEVNP 157
QY 121 ANRNOETSEERYQIKAMTDFRPPGKNTYSDPKMWHFDGADWDESKISRIFFRGEQK 180
DB 158 ANRNOETSEERYQIKAMTDFRPPGKNTYSDPKMWHFDGADWDESKISRIFFRGEQK 217
QY 181 AMDWEVSENGNVDYLMYADVVDYHPVVAETKKMGIMYANELSLDGRIDAAGHIKFSF 240
DB 218 AMDWEVSENGNVDYLMYADVVDYHPVVAETKKMGIMYANELSLDGRIDAAGHIKFSF 277
QY 241 LRDVQAVRQATGEMFTVAEYMONNAGKLENYLNTKTSFNQSVDPVPLHFNLOAASSQGG 300
DB 278 LRDVQAVRQATGEMFTVAEYMONNAGKLENYLNTKTSFNQSVDPVPLHFNLOAASSQGG 337
QY 301 GYDMRRLDGTVVSRRHPEKAVTFVENHDTQPGSLSESTVQTFKPLAVAFILITRESGYPQ 360
DB 338 GYDMRRLDGTVVSRRHPEKAVTFVENHDTQPGSLSESTVQTFKPLAVAFILITRESGYPQ 397
QY 361 VFYGDWYGTGKTSPEKIPSLKDNIEPLIKARKEYAYGPQHDYIDHPVIGWTRGDSAA 420
DB 398 VFYGDWYGTGKTSPEKIPSLKDNIEPLIKARKEYAYGPQHDYIDHPVIGWTRGDSAA 457
QY 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKISGDSGGEFFHNDGSYSIY 480
DB 458 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKISGDSGGEFFHNDGSYSIY 517
QY 481 VQK 483
DB 518 VQK 520
```

RESULT 13
AA01584
ID AA01584 standard; protein; 520 AA.

AC AA01584;

XX 17-JUN-1999 (first entry)

DE An alpha-amylase (Am-Amy1o) protein sequence.

XX Alpha-amylase; mutant; liquefaction; starch processing;
KW alcohol production; cleaning agent; detergent matrix; starch desizing.
XX Bacillus amyloliquefaciens.

XX MO9909183-A1.

XX 25-FEB-1999.

XX 14-AUG-1998; 98WO-US016906.

XX 19-AUG-1997; 97US-00914679.

XX

PA (GENV) GENECOR INT INC.

XX Day A.; Swanson B;

XX WPI; 1999-190168/16.

XX New mutant Bacillus licheniformis -a-amylase - useful in starch

PT liquefaction processes and detergents.

XX Disclosure; Fig 3; 35pp; English.

XX The present sequence represents an alpha-amylase from Bacillus
CC amyloliquefaciens. The specification describes a mutant alpha-amylase
CC derived from a precursor alpha-amylase by the deletion, substitution, or
CC addition of a residue corresponding to A210, H405, and/or T412 in B.
CC licheniformis alpha-amylase. The mutant alpha-amylase is used in the
CC initial stages (liquefaction) of starch processing, in alcohol
CC production, as a cleaning agent in detergent matrices, and in the textile
CC industry for starch desizing. The enzyme can be used in a detergent for
CC cleaning soiled laundry and/or dishes, and to liquefy starch

XX Sequence 520 AA;

Query Match 100.0%; Score 2638; DB 2; Length 520;
Best Local Similarity 100.0%; Pred. No. 6,8e-219;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 VNGTLMQYFEMWTPNDGQHWKRLONDAEHLSDIGITAVWIPPAKYGISQSDNGGYPDLY 60
DB 38 VNGTLMQYFEMWTPNDGQHWKRLONDAEHLSDIGITAVWIPPAKYGISQSDNGGYPDLY 97
QY 61 DLGEFOQKGVTRTKYGTGKSELQDAIGSLHSRNVOYGVVNLHAKAGADATEDVAVEVNP 120
DB 98 DLGEFOQKGVTRTKYGTGKSELQDAIGSLHSRNVOYGVVNLHAKAGADATEDVAVEVNP 157
QY 121 ANRNOETSEERYQIKAMTDFRPPGKNTYSDPKMWHFDGADWDESKISRIFFRGEQK 180
DB 158 ANRNOETSEERYQIKAMTDFRPPGKNTYSDPKMWHFDGADWDESKISRIFFRGEQK 217
QY 181 AMDWEVSENGNVDYLMYADVVDYHPVVAETKKMGIMYANELSLDGRIDAAGHIKFSF 240
DB 218 AMDWEVSENGNVDYLMYADVVDYHPVVAETKKMGIMYANELSLDGRIDAAGHIKFSF 277
QY 241 LRDVQAVRQATGEMFTVAEYMONNAGKLENYLNTKTSFNQSVDPVPLHFNLOAASSQGG 300
DB 278 LRDVQAVRQATGEMFTVAEYMONNAGKLENYLNTKTSFNQSVDPVPLHFNLOAASSQGG 337
QY 301 GYDMRRLDGTVVSRRHPEKAVTFVENHDTQPGSLSESTVQTFKPLAVAFILITRESGYPQ 360
DB 338 GYDMRRLDGTVVSRRHPEKAVTFVENHDTQPGSLSESTVQTFKPLAVAFILITRESGYPQ 397
QY 361 VFYGDWYGTGKTSPEKIPSLKDNIEPLIKARKEYAYGPQHDYIDHPVIGWTRGDSAA 420
DB 398 VFYGDWYGTGKTSPEKIPSLKDNIEPLIKARKEYAYGPQHDYIDHPVIGWTRGDSAA 457
QY 421 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKISGDSGGEFFHNDGSYSIY 480
DB 458 KSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKISGDSGGEFFHNDGSYSIY 517
QY 481 VQK 483
DB 518 VQK 520
```

RESULT 14
AAG65878
ID AAG65878 standard; protein; 520 AA.

XX AAG65878;

XX 11-FEB-2002 (first entry)

DE B. amyloliquefaciens alpha-amylase.

```
XX  Bacillus; mutant; alpha-amylase; oxidative stability; thermal stability;
KM  detergent; starch.
XX
OS  Bacillus amyloliquefaciens.
XX  US6297037-B1.
XX  02-OCT-2001.
XX
PF  10-FEB-1994; 94US-00194664.
XX
PR  11-FEB-1993; 93US-00016395.
XX
XX  (BARN/) BARNETT C. C.
PA  (MITC/) MITCHINSON C.
PA  (POWE/) POWER S. D.
PA  (REQU/) REQUADT C. A.
XX
PI  Barnett CC, Mitchinson C, Power SD, Requadt CA;
XX  WPI; 2001-638043/73.
XX
PT  Mutant alpha amylase, derived from Bacillus, for use in detergents and
XX  starch liquefaction compositions, comprising substituted amino acids.
XX
PS  Example; Fig 3A-B; 57pp; English.
XX
XX  The invention relates to a mutant alpha-amylase, derived from Bacillus.
CC  The mutant has a substitution or a deletion of a methionine residue in
CC  Bacillus licheniformis alpha amylase. The mutant alpha-amylases have
CC  altered oxidative stability and/or altered thermal stability and altered
CC  pH performance profiles. They are useful in detergents or starch
CC  liquefaction compounds. The present sequence represents the B.
CC  amyloliquefaciens alpha-amylase
XX
SQ  Sequence 520 AA;

Query Match      100.0%; Score 2638; DB 4; Length 520;
Best Local Similarity 100.0%; Pred. No. 6.8e-219;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1  VNGTLMQYFEWYTPNDGQHMRLQNDAEHLSDIGITAVMIPPAKGLSOSDNGGYPDLY 60
DB  |||||||
38  VNGTLMQYFEWYTPNDGQHMRLQNDAEHLSDIGITAVMIPPAKGLSOSDNGGYPDLY 97
QY  61  DLGEFOQKGTVRTKYGKSELQDAIGSLHSRNVOYGVVNLNKAAGADATEDVTAVERN 120
DB  |||||||
98  DLGEFOQKGTVRTKYGKSELQDAIGSLHSRNVOYGVVNLNKAAGADATEDVTAVERN 157
QY  121 ANRNOETSEERYQIKAWTDFRPPRGNTYSDPKMWHYHFDGADWDESKRSIRIFRGE 180
DB  |||||||
158 ANRNOETSEERYQIKAWTDFRPPRGNTYSDPKMWHYHFDGADWDESKRSIRIFRGE 217
QY  181 AMDREVSEENYQIYAWDVADYDHPVVAETKMGITWANEISLDGFRIDAANKHIFES 240
DB  |||||||
218 AMDREVSEENYQIYAWDVADYDHPVVAETKMGITWANEISLDGFRIDAANKHIFES 277
QY  241 LRDVQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFPOSYEDVYLHFNLAASOG 300
DB  |||||||
278 LRDVQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFPOSYEDVYLHFNLAASOG 337
QY  301 GYDNRRLIDGTVVRNRHBEKAVTVYENHDTQPGSLESTVQTWKPLAAYAFILTR 360
DB  |||||||
338 GYDNRRLIDGTVVRNRHBEKAVTVYENHDTQPGSLESTVQTWKPLAAYAFILTR 397
QY  361 VFYGDMTGKTGTSKPELPSLKDNTEPILKARKKAYAVPOHDYLDHNDVIGMTREG 420
DB  |||||||
398 VFYGDMTGKTGTSKPELPSLKDNTEPILKARKKAYAVPOHDYLDHNDVIGMTREG 457
QY  421 KSGIALAIIITDGPQSGSKMYAGLAKNAGETWYDITGNRSDTVKIGSDMGFFHVND 480
DB  |||||||
458 KSGIALAIIITDGPQSGSKMYAGLAKNAGETWYDITGNRSDTVKIGSDMGFFHVND 517
```

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QY  481 VQK 483
DB  |||
518 VQK 520

RESULT 15
AAB12431
ID  AAB12431 standard; protein; 514 AA.
XX
AC  AAB12431;
XX
DT  19-OCT-2000 (first entry)
XX
XX  Bacillus amyloliquefaciens clone number 24 protein SEQ ID NO:5.
DE  Bacillus amyloliquefaciens; alpha-amylase; thermostable; bread.
XX
XX  Bacillus amyloliquefaciens.
OS  Bacillus amyloliquefaciens.
XX  JP2000135093-A.
XX
XX  16-MAY-2000.
XX
XX  20-AUG-1999; 99UP-00234813.
XX
XX  24-AUG-1998; 98UP-00237839.
XX
XX  (DAIW ) DAIWA KASEI KK.
XX
XX  WPI; 2000-403584/35.
XX
XX  N-PSDB; AAA60578.
XX
PT  Novel thermostable alpha-amylase, useful for improving the preparation of
XX  bread, comprises alpha-amylase activity with less than 80% activity after
XX  treatment at 65degreesC for 30 min.
XX
PS  Example 6; Page 15-16; 22pp; Japanese.
XX
XX  The present invention describes a thermostable alpha-amylase (1)
CC  comprising the sequence given in AAB12431 (A) or deletions, replacements
CC  or insertions of one or more amino acid(s) in the sequence and alpha-
CC  amylase activity with less than 80% activity after treatment at 65 plus
CC  degrees Celsius for 30 minutes. Also described are: (1) DNAs encoding (1)
CC  ; (2) DNAs containing one of 4 nucleotide sequences comprising 1545 base
CC  pairs (see AAA60576 to AAA60579); (3) expression vectors containing the
CC  above mentioned DNAs; (4) host cells containing the above mentioned
CC  expression vectors; (5) preparation of a polypeptide having alpha-amylase
CC  activity by culture of the recombinant host cells; and (6) preparation of
CC  bread including a process to add (1) to the dough. (1) is useful in the
CC  preparation of bread. (1) improves the soft volume of the bread and
CC  prevents it aging. The present sequence represents a Bacillus
CC  amyloliquefaciens clone number 24 protein, which is used in the
CC  exemplification of the present invention
XX
SQ  Sequence 514 AA;

Query Match      99.9%; Score 2635; DB 3; Length 514;
Best Local Similarity 99.8%; Pred. No. 1.2e-218;
Matches 482; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1  VNGTLMQYFEWYTPNDGQHMRLQNDAEHLSDIGITAVMIPPAKGLSOSDNGGYPDLY 60
DB  |||||||
32  VNGTLMQYFEWYTPNDGQHMRLQNDAEHLSDIGITAVMIPPAKGLSOSDNGGYPDLY 91
QY  61  DLGEFOQKGTVRTKYGKSELQDAIGSLHSRNVOYGVVNLNKAAGADATEDVTAVERN 120
DB  |||||||
92  DLGEFOQKGTVRTKYGKSELQDAIGSLHSRNVOYGVVNLNKAAGADATEDVTAVERN 151
QY  121 ANRNOETSEERYQIKAWTDFRPPRGNTYSDPKMWHYHFDGADWDESKRSIRIFRGE 180
DB  |||||||
152 ANRNOETSEERYQIKAWTDFRPPRGNTYSDPKMWHYHFDGADWDESKRSIRIFRGE 211
```


Qy	181	AMDEVSSENGNYDYLNAVADVDYDHPVVAETKKMGIMYANELSLDGFRIIDAKHIXSF	240
Db	212	AMDEVSSENGNYDYLNAVADVDYDHPVVAETKKMGIMYANELSLDGFRIIDAKHIXSF	271
Qy	241	LRDWVQAVROATGKEMFTVAETWONNAGKLENYLNKTSFNOSVDPVPLHFNLOAASSQGG	300
Db	272	LRDWVQAVROATGKEMFTVAETWONNAGKLENYLNKTSFNOSVDPVPLHFNLOAASSQGG	331
Qy	301	GYPDRLDGTIVSRHPEKATFVENHDTOPGQSLSESTVQTFEKLAYAFILITRESGYPO	360
Db	332	GYPDRLDGTIVSRHPEKATFVENHDTOPGQSLSESTVQTFEKLAYAFILITRESGYPO	391
Qy	361	VFYGDMYGTGKTSPEKEIPSLKONIEPILKARKEAYAGPOHDYIDHPVYIGWTRREGDSSAA	420
Db	392	VFYGDMYGTGKTSPEKEIPSLKONIEPILKARKEAYAGPOHDYIDHPVYIGWTRREGDSSAA	451
Qy	421	KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSPTYKIGSDGNGEFHNDGSYSIX	480
Db	452	KSGLAALITDGPQGSKMYAGLKNAGETWYDITGNRSPTYKIGSDGNGEFHNDGSYSIX	511
Qy	481	VQK 483	
Db	512	VQK 514	

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 Job time : 60.3101 secs

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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:01:38 ; Search time 14.8246 Seconds
(without alignments)
3134.012 Million cell updates/sec

Title: US-09-925-576C-10

Perfect score: 2638
Sequence: 1 VNGTLMQYFEMVTPNDGQHW.....SDGNGEPHVDGVSIVYQK 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2638	100.0	514	1	ALBSN
2	2184	82.8	512	1	ALBSL
3	1835	69.6	518	1	A27705
4	1773.5	67.2	549	1	A54541
5	1759.5	66.8	549	1	A24436
6	1759.5	66.7	549	1	A24549
7	1700	64.4	548	1	ALBSF
8	1253	47.5	493	2	ALBSF
9	1217	46.1	484	2	G95160
10	1212	45.9	484	2	P98026
11	1206	45.7	492	2	AH2079
12	1136	43.1	491	2	C86781
13	1054	40.0	495	2	AD3038
14	1054	40.0	506	2	G98247
15	1019	38.6	494	1	B45738
16	1010	38.3	494	2	AD0751
17	1003	38.0	495	2	B90962
18	1002	38.0	495	1	A45738
19	984	37.3	495	1	B85810
20	620	23.5	217	2	A19506
21	351.5	13.3	826	2	B36720
22	346	13.1	826	2	B36720
23	333.5	12.6	421	2	S10514
24	324	12.3	437	2	S14956
25	323	12.2	1196	2	A29130
26	319	12.1	438	2	S14957
27	318	12.1	435	2	S12625
28	317	12.0	435	2	UC7137
29	315.5	12.0	437	2	UT0946

30	315.5	12.0	437	2	UC7138	alpha-amylase (EC
31	315	11.9	413	1	ALMT3	alpha-amylase (EC
32	310	11.8	504	2	A55861	alpha-amylase (EC
33	307.5	11.7	423	2	T09942	alpha-amylase (EC
34	307.5	11.7	438	1	ALBH	alpha-amylase (EC
35	305	11.6	439	2	T02956	alpha-amylase (EC
36	289	11.0	429	1	JE0406	alpha-amylase (EC
37	287	10.9	428	2	T05521	alpha-amylase (EC
38	285.5	10.8	713	2	S09196	cyclomaltoextrin
39	284.5	10.8	443	2	Q01527	alpha-amylase (EC
40	284.5	10.8	445	2	S19990	alpha-amylase (EC
41	283	10.7	427	1	ALBHB	alpha-amylase (EC
42	282.5	10.7	437	2	S07040	alpha-amylase (EC
43	279.5	10.6	482	2	S31478	alpha-amylase (EC
44	277.5	10.5	713	2	A58800	cyclomaltoextrin
45	272	10.3	713	1	ALBSG7	cyclomaltoextrin

ALIGNMENTS

RESULT 1

ALBSN
alpha-amylase (EC 3.2.1.1) precursor - Bacillus amyloliquefaciens

N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C/Species: Bacillus amyloliquefaciens

C/Date: 30-Nov-1980 #sequence_revision 30-Jun-1987 #text_change 18-Jun-1999

C/Accession: A92389; A90307; I39756; I39763; A00843

J/Takkinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L

U. Biol. Chem. 258, 1007-1013, 1983

A/Title: Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens deduced fr

A/Reference number: A92389; MUID:63108808; PMID:6185474

A/Contents: PUB110

A/Accession: A92389

A/Molecule type: DNA

A/Residues: 1-514 <TAX>

A/Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:G142428; PIDN:AAA221

A/Title: Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-amylase.

A/Reference number: A90307; MUID:80241725; PMID:6156671

A/Accession: A90307

A/Molecule type: protein

A/Residues: 32-53, 'I', 55-63, 'L', 65-78, 'D', 80-83, 'S', 85-222 <CHU>

R/Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtoavaara, P.; Sarvas, M.; Soderlund, H.;

Gene 15, 43-51, 1981

A/Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of t

A/Reference number: I39756; MUID:82051296; PMID:6170539

A/Accession: I39756

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-96 <RES>

A/Cross-references: EMBL:V00092; NID:G39297; PIDN:CAA23430.1; PID:G39298

R/Ruohonen, L.; Hackman, P.; Lehtoavaara, P.; Knowles, J.K.C.; Karanen, S.

Gene 59, 161-170, 1987

A/Title: Efficient secretion of Bacillus amyloliquefaciens alpha-amylase cells by its ow

A/Reference number: I39763; MUID:88137952; PMID:2830166

A/Accession: I39763

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-39 <RES>

A/Cross-references: GB:M18424; NID:G142430; PIDN:AAA22192.1; PID:G142431

C/Function: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A/Pathway: glycogen/starch degradation

C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F:32-514/Product: signal sequence #status predicted <SIG>

F:229-362/Domains: alpha-amylase core homology <AMY>

F:133,221,266/Binding site: calcium (Asn, Asp, His) #status predicted

F:262,292,359/Active site: Asp, Glu, Asp #status predicted

Query Match 100.0%; Score 2638; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 4, 7e-182;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPPAVKGLSGSDNGYGPYDLY 60
 DB 32 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPPAVKGLSGSDNGYGPYDLY 91

QY 61 DLGEFOOKGTVFRKYGKSKSLQDAIGSLSRNVOYGVVLAHKAQADTEVTAVEVNP 120
 DB 92 DLGEFOOKGTVFRKYGKSKSLQDAIGSLSRNVOYGVVLAHKAQADTEVTAVEVNP 151

QY 121 ANRNGTSEBYQIKAWTDFRPFGRGNTYSDFKWHYFPGADWDSRKISRIFKRGSECK 180
 DB 152 ANRNGTSEBYQIKAWTDFRPFGRGNTYSDFKWHYFPGADWDSRKISRIFKRGSECK 211

QY 181 AMDWEVSSNGNYDLYMADVDYDHPDVVAETKKGCIWYANELSLDGFRIIDAKHIFKSF 240
 DB 212 AMDWEVSSNGNYDLYMADVDYDHPDVVAETKKGCIWYANELSLDGFRIIDAKHIFKSF 271

QY 241 LRDWVOAVRQATGKEMFTVAEYVONNAGLENYLNTKTSNOSVDPVPLHPNLQAASQGG 300
 DB 272 LRDWVOAVRQATGKEMFTVAEYVONNAGLENYLNTKTSNOSVDPVPLHPNLQAASQGG 331

QY 301 GTDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLESTVQTFKFLAVALITRBSGPQ 360
 DB 332 GTDMRRLDGTIVVSRHPEKAVTFVENHDTQPGQSLESTVQTFKFLAVALITRBSGPQ 391

QY 361 VVYGMWYKGTSPKEIPBLKNIPBLKARKEYAVGQHDYIDHPDYIGMTRESDSAA 420
 DB 392 VVYGMWYKGTSPKEIPBLKNIPBLKARKEYAVGQHDYIDHPDYIGMTRESDSAA 451

QY 421 KSGLAALITDGPGRKMYAGLKNAGETWYDITGRNSPTVKISPDGMEFPYNDGSVSY 480
 DB 452 KSGLAALITDGPGRKMYAGLKNAGETWYDITGRNSPTVKISPDGMEFPYNDGSVSY 511

QY 481 VOK 483
 DB 512 VOK 514

RESULT 2
 ALBTL
 alpha-amylase (EC 3.2.1.1) precursor [validated] - Bacillus licheniformis
 N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C/Species: Bacillus licheniformis
 C/Date: 30-Jun-1987 #sequence revision 24-Apr-1998 #text change 15-Sep-2000
 C/Accession: A91997; B24549; A91796; A21663; I39772; A26151; S53788; A00844
 R/Yuuki, T.; Nomura, T.; Teruka, H.; Tsuboi, A.; Yamagata, H.; Tsukagoshi, N.; Uda, S.
 J. Biochem. 98, 1147-1156, 1985
 A/Title: Complete nucleotide sequence of a gene coding for heat- and pH-stable alpha-amylase deduced from the DNA sequences.
 A/Reference number: A91997; MUID:86111694; PMID:2418011
 A/Accession: A91997
 A/Molecule type: DNA
 A/Residues: 1-162, 'R', 164-512 <YU>
 A/Cross-references: GB:X03236; NID:939551; PIDN:CAA26981.1; PID:939552
 A/Experimental source: ATCC 27811
 R/Gray, G.L.; Mailzner, S.E.; Rey, M.W.; Lamsa, M.H.; Kindle, K.L.; Carmona, C.; Requadt, J. Bacteriol. 166, 635-643, 1986
 A/Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus
 A/Reference number: A91817; MUID:86195857; PMID:3009417
 A/Accession: B24549
 A/Molecule type: DNA
 A/Residues: 1-338, 'G', 340-348, 'S', 350-512 <GRA>
 A/Cross-references: GB:M13256; NID:g142510; PIDN:AAA22240.1; PID:g142511
 A/Experimental source: NCIB 8061
 R/Stephens, M.A.; Orlepp, S.A.; Ollington, J.F.; McConnell, D.J.
 J. Bacteriol. 158, 369-372, 1984
 A/Title: Nucleotide sequence of the 5' region of the Bacillus licheniformis alpha-amylase
 A/Reference number: A91796; MUID:84185455; PMID:6609154
 A/Accession: A91796
 A/Molecule type: DNA

A/Residues: 1-104 <STE>
 A/Cross-references: GB:X01984; NID:g142432; PIDN:AAA22193.1; PID:g142433
 R/Sibakov, M.; Palva, I.
 Eur. J. Biochem. 145, 567-572, 1984
 A/Title: Isolation and the 5'-end nucleotide sequence of Bacillus licheniformis alpha-amylase
 A/Reference number: A21663; MUID:85076654; PMID:6334606
 A/Accession: A21663
 A/Molecule type: DNA
 A/Residues: 1-3, 'H', 5-12, 'P', 14-47, 'R', 49-61, 'V', 63, 'D', 65-67, 'VA', 70-71, 'S', 73-80, 'D', 82
 A/Experimental source: chromosomal DNA of ATCC 14580
 A/Note: the authors translated the codon CGT for residue 48 as Gly and GAC for residue 64
 R/Laoid, B.M.; Chambliss, G.H.; McConnell, D.J.
 J. Bacteriol. 171, 2435-2442, 1989
 A/Title: Bacillus licheniformis alpha-amylase gene, amyL, is subject to promoter-independent
 A/Reference number: I39773; MUID:89213924; PMID:2540150
 A/Accession: I39774
 A/Molecule type: DNA
 A/Status: translated from GB/EMBL/DBJ
 A/Residues: 1-29 <LAC>
 A/Cross-references: GB:M26412; NID:g341477; PIDN:AAA22237.1; PID:g516590
 R/Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Didrichsen, B.
 Gene 96, 37-41, 1990
 A/Title: In vivo genetic engineering: homologous recombination as a tool for plasmid construction
 A/Reference number: I39772; MUID:91092499; PMID:2265757
 A/Accession: I39772
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-32, 'T' <DOR>
 A/Cross-references: GB:M62637; NID:g142498; PIDN:AAA22232.1; PID:g142499
 R/Kuhn, H.; Fietzek, P.P.; Lampen, J.O.
 J. Bacteriol. 149, 372-373, 1982
 A/Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: comparison
 A/Reference number: A26151; MUID:82098050; PMID:6172418
 A/Accession: A26151
 A/Molecule type: protein
 A/Residues: 30-37, 'E', 39-41, 'X', 43-47 <KUH>
 R/Machius, M.; Wiegand, G.; Huber, R.
 J. Mol. Biol. 246, 545-559, 1995
 A/Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2.2 Å
 A/Reference number: S53788; MUID:95182462; PMID:7877175
 A/Accession: S53788
 A/Molecule type: protein
 A/Residues: 'D', 220-227 <MAC>
 A/Note: sequence represents amino end of an internal fragment created by a single enzymatic
 R/Machius, M.; Wiegand, G.; Huber, R.
 submitted to the Brookhaven Protein Data Bank, July 1995
 A/Reference number: A65206; PDB:1BPL
 A/Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 32-210, 222-511
 A/Note: these structural studies suggest 163 is Leu rather than Arg
 R/Song, H.K.; Hwang, K.Y.; Chang, C.; Suh, S.W.
 submitted to the Brookhaven Protein Data Bank, October 1996
 A/Reference number: A66860; PDB:1VDS
 A/Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210, 222-511
 C/Genetics:
 A/Gene: amyL
 C/Function:
 A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 C/Pathway: glycogen/starch degradation
 C/Superfamily: alpha-amylase, amyloliqueficans type; alpha-amylase core homology
 C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide
 F/1-23/Domain: signal sequence #status predicted <SIG>
 F/30-512/Product: alpha-amylase #status experimental <WAT>
 F/227-360/Domain: alpha-amylase core homology <AMY>
 F/133, 229, 264/Binding site: calcium (ben, Asp, His) #status experimental
 F/260, 290, 357/Active site: Asp, Glu, Asp #status experimental

Query Match 82.8%; Score 2184; DB 1; Length 512;
 Best Local Similarity 80.5%; Pred. No. 2, 2e-149;
 Matches 389; Conservative 42; Mismatches 50; Indels 2; Gaps 1;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPPAVKGLSGSDNGYGPYDLY 60
 DB 32 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIIPPAVKGLSGSDNGYGPYDLY 91

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Qy 61 DLGFOQKGTVRTKYGKSELQDAIGSLHSRNVQYGVVNLNKAAGADATEDVTAVERNPN 120
Db 92 DLGFEHQKGTVRTKYGKSELQDAIGSLHSRNVQYGVVNLNKAAGADATEDVTAVERNPN 151
Qy 121 ANRQETSEEOYQIKAMTDFRPPRGNTYSDPKMWHYHFDGADMDSESRKI-SRIFFRGEK 180
Db 152 ADNRNRVTSGLHLLQAMWHFHFPGRGSTYSDFKMHWHFDGDMDESKLRIRYF--QSK 209
Qy 181 AMDMEVSENGNDYLYMAYADVVDYHPVVAETKKMGIMYANELSLDGFRIDAANKIKRSP 240
Db 210 AMDMEVSENGNDYLYMAYADIDYHPVVAEIKRGMWYANELQDGFRLDAVGHIFSF 269
Qy 241 LRDVQAVRQATGKEMFTVAEYQNNAGKLENTYKTSFNQSVFDPVLPHEMLQAASSQGG 300
Db 270 LRDVNHVRREKTGKEMFTVAEYQNNAGKLENTYKTSFNQSVFDPVLPHEMLQAASSQGG 329
Qy 301 GYDMRLLDGTIVSRHEKAVTPEVNDHDPGQSLSESTVQTFKPLAVAFILITRESGYPQ 360
Db 330 GYDMRKLNTSTVSKHPLKATFVDNHDTPGQSLSESTVQTFKPLAVAFILITRESGYPQ 389
Qy 361 VFYGDYGTGTSPEIKSLKONIEPILKARKEVAYGPQHDYIDHPVIGMTREGSSAA 420
Db 390 VFYGDYGTGTSPEIKSLKONIEPILKARKEVAYGPQHDYIDHPVIGMTREGSSAA 449
Qy 421 KSGGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKIGSDGMEFHVNDGSYSY 480
Db 450 NSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKIGSDGMEFHVNDGSYSY 509
Qy 481 VQK 483
Db 510 VQK 512

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RESULT 3

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alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase
C/Species: Bacillus sp.
C/Date: 31-Mar-1999 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
R/Jukamoto, A.; Kimura, K.; Ishii, Y.; Takano, T.; Yamane, K.
Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A/Title: Nucleotide sequence of the maltotriose-producing amylase gene from an alkalophilic bacterium, Bacillus sp.
A/Reference number: A27705; MUID:86162814; PMID:3258152
A/Accession: A27705
A/Molecule type: DNA
A/Residues: 1-518 <TSU>
A/Cross-references: GB:M18662; NID:g142496; PID:AAA2231.1; PID:g142497
A/Experimental source: Chromosomal DNA of strain 707
A/Note: amino end of mature protein also determined
C/Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F/1-33/Domain: signal sequence #status predicted <SIG>
F/34-518/Product: alpha-amylase #status experimental <WAT>
F/236-369/Domain: alpha-amylase core homology <AMY>
F/139,237,272/Binding site: calcium (Asn, Asp, His) #status predicted
F/269,299,366/Active site: Asp, Glu, Asp #status predicted

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Query Match 69.6%; Score 1835; DB 1; Length 518;
Best Local Similarity 66.6%; Pred. No. 2.8e-124;
Matches 323; Conservative 63; Mismatches 91; Indels 8; Gaps 3;
Qy 2 NGTLMQFEWYTPNDGQHWKRLQNDABHLSIDGTTAWIIPRAYKGLSGSDNGYGPYDLYD 61
Db 39 NGTLMQFEWYTPNDGQHWKRLQNDABHLSIDGTTAWIIPRAYKGLSGSDNGYGPYDLYD 98
Qy 62 LGFEQKGTVRTKYGKSELQDAIGSLHSRNVQYGVVNLNKAAGADATEDVTAVERNPN 121
Db 92 LGFEQKGTVRTKYGKSELQDAIGSLHSRNVQYGVVNLNKAAGADATEDVTAVERNPN 151

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Db 99 LGFEHQKGTVRTKYGKSELQDAIGSLHSRNVQYGVVNLNKAAGADATEDVTAVERNPN 158
Qy 122 ANRQETSEEOYQIKAMTDFRPPRGNTYSDPKMWHYHFDGADMDSESRKI-SRIFFRGEK 180
Db 159 ADNRNRVTSGLHLLQAMWHFHFPGRGSTYSDFKMHWHFDGDMDESKLRIRYF--QSK 209
Qy 181 AMDMEVSENGNDYLYMAYADVVDYHPVVAETKKMGIMYANELSLDGFRIDAANKIKRSP 240
Db 210 AMDMEVSENGNDYLYMAYADIDYHPVVAEIKRGMWYANELQDGFRLDAVGHIFSF 269
Qy 241 LRDVQAVRQATGKEMFTVAEYQNNAGKLENTYKTSFNQSVFDPVLPHEMLQAASSQGG 300
Db 270 LRDVNHVRREKTGKEMFTVAEYQNNAGKLENTYKTSFNQSVFDPVLPHEMLQAASSQGG 329
Qy 301 GYDMRLLDGTIVSRHEKAVTPEVNDHDPGQSLSESTVQTFKPLAVAFILITRESGYPQ 360
Db 330 GYDMRKLNTSTVSKHPLKATFVDNHDTPGQSLSESTVQTFKPLAVAFILITRESGYPQ 389
Qy 361 VFYGDYGTGTSPEIKSLKONIEPILKARKEVAYGPQHDYIDHPVIGMTREGSSAA 420
Db 390 VFYGDYGTGTSPEIKSLKONIEPILKARKEVAYGPQHDYIDHPVIGMTREGSSAA 449
Qy 421 KSGGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKIGSDGMEFHVNDGSYSY 480
Db 450 NSGLAALITDGPQSGSKMYAGLKNAGETWYDITGNRSDTYKIGSDGMEFHVNDGSYSY 509
Qy 481 VQK 483
Db 510 VQK 512

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RESULT 4

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alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DN1792)
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: Bacillus stearothermophilus
C/Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
R/Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEBS Microbiol. Lett. 77, 271-276, 1991
A/Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
A/Reference number: A54541
A/Accession: A54541
A/Molecule type: DNA
A/Residues: 1-549 <DOR>
A/Cross-references: GB:X59476
A/Experimental source: Chromosomal DNA of strain DN1792
C/Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the chromosome.
C/Genetics:
A/Start codon: GTG
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide degradation
F/1-34/Domain: signal sequence #status predicted <SIG>
F/35-549/Product: alpha-amylase #status predicted <WAT>
F/235-368/Domain: alpha-amylase core homology <AMY>
F/139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F/266,298,365/Active site: Asp, Glu, Asp #status predicted

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Query Match 67.2%; Score 1773.5; DB 1; Length 549;
Best Local Similarity 65.4%; Pred. No. 8.2e-120;
Matches 316; Conservative 57; Mismatches 105; Indels 5; Gaps 2;
Qy 2 NGTLMQFEWYTPNDGQHWKRLQNDABHLSIDGTTAWIIPRAYKGLSGSDNGYGPYDLYD 61
Db 39 NGTLMQFEWYTPNDGQHWKRLQNDABHLSIDGTTAWIIPRAYKGLSGSDNGYGPYDLYD 98
Qy 62 LGFEQKGTVRTKYGKSELQDAIGSLHSRNVQYGVVNLNKAAGADATEDVTAVERNPN 121
Db 99 LGFEQKGTVRTKYGKSELQDAIGSLHSRNVQYGVVNLNKAAGADATEDVTAVERNPN 158

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Qy 122 NNNQETSEBYOIKAMTDFRPGRGNTYSDPKMHWYHFGADWDESRLKSRIFKRGEGKA 181
Db 159 DRNGEISGTYOIAMTKFDFPGRGNTYSSFKRWYHFDGVDWDESRLKSRIFKRGEGKA 218
Qy 182 WDEVSSENGYDYLYMAYADVDPVVAETKKMGWYANELSLDGFRIIDAAKHIFSL 241
Db 219 WDEVDTENGYDYLYMAYADLDMDHPEVVELTKMGKMYVTNTIIDGFRIDVKKHIFSL 278
Qy 242 RDVQAVRQATGEMFTVAEYQNNAGKLENTYKTSFNQSVFVDFLHFNLOAASQGG 301
Db 279 PDMLSVRSQTKFPLTVGEYWSYINLKHNYITLDTGMSLFDAPLHKKFYTASKSGA 338
Qy 302 YMRRLDGTIVSRPEKAVTFVENHDTPQGSLSTVQWTKFKPLAAYFILTRESGYOV 361
Db 339 FMRRLMTNTLTKDQPTLAVTFVDNHDTEPGALQSWDPWFKPLAAYFILTREGYPCV 398
Qy 362 FYGDMYGTGKTSFK-ELPSLKDNIETPLKARKEYAVGPQHDYIDHPVIGWTRGDSAA 420
Db 399 FYGDIYGI---PQYNIPLSKSIDPLLIARRDYAVGQHDYIDHSDIIGWTRGTEPK 454
Qy 421 KSGLAALITDGPGRKMYAGLKNAGETWYDITGNRSPTYKIGSGMGEEFHVNDGSVSIY 480
Db 455 GSGLAALITDGPGRKMYVKGQAHAKVFDLTGNRSPTYKINSDDGGEFHVNDGSVSIY 514
Qy 481 VQK 483
Db 515 VPR 517

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RESULT 5

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A24436
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid PAT5
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: Bacillus stearothermophilus
C/Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C/Accession: A24436; I39777
R/Nakajima, R.; Imanaka, T.; Aiba, S.
J. Bacteriol. 163, 401-406, 1985
A/Reference number: A24436; UID:85234394; PMID:3924897
A/Accession: A24436
A/Molecule type: DNA
A/Residues: 1-549 <NAB>
A/Cross-references: GB:M11450
A/Experimental source: plasmid PAT5
A/Note: amino end of the mature protein also determined
Gene 96, 37-41, 1990
A/Title: In vivo genetic engineering: homologous recombination as a tool for plasmid cor
A/Reference number: I39772; UID:91092499; PMID:2265757
A/Accession: I39777
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-45 <RES>
A/Cross-references: GB:M62638; NID:G142514; PIDN:AAA22242.1; PID:G142515
C/Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
A/Genes: amyS
A/Genome: plasmid
A/Start codon: GTG
C/Function:
A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A/Pathway: glycogen/starch degradation
C/Superfamily: alpha-amylase, amyloliquefactans type; alpha-amylase core homology
C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F.1-34/Domian: signal sequence #status predicted <SIG>
F.135-549/Product: alpha-amylase #status experimental <AMT>
F.135-368/Domian: alpha-amylase core homology <AMT>
F.133,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F.1268,298,365/Active site: Asp, Glu, Asp #status predicted

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```

Query Match 66.8%; Score 1763.5; DB 1; Length 549;
Best Local Similarity 65.2%; Pred. No. 4.3e-119;
Matches 315; Conservative 58; Mismatches 105; Indels 5; Gaps 2;

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Qy 2 NGTLMQFEMWYTPNDQOHKRLQNDAEHLSDIGITAVWIPRAYKLSQSDNGYCPDLYD 61
Db 39 NGTLMQFEMWYTPDQOHKRLQNDAEHLSDIGITAVWIPRAYKLSQSDNGYCPDLYD 98
Qy 62 LGEFQKGVTRKTKYKSELDALIGSLHSRNQYGVVNLHKAQADATEDVTAVEVPA 121
Db 99 LGEFQKGVTRKTKYKSELDALIGSLHSRNQYGVVNLHKAQADATEDVTAVEVPA 158
Qy 122 NNNQETSEBYOIKAMTDFRPGRGNTYSDPKMHWYHFGADWDESRLKSRIFKRGEGKA 181
Db 159 DRNGEISGTYOIAMTKFDFPGRGNTYSSFKRWYHFDGVDWDESRLKSRIFKRGEGKA 218
Qy 182 WDEVSSENGYDYLYMAYADVDPVVAETKKMGWYANELSLDGFRIIDAAKHIFSL 241
Db 219 WDEVDTENGYDYLYMAYADLDMDHPEVVELTKMGKMYVTNTIIDGFRIDVKKHIFSL 278
Qy 242 RDVQAVRQATGEMFTVAEYQNNAGKLENTYKTSFNQSVFVDFLHFNLOAASQGG 301
Db 279 PDMLSVRSQTKFPLTVGEYWSYINLKHNYITLDTGMSLFDAPLHKKFYTASKSGA 338
Qy 302 YMRRLDGTIVSRPEKAVTFVENHDTPQGSLSTVQWTKFKPLAAYFILTRESGYOV 361
Db 339 FMRRLMTNTLTKDQPTLAVTFVDNHDTEPGALQSWDPWFKPLAAYFILTREGYPCV 398
Qy 362 FYGDMYGTGKTSFK-ELPSLKDNIETPLKARKEYAVGPQHDYIDHPVIGWTRGDSAA 420
Db 399 FYGDIYGI---PQYNIPLSKSIDPLLIARRDYAVGQHDYIDHSDIIGWTRGTEPK 454
Qy 421 KSGLAALITDGPGRKMYAGLKNAGETWYDITGNRSPTYKIGSGMGEEFHVNDGSVSIY 480
Db 455 GSGLAALITDGPGRKMYVKGQAHAKVFDLTGNRSPTYKINSDDGGEFHVNDGSVSIY 514
Qy 481 VQK 483
Db 515 VPR 517

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RESULT 6

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A24549
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)
N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C/Species: Bacillus stearothermophilus
C/Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C/Accession: A24549; I39501; I39770
R/Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamea, M.H.; Kindle, K.L.; Reguadt,
J. Bacteriol. 166, 635-643, 1986
A/Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothe
A/Reference number: A91817; UID:86195857; PMID:3009417
A/Accession: A24549
A/Molecule type: DNA
A/Residues: 1-549 <GRA>
A/Cross-references: GB:M3255; NID:G142512; PIDN:AAA22241.1; PID:G142513
A/Experimental source: genomic DNA of strain NZ-3
R/Sach, H.; Nishida, H.; Isono, K.
J. Bacteriol. 170, 1034-1040, 1988
A/Title: Evidence for movement of the alpha-amylase gene into two phylogenetically dista
A/Reference number: I39501; UID:88139156; PMID:3257753
A/Accession: I39501
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 536-549 <RES>
A/Cross-references: GB:M29577; NID:G142476; PIDN:AAA22225.1; PID:G142478
A/Experimental source: strain DY-5
A/Accession: I39770
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 536-549 <RE2>
A/Cross-references: GB:M29578; NID:G142484; PIDN:AAA22228.1; PID:G142486
A/Experimental source: strain 799
C/Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
A/Genes:
A/Start codon: GTG

```

C/Function:

A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A/Pathway: glycogen/starch degradation
 C/Superfamily: alpha-amylose, amyloliquefaciens type; alpha-amylose core homology
 C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
 F/1-34/Domain: signal sequence #status predicted <SIG>
 F/35-549/Product: alpha-amylose #status predicted <MAT>
 F/235-368/Domain: alpha-amylose core homology <AMY>
 F/139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
 F/268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 66.7%; Score 1759.5; DB 1; Length 549;
 Best Local Similarity 65.0%; Pred. No. 8.3e-119;
 Matches 314; Conservative 59; Mismatches 105; Indels 5; Gaps 2;

```

QY 2 NGTLMQFEMWTPDDGQHWKRLQNDADHLSDIGTAVWIPAYKGLSOSNGVGYLYD 61
DB 39 NGTLMQFEMWTPDDGQHWKRLQNDADHLSDIGTAVWIPAYKGLSOSNGVGYLYD 98
QY 62 LGSEFOQKGTVRTKTKYKSELDALIGSLHSRNVOYGVGVNLHKGADATEDVTAVERNPA 121
DB 99 LGSEFOQKGTVRTKTKYKSELDALIGSLHSRNVOYGVGVNLHKGADATEDVTAVERNPA 158
QY 122 NNOQTSSEYQIAWTFDFPGRGNTYSDFKMWHYHFDGADWDSESKISRIKFRGEGKA 181
DB 159 DRNOEISGTYQIAWTFDFPGRGNTYSDFKMWHYHFDGADWDSESKISRIKFRGEGKA 218
QY 182 WDMEVSENGNYLYMADVDYDHPVVAETKKMGWYANELSDGGRIDAARKIKSF 241
DB 219 WDMEVSENGNYLYMADVDYDHPVVAETKKMGWYANELSDGGRIDAARKIKSF 278
QY 242 RDWVOAVRQATGKEMFVAEYQWNNAGKLENYLNTKTSFNOSVDFVPLHFMLOAASQGGG 301
DB 279 PDLSTVRSQGTGRPLFTVGSYMSYDINKLNYITKNGTMSLDPAHNFYTAASKGGA 338
QY 302 YDMRRLDGTVSRRPEKAVTVEENHDTPQGSLESTVQTFKPLAAYAFILTRBSGYPOV 361
DB 339 FDMSTLMTNTLMKDQPTLAVTFVDNHDTPQGSLESTVQTFKPLAAYAFILTRBSGYPOV 398
QY 362 FYGDWYGTGKTSRK-ELPSLKDNIEPLTKARKAYAPQHDYIDHPVLTGWTREGSSAA 420
DB 399 FYGDWYGTGKTSRK-ELPSLKDNIEPLTKARKAYAPQHDYIDHPVLTGWTREGSSAA 454
QY 421 KSGIALITDGPGRSKMYAGLKNAGETWYDITGNRSDTYKISGDSGGEFHVNDGSSY 480
DB 455 GSGIALITDGPGRSKMYAGLKNAGETWYDITGNRSDTYKISGDSGGEFHVNDGSSY 514
QY 481 VOK 483
DB 515 VPR 517

```

RESULT 7

ALBSF

alpha-amylose (EC 3.2.1.1) precursor - *Bacillus stearothermophilus* (strain DY-5) plasmid
 N/Alternate names: 1,4-alpha-D-glucan glucanohydrolase
 C/Species: *Bacillus stearothermophilus*
 C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Feb-1997
 C/Accession: A91999; B91999; A91804; A00845
 J/Ihara, H.; Sasaki, T.; Teubot, A.; Yamagata, H.; Teukagoshi, N.; Uda, S.
 J. Biochem. 98, 95-103, 1985
 A/Title: Complete nucleotide sequence of a thermophilic alpha-amylose gene: homology bet
 A/Reference number: A91999; MUID:86008166; PMID:3876333
 A/Accession: A91999
 A/Molecule type: DNA
 A/Residues: 1-548 <1H1>
 A/Cross-references: GB:X02769
 A/Experimental source: plasmid pHI300 from strain DY-5
 A/Accession: B91999
 A/Molecule type: protein
 A/Residues: 35-48 <1H2>
 R/Teukagoshi, N.; Iritani, S.; Sasaki, T.; Takemura, T.; Ihara, H.; Idota, Y.; Yamagata,

J. Bacteriol. 164, 1182-1187, 1985

A/Title: Efficient synthesis and secretion of a thermophilic alpha-amylose by protein-pr
 A/Reference number: A91804; MUID:86059211; PMID:2999073
 A/Contents: pBAM101
 A/Accession: A91804
 A/Molecule type: DNA
 A/Residues: 1-29, 'Q', 31-75, 'W', 77-122 <TSU>
 C/Comment: Alpha-amylose genes have been found on plasmids and in multiple copies on the
 C/Genetics:
 A/Genome: Plasmid
 A/Start codon: GTC
 C/Function:
 A/Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
 A/Pathway: glycogen/starch degradation
 C/Superfamily: alpha-amylose, amyloliquefaciens type; alpha-amylose core homology
 C/Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
 F/1-34/Domain: signal sequence #status predicted <SIG>
 F/35-548/Product: alpha-amylose #status experimental <MAT>
 F/235-368/Domain: alpha-amylose core homology <AMY>
 F/139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
 F/268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 64.4%; Score 1700; DB 1; Length 548;
 Best Local Similarity 63.8%; Pred. No. 1.6e-114;
 Matches 308; Conservative 57; Mismatches 112; Indels 6; Gaps 3;

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QY 2 NGTLMQFEMWTPDDGQHWKRLQNDADHLSDIGTAVWIPAYKGLSOSNGVGYLYD 61
DB 39 NGTLMQFEMWTPDDGQHWKRLQNDADHLSDIGTAVWIPAYKGLSOSNGVGYLYD 98
QY 62 LGSEFOQKGTVRTKTKYKSELDALIGSLHSRNVOYGVGVNLHKGADATEDVTAVERNPA 121
DB 99 LGSEFOQKGTVRTKTKYKSELDALIGSLHSRNVOYGVGVNLHKGADATEDVTAVERNPA 158
QY 122 NNOQTSSEYQIAWTFDFPGRGNTYSDFKMWHYHFDGADWDSESKISRIKFRGEGKA 181
DB 159 DRNOEISGTYQIAWTFDFPGRGNTYSDFKMWHYHFDGADWDSESKISRIKFRGEGKA 218
QY 182 WDMEVSENGNYLYMADVDYDHPVVAETKKMGWYANELSDGGRIDAARKIKSF 241
DB 219 WDMEVSENGNYLYMADVDYDHPVVAETKKMGWYANELSDGGRIDAARKIKSF 278
QY 242 RDWVOAVRQATGKEMFVAEYQWNNAGKLENYLNTKTSFNOSVDFVPLHFMLOAASQGGG 301
DB 279 PDLSTVRSQGTGRPLFTVGSYMSYDINKLNYITKNGTMSLDPAHNFYTAASKGGA 338
QY 302 YDMRRLDGTVSRRPEKAVTVEENHDTPQGSLESTVQTFKPLAAYAFILTRBSGYPOV 361
DB 339 FDMSTLMTNTLMKDQPTLAVTFVDNHDTPQGSLESTVQTFKPLAAYAFILTRBSGYPOV 397
QY 362 FYGDWYGTGKTSRK-ELPSLKDNIEPLTKARKAYAPQHDYIDHPVLTGWTREGSSAA 420
DB 399 FYGDWYGTGKTSRK-ELPSLKDNIEPLTKARKAYAPQHDYIDHPVLTGWTREGSSAA 453
QY 421 KSGIALITDGPGRSKMYAGLKNAGETWYDITGNRSDTYKISGDSGGEFHVNDGSSY 480
DB 454 GSGIALITDGPGRSKMYAGLKNAGETWYDITGNRSDTYKISGDSGGEFHVNDGSSY 513
QY 481 VOK 483
DB 514 VPR 516

```

RESULT 8

alpha-amylose (EC 3.2.1.1) - *Bacillus circulans*
 C/Species: *Bacillus circulans*
 C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
 C/Accession: S15713
 R/Marcel, T.
 submitted to the EMBL Data Library, May 1991
 A/Reference number: S15713
 A/Accession: S15713

QY 418 SAAKSGLAALITDQPGSKMYAGLNAGETWYDITGNRSDTVTKIGSDGWFHNDGVS 477
Db 413 DNKEYGLSCILTNKNGSKMTIIDKAYAGKVYIDLFGRHEIPIITLDQNGGAEFYNDGVS 472

QY 478 SIYVQK 483
Db 473 SVWVDK 478

RESULT 13
AD3038
alpha-amylase amYA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AD3038
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan
Science 294, 2317-2323, 2001
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AD3038
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-495 <KUR>
A:Cross-references: GB:AE008689; PIDN:AAL44722.1; PID:g17742354; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: amyA
A:Map position: linear chromosome
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 40.0%; Score 1054; DB 2; Length 495;
Best Local Similarity 43.7%; Pred. No. 4.2e-68;
Matches 214; Conservative 77; Mismatches 183; Indels 16; Gaps 6;

QY 4 TLMQYFEWYTPNDGQHWKQLQNDAEHLSDIGITAVIWPAYKGLSQSDN-GYGFYDLYL 62
Db 5 TLLQFFHYYPDGKLMSEVAEKAESLAKMGITDWLPPAYKGAAGGYSVGYDTYDL 64

QY 63 GEFQKQKTVRTKYTKSELODAIGSLHSRNQVGVVNLNKHAGADATEDVAVEVNPAN 122
Db 65 GEFQKQKTVATKYGDRAALEHAGTKLKDNGIRVHDVVLNKHMGADKEKEKVRVRNPDD 124

QY 123 RNQETSEYQIKAWTDFFPGRGNYSDFKWHYHFDGADWDSRKISRIFKP---RREG 179
Db 125 RTDIDDEDFPALAYTRFTFPGRNKHSKFIWDLKCFSGVDHIEPTEDGIFRLVNEYG 184

QY 180 KAMDVESSNGNYDLYMADVDYDHPDVAETKKGWYANLSLDGFRIDAAKHIKFS 239
Db 185 E-WNEEVDQENGFDYLMGADVEFRNRAVYELKYWRMLSEQVQVDGFRIDAACHIPAW 243

QY 240 FLRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVDFVPLHNLQAASSOG 299
Db 244 FFRDVGVMHRETVPDLFVVAEYHWPDLKSYLELVKQLMFLDVALHHSFHDASKQ 303

QY 300 GGYDMRLLDGTVSRHPEKAVTFVENHDTQPGQSLSTVQTWFKPLAYAFILTRREG 359
Db 304 GDFDMRSIFDGLSVSAVPDHAVTLDVNDHTQPLQSLSEAPVEPWFKPLAYAIIILLRE 363

QY 360 QVFYCDMYGTGKTSKP-----EIPSLKDNIEPIILKARKEYAGVQPHDYIDHPDVIGW 411
Db 364 CVFYPDLPFGTSYTDGNGNEYKIDIPAI-ECULPKLEARSFANGPQTDIFDDASCI 422

QY 412 TREGDSSAAKSGLAALITDQPGSKMYAGLNAGETWYDITGNRSDTVTKIGSDGWFH 471
Db 423 IRHGTADA--PGCVVVMNSGEPGEKQADLGPERRAGSVWRDFLGHREHITLDESCKGTF 480

QY 472 VNDGVSIVY 481
Db 481 TNGGVSVMV 490

RESULT 14
G98247
cytoplasmic alpha-amylase (1,4-alpha-d-glucan glucanohydrolase) [imported] - Agrobacterium
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C:Accession: G98247
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman, I.
A.; Liu, F.; Woliam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.,
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: G98247
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-506 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK89505.1; PID:g15159379; GSPDB:GN00170
C:Genetics:
A:Gene: AGR L 1863
A:Map position: linear chromosome
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 40.0%; Score 1054; DB 2; Length 506;
Best Local Similarity 43.7%; Pred. No. 4.3e-68;
Matches 214; Conservative 77; Mismatches 183; Indels 16; Gaps 6;

QY 4 TLMQYFEWYTPNDGQHWKQLQNDAEHLSDIGITAVIWPAYKGLSQSDN-GYGFYDLYL 62
Db 16 TLLQFFHYYPDGKLMSEVAEKAESLAKMGITDWLPPAYKGAAGGYSVGYDTYDL 75

QY 63 GEFQKQKTVRTKYTKSELODAIGSLHSRNQVGVVNLNKHAGADATEDVAVEVNPAN 122
Db 76 GEFQKQKTVATKYGDRAALEHAGTKLKDNGIRVHDVVLNKHMGADKEKEKVRVRNPDD 135

QY 123 RNQETSEYQIKAWTDFFPGRGNYSDFKWHYHFDGADWDSRKISRIFKP---RREG 179
Db 136 RTDIDDEDFPALAYTRFTFPGRNKHSKFIWDLKCFSGVDHIEPTEDGIFRLVNEYG 195

QY 180 KAMDVESSNGNYDLYMADVDYDHPDVAETKKGWYANLSLDGFRIDAACHIKFS 239
Db 196 E-WNEEVDQENGFDYLMGADVEFRNRAVYELKYWRMLSEQVQVDGFRIDAACHIPAW 254

QY 240 FLRDWQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVDFVPLHNLQAASSOG 299
Db 255 FFRDVGVMHRETVPDLFVVAEYHWPDLKSYLELVKQLMFLDVALHHSFHDASKQ 314

QY 300 GGYDMRLLDGTVSRHPEKAVTFVENHDTQPGQSLSTVQTWFKPLAYAFILTRREG 359
Db 315 GDFDMRSIFDGLSVSAVPDHAVTLDVNDHTQPLQSLSEAPVEPWFKPLAYAIIILLRE 374

QY 360 QVFYCDMYGTGKTSKP-----EIPSLKDNIEPIILKARKEYAGVQPHDYIDHPDVIGW 411
Db 375 CVFYPDLPFGTSYTDGNGNEYKIDIPAI-ECULPKLEARSFANGPQTDIFDDASCI 433

QY 412 TREGDSSAAKSGLAALITDQPGSKMYAGLNAGETWYDITGNRSDTVTKIGSDGWFH 471
Db 434 IRHGTADA--PGCVVVMNSGEPGEKQADLGPERRAGSVWRDFLGHREHITLDESCKGTF 491

QY 472 VNDGVSIVY 481
Db 492 TNGGVSVMV 501

RESULT 15
B45738
alpha-amylase (EC 3.2.1.1), cytosolic - Salmonella typhimurium
N:Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C:Species: Salmonella typhimurium
C:Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C:Accession: B45738
R:Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.
J. Bacteriol. 174, 6644-6652, 1992

00000 : OT :

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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:46:32 ; Search time 8.47121 Seconds
(without alignments)
2968.867 Million cell updates/sec

Title: US-09-925-576C-10
Perfect score: 2638
Sequence: 1 VNGTLMQYFEWYTPNDGQHW.....SDGWBGFHVDGVSIVYQK 483

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2638	100.0	514	1 AMY_BACAM	P06692 bacillus li
2	2187	82.9	512	1 AMY_BACLI	P06278 bacillus li
3	1835	69.6	518	1 AMY2_BACS7	P19571 bacillus sp
4	1763.5	66.8	549	1 AMY_BACST	P06279 bacillus st
5	1017	38.6	494	1 AMY2_SALTY	P26613 salmonella
6	1002	38.0	495	1 AMY2_ECOLI	P26612 escherichia
7	345	13.1	440	1 AMY3_ORYSA	P27932 oryza sativ
8	333.5	12.6	421	1 AMY3_VIGMU	P17859 vigna mungo
9	324	12.3	437	1 AMY3_ORYSA	P27939 oryza sativ
10	323	12.2	1196	1 AMYB_PAEPO	P21543 paenibacill
11	319	12.1	438	1 AMY3_ORYSA	P27937 oryza sativ
12	318	12.1	435	1 AMY3_ORYSA	P27933 oryza sativ
13	315.5	12.0	437	1 AMY3_ORYSA	P27934 oryza sativ
14	315	11.9	413	1 AMY3_WHEAT	P08117 triticum ae
15	307.5	11.7	438	1 AMY1_HORVU	P00693 hordeum vul
16	289	11.0	429	1 AMY1_HORVU	P04750 hordeum vul
17	285.5	10.8	713	1 CDGT_BACS8	P17692 bacillus sp
18	284.5	10.8	443	1 AMY2_ORYSA	P27935 oryza sativ
19	284.5	10.8	445	1 AMY2_ORYSA	P27941 oryza sativ
20	283	10.7	427	1 AMY2_HORVU	P04063 hordeum vul
21	282	10.7	368	1 AMY3_HORVU	P04747 hordeum vul
22	277.5	10.5	713	1 CDGT_BACCI	P43379 bacillus ci
23	272	10.3	713	1 CDGT_BACSP	P30921 bacillus sp
24	270	10.2	428	1 AMY1_ORYSA	P17654 oryza sativ
25	267.5	10.1	919	1 AMY_STRLI	Q05884 streptomyce
26	255	9.7	712	1 CDGT_BACS3	P09121 bacillus sp
27	253	9.6	718	1 CDGT_BACCI	P30920 bacillus ci
28	253	9.6	718	1 CDGT_BACSS	P31747 bacillus sp
29	251	9.5	713	1 CDGT_BACS0	P05618 bacillus sp
30	246.5	9.3	581	1 AMY1_SCHPO	Q09840 schizosacch
31	245	9.3	719	1 AMYM_BACST	P19531 bacillus st
32	244.5	9.3	478	1 Y029_SCHPO	Q10427 schizosacch
33	244.5	9.3	528	1 AMY_BACCI	P08137 bacillus ci

ALIGNMENTS

RESULT 1

ID	AMY_BACAM	STANDARD;	PRT;	514 AA.
AC	P00692;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-JAN-1988 (Rel. 06, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan Glucanohydrolase).			
OS	Bacillus amyloliquefaciens.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1390;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=IH;			
RX	MEDLINE=83108808; PubMed=6185474;			
RA	Takkinen K., Pettersson R.F., Kalkkinen N., Palva I., Soederlund H., Kaeerlaeinen L.;			
RT	"Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens deduced from the nucleotide sequence of the cloned gene.";			
RL	J. Biol. Chem. 258:1007-1013 (1983).			
RN	[2]			
RP	SEQUENCE OF 32-222.			
RX	MEDLINE=80241725; PubMed=6156671;			
RA	Chung H.S., Friedberg F.;			
RT	"Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha- amylase.";			
RL	Biochem. J. 185:387-395 (1980).			
RN	[3]			
RP	SEQUENCE OF 1-96 FROM N.A.			
RX	MEDLINE=8201296; PubMed=6170539;			
RA	Palva I., Pettersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M., Soederlund H., Takkinen K., Kaeerlaeinen L.;			
RT	"Nucleotide sequence of the promoter and NH2-terminal signal peptide region of the alpha-amylase gene from Bacillus amyloliquefaciens.";			
RL	Gene 15:43-51 (1981).			
RN	[4]			
RP	SEQUENCE OF 1-39 FROM N.A.			
RX	MEDLINE=88137952; PubMed=2830166;			
RA	Ruohonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Karaenen S.;			
RT	"Efficient secretion of Bacillus amyloliquefaciens alpha-amylase by its own signal peptide from Saccharomyces cerevisiae host cells.";			
RL	Gene 59:161-170 (1987).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.			
RX	MEDLINE=20384196; PubMed=10924103;			
RA	Brzozowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H., Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;			
RT	"Structural analysis of a chimeric bacterial alpha-amylase. High-resolution analysis of native and ligand complexes.";			
RL	Biochemistry 39:9099-9107 (2000).			
CC	-1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.			
CC	-1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.			
CC	-1- SUBUNIT: Monomer.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			

P14014 bacillus li
Q9y789 schizosacch
P26827 thermoanaer
P21567 saccharomyc
P31797 bacillus st
P14859 dictyoglomu
P80039 thermotoga
P10529 aspergillus
P25718 escherichia
O86956 thermotoga
P30292 aspergillus
Q02905 aspergillus

34 242.5 9.2 718 1 CDGT_BACLI
35 241 9.1 564 1 AMY4_SCHPO
36 240.5 9.1 710 1 CDGT_THETU
37 240 9.1 494 1 AMY1_SACFI
38 234.5 8.9 711 1 CDGT_BACST
39 232 8.8 498 1 AMY3_DICTH
40 229 8.7 441 1 NGTA_THEMA
41 228.5 8.7 499 1 AMYA_ASFOR
42 228 8.6 676 1 AMY1_ECOLI
43 225.5 8.5 442 1 NGTA_THENE
44 225.5 8.5 499 1 AMY_ASPSH
45 222.5 8.4 498 1 AMYA_ASPAW

FT	METAL	233	233	CALCIUM 2.	
	Query Match	82.9%;	Score 2187;	DB 1;	Length 512;
	Best Local Similarity	80.5%;	Pred. No. 2.5e-147;		
	Matches 389;	Conservative 43;	Mismatches 49;	Indels 2;	Gaps 1;
QY	1	VNGLMQYFEWYTNDDGQHWKRLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	60		
Db	32	LNGLMQYFEWYTNDDGQHWKRLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	91		
QY	61	DLGFEFOQKGTVRTKYTKSELQDAIGLSHNSVVOYGDVVLNKHAGADATEDVAVENP	120		
Db	92	DLGFEFOQKGTVRTKYTKSELQDAIGLSHNSVVOYGDVVLNKHAGADATEDVAVENP	151		
QY	121	ANRNQETSEYQIKAWTDTRFPGRGNTYSDFKWHYHFDGADWDESKIRIKFRGEK	180		
Db	152	ADNRNVISGEHRIKAWTHFPPGRGNTYSDFKWHYHFDGADWDESKIRIKFRGEK	209		
QY	181	AWDWEVSSENGYDILMYADVVDYDHPDVVAETKKGWIYANELSLDGRIDAAGHKFSF	240		
Db	210	AWDWEVSSENGYDILMYADVVDYDHPDVVAETKKGWIYANELSLDGRIDAAGHKFSF	269		
QY	241	LRDWVQAVROATGKEMFTVAEYMNAGKLENYLNKTSFNQSDVDPVPLHFNLOAASQGG	300		
Db	270	LRDWVHREKTKGEMFTVAEYMNAGKLENYLNKTSFNQSDVDPVPLHFNLOAASQGG	329		
QY	301	GYDMRLLDGTVVRSHPEKAVTFVENHDTQPGSLESTVQTFKPLAYAFILTRSGYPQ	360		
Db	330	GYDMRLLDGTVVRSHPEKAVTFVENHDTQPGSLESTVQTFKPLAYAFILTRSGYPQ	389		
QY	361	VFYGDMYGTGTSPEKIPSLKDNIEPIKARKEYAYGPOHDIYDHPDVIGTWREGDSSAA	420		
Db	390	VFYGDMYGTGTSPEKIPSLKDNIEPIKARKEYAYGPOHDIYDHPDVIGTWREGDSSAA	449		
QY	421	KSLGALALITDGPCKRMYAGLNAGETWYDITGNRSDTVKIGDSCGWGEFHVNDGVSIV	480		
Db	450	NSGLAALITDGPCKRMYAGLNAGETWYDITGNRSDTVKIGDSCGWGEFHVNDGVSIV	509		
QY	481	VQK 483			
Db	510	VQR 512			
RESULT 3					
AMT6	BACS7	STANDARD;	PRT;	518 AA.	
AC	P19571;				
DT	01-FEB-1991	(Rel. 17, Created)			
DT	01-FEB-1991	(Rel. 17, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (G6-amyase)				
OS	Bacillus sp. (strain 707).				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX	NCBI_TaxID=1416;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.				
RX	MEDLINE=88162814; PubMed=3258152;				
RA	Tsukamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;				
RT	"Nucleotide sequence of the maltohexaoside-producing amylase gene from				
RT	an alkalophilic Bacillus sp. #707 and structural similarity to				
RT	liquefying type alpha-amyloses."				
RL	Biochem. Biophys. Res. Commun. 151:25-31(1988).				
CC	-!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages				
CC	in amylaceous polysaccharides so as to remove successive				
CC	maltohexaoside residues from the non-reducing chain ends.				
CC	-!- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By				
CC	similarity).				
CC	-!- PATHWAY: Starch degradation.				
CC	-!- SUBCELLULAR LOCATION: Secreted.				
CC	-!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.				
CC	-----				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; M18862; AAA22231.1; -.				
DR	PIR; A27705; A27705.				
DR	HSPP; P06278; LVJS.				
DR	InterPro; IPR006589; Alp_aml_cat_sub.				
DR	InterPro; IPR006047; Alpha_aml_cat.				
DR	InterPro; IPR006046; Glyco_hydro_13.				
DR	Pfam; PF00128; alpha-amyLase; 1_13.				
DR	PRINTS; PR00110; ALPHAAMYLASE.				
DR	SMART; SM00642; Amy; 1.				
KW	Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.				
FT	SIGNAL	1	33		
FT	CHAIN	34	518		GLUCAN 1,4-ALPHA-MALTOHEXAOSIDASE.
FT	ACT_SITE	269	269		BY SIMILARITY.
FT	ACT_SITE	273	273		BY SIMILARITY.
FT	ACT_SITE	366	366		BY SIMILARITY.
FT	METAL	139	139		CALCIUM 1 (BY SIMILARITY).
FT	METAL	196	196		CALCIUM 2 AND SODIUM (BY SIMILARITY).
FT	METAL	219	219		CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
FT					SIMILARITY).
FT	METAL	221	221		CALCIUM 2 AND SODIUM (BY SIMILARITY).
FT	METAL	232	232		CALCIUM 1 AND SODIUM (BY SIMILARITY).
FT	METAL	238	238		CALCIUM 1 AND SODIUM (BY SIMILARITY).
FT	METAL	240	240		CALCIUM 2 (BY SIMILARITY).
FT	METAL	242	242		CALCIUM 2 (BY SIMILARITY).
FT	METAL	273	273		CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
FT					SIMILARITY).
SQ	SEQUENCE	518 AA;	59009 MW;	3A961E21612682C4	CRC64;
	Query Match	69.6%;	Score 1835;	DB 1;	Length 518;
	Best Local Similarity	66.6%;	Pred. No. 2e-122;		
	Matches 323;	Conservative 63;	Mismatches 91;	Indels 8;	Gaps 3;
QY	2	NGTLMQYFEWYTNDDGQHWKRLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	61		
Db	39	NGTLMQYFEWYTNDDGQHWKRLQNDABHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	98		
QY	62	LCEFOQKGTVRTKYTKSELQDAIGLSHNSVVOYGDVVLNKHAGADATEDVAVENP	121		
Db	99	LCEFOQKGTVRTKYTKSELQDAIGLSHNSVVOYGDVVLNKHAGADATEDVAVENP	158		
QY	122	NRNQTSEYQIKAWTDTRFPGRGNTYSDFKWHYHFDGADWDESKRI-SRIFKFRGEK	180		
Db	159	NRNQTSEYQIKAWTDTRFPGRGNTYSDFKWHYHFDGADWDESKRI-SRIFKFRGEK	218		
QY	181	AWDWEVSSENGYDILMYADVVDYDHPDVVAETKKGWIYANELSLDGRIDAAGHKFSF	240		
Db	219	AWDWEVSSENGYDILMYADVVDYDHPDVVAETKKGWIYANELSLDGRIDAAGHKFSF	278		
QY	241	LRDWVQAVROATGKEMFTVAEYMNAGKLENYLNKTSFNQSDVDPVPLHFNLOAASQGG	300		
Db	279	LRDWVQAVROATGKEMFTVAEYMNAGKLENYLNKTSFNQSDVDPVPLHFNLOAASQGG	338		
QY	301	GYDMRLLDGTVVRSHPEKAVTFVENHDTQPGSLESTVQTFKPLAYAFILTRSGYPQ	360		
Db	339	GYDMRLLDGTVVRSHPEKAVTFVENHDTQPGSLESTVQTFKPLAYAFILTRSGYPQ	398		
QY	361	VFYGDMYGTGTSPEKIPSLKDNIEPIKARKEYAYGPOHDIYDHPDVIGTWREGDSS	418		
Db	399	VFYGDMYGTGTSPEKIPSLKDNIEPIKARKEYAYGPOHDIYDHPDVIGTWREGDSS	453		
QY	419	AAKSLAALITDGPCKRMYAGLNAGETWYDITGNRSDTVKIGDSCGWGEFHVNDGVSIV	478		
Db	454	HPNSGLATIMSDGAGGSKMVFVGRNKGAGQVWSDITGNRTGTITINADGWNFSVNGSVS	513		
QY	479	IYVOK 483			

Db 514 IWVKN 518

RESULT 4

AMY_BACST STANDARD; PRT; 549 AA.

AC P06279; Q45519;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan

DE glucanohydrolase).

GN AMYS.

OS Bacillus stearothermophilus.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.

OX NCBI_TaxID=1422;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 35-39.

RX MEDLINE=85234394; PubMed=3924897;

RA Nakajima R., Imanaka T., Aiba S.;

RT "Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase

RT gene.";

RL J. Bacteriol. 163:401-406(1985).

RN [2]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX STRAIN=DY5/PHI300;

RC MEDLINE=86008166; PubMed=3876333;

RA Ihara H., Saaki T., Teuboi A., Yamagata H., Teukagoshi N., Uda S.;

RT "Complete nucleotide sequence of a thermophilic alpha-amylase gene:

RT homology between prokaryotic and eukaryotic alpha-amylases at the

RT active sites.";

RL J. Biochem. 98:95-103(1985).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=NZ-3.

RX MEDLINE=86195857; PubMed=3009417;

RA Gray G.L., Mainzer S.E., Rey M.W., Lamea M.H., Kindle K.L.,

RT Carmona C., Reguadt C.;

RT "Structural genes encoding the thermophilic alpha-amylases of

RT Bacillus stearothermophilus and Bacillus licheniformis.";

RL J. Bacteriol. 166:635-643(1986).

RN [4]

RP SEQUENCE FROM N.A.

RA Suominen I., Karp M., Lautamo J., Knowles J., Mantsaelae P.;

RT "Thermostable alpha amylase of Bacillus stearothermophilus: cloning,

RT expression, and secretion by Escherichia coli.";

RL (In) Chaloupka J., Krumphanz V. (eds.);

RL Extracellular enzymes of microorganisms, pp.129-137, Plenum Press,

RL New York (1987).

RN [5]

RP SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48.

RC STRAIN=DY-5;

RX MEDLINE=86059211; PubMed=2999073;

RA Teukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H.,

RA Idota Y., Yamagata H., Uda S.;

RT "Efficient synthesis and secretion of a thermophilic alpha-amylase by

RT protein-producing Bacillus brevis 47 carrying the Bacillus

RT stearothermophilus amylase gene.";

RL J. Bacteriol. 164:1182-1187(1985).

RN [6]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

RX MEDLINE=21125602; PubMed=11226887;

RA Svud D., Fujimoto Z., Takase K., Matsumura M., Mizuno H.;

RT "Crystal structure of Bacillus stearothermophilus alpha-amylase:

RT possible factors determining the thermostability.";

RL J. Biochem. 129:461-468(2001).

CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic

CC linkages in oligosaccharides and polysaccharides.

CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.

CC -1- SUBUNIT: Monomer.

CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.

CC -----

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EMBL; M11450; AAA22235.2; -

EMBL; X02769; CAA26547.1; -

EMBL; M57457; AAA22227.1; -

EMBL; M13255; AAA22241.1; -

PIR; A24436; A24436.

PIR; A91999; ALBSF.

PDB; 1HVX; 05-AUG-03.

InterPro; IPR006589; Alp_aml cat sub.

InterPro; IPR006047; Alpha_aml cat.

InterPro; IPR006046; Glyco_hydro_13.

Pfam; PF00128; alpha-amylase; 1.

PRINTS; SM00110; ALPHAAMYLASE.

SMART; SM00642; Amy; 1.

KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;

KW Signal; 3D-structure.

FT SIGNAL 1 34

FT CHAIN 35 549

FT ACT SITE 268 268

FT ACT SITE 272 272

FT ACT SITE 365 365

FT METAL 139 139

FT METAL 196 196

FT METAL 218 218

FT METAL 220 220

FT METAL 231 231

FT METAL 237 237

FT METAL 238 238

FT METAL 239 239

FT METAL 272 272

FT METAL 337 337

FT METAL 339 339

FT METAL 440 440

FT METAL 441 441

FT METAL 464 464

FT CONFLICT 13 13

FT CONFLICT 19 19

FT CONFLICT 23 23

FT CONFLICT 31 31

FT CONFLICT 107 107

FT CONFLICT 167 167

FT CONFLICT 179 179

FT CONFLICT 251 251

FT CONFLICT 260 260

FT CONFLICT 284 284

FT CONFLICT 312 312

FT CONFLICT 338 338

FT CONFLICT 342 342

FT CONFLICT 346 346

FT CONFLICT 376 376

FT CONFLICT 526 526

FT CONFLICT 527 527

FT CONFLICT 535 535

SEQUENCE 549 AA; 62670 MW; 3A2DD93A955E79D3 CRC64;

Query Match 66.8%; Score 1763.5; DB 1; Length 549;

Best Local Similarity 65.2%; Pred. No. 2.5e-117;

Matches 315; Conservative 58; Mismatches 105; Indels 5; Gaps 2;

Oy 2 NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGTAVWIPPAYKGLSCSNGYGFYDLYD 61

Db 39 NGTMMQYFEWYLPDDGTLTKVANEANNSLSGITALWLPPAYKGTSDYGVGYDLYD 98

Oy 62 LGFEQOQGTVTRTKYGTSEKSLQDAIGSLHSRNVQYGVNLNHNKAGADATEDVTAVERNPA 121

Db 99 LGFEQKQGVTRTKYGTQYLAQIAAFAAGMAYVADVDFHKGAGDGTWDAVERNPS 158

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QY 122 NRNOETSEYQIKAWTDPRFPGRGNTYSDFKWHWHYHFDGADWDESRKISRIFKPRGKA 181
Db 159 DRNQEISGTYQIQAWTKDFPGRGNTYSSFKRWYHFDGVDWDESRKSRIFKPRGIGA 218
QY 182 WDWVESSENGNDYLMYADVDYHDPDVAETKKGWIWYANELSLDGFRIIDAKHFKPSFL 241
Db 219 WDWVEDTNGNDYLMYADLDMDHPEVVTLSKWKYVNTNIDGFRDLDAVHKHKPSFF 278
QY 242 RDWQAVROATKEMFTVAEYQNNAGKLENLNTKTSFNQSVDFVPLHFNLOAASSQGG 301
Db 279 PDLSDSVRSQTKPLFTVGXYWSYDINKLHNYIMKTNGTMSLFDAPLHNFYTASKSGGT 338
QY 302 YDMRLLDGTGTVSRPEKAVTEVNHDTOPGOSLESTVQTFKPLAYAFILTRSGYPOV 361
Db 339 FDMRTLMTNTLMKDQPTLATVFDVNDHTEFGALQSWDPMPKPLAYAFILTRQEGYPCV 398
QY 362 FYGDMYGTGTSKP-EIPSLKDNIBPILKARKEYAYGPHDYIDHPDVIGWTRGDSAA 420
Db 399 FYGDIYGI---PQYNIPSLKSDIPLLIARDYAYGQHDYLDHSDIIGWTRGVTKEP 454
QY 421 KSLGAAALITDGGGSKRWYAGLKNAGETWYDITGNRSYTVKIGSDGWFPHVNDGVSIIY 480
Db 455 SGSLAALITDGGGSKRWYAGKQAGKVFYDLTGNRSDTVTINSDGWGEFKVNGSVSW 514
QY 481 VQK 483
Db 515 VPR 517

RESULT 5
AMY2_SALTY
ID AMY2_SALTY STANDARD; PRT; 494 AA.
AC P26613;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYA OR STM1963.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=SJW1103;
RC MEDLINE=93015717; PubMed=1400215;
PX Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RA "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA.";
RL J. Bacteriol. 174:6644-6652(1992).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=LT2 / SGSC1412 / ATCC 700720;
RC MEDLINE=21534948; PubMed=11677609;
PX McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
[3]
RN SEQUENCE OF 1-6 FROM N.A.
RP STRAIN=SJW1103;
RC MEDLINE=92407478; PubMed=1527488;
PX Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RA "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes.";
RL J. Gen. Microbiol. 138:1051-1065(1992).
[4]
RN SEQUENCE OF 476-494 FROM N.A.
RP
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RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIa and IIb, including a
RT large non-coding region.";
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC or send an email to license@isb-sib.ch)
CC
CC EMBL; L01643; AAA27110.1; -.
CC EMBL; AE008787; AAL20875.1; -.
CC EMBL; M85241; AAA27079.1; -.
CC EMBL; L13280; AAA1970.1; -.
CC PIR; B45738; B45738.
CC HSP; P06278; B45738.
CC StyGene; SG10011; amyA.
CC InterPro; IPR006589; Alp_amy1_cat_sub.
CC InterPro; IPR006047; Alp_amy1_cat.
CC Pfam; PF00128; alpha-amylase; 1.
CC SMART; SM00642; Amy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Complete proteome.
FT ACT_SITE 235 BY SIMILARITY.
FT ACT_SITE 265 265 BY SIMILARITY.
FT ACT_SITE 332 332 BY SIMILARITY.
FT METAL 104 104 CALCIUM (BY SIMILARITY).
FT METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT CONFLICT 462 462 L -> S (IN REF. 1).
SQ SEQUENCE 494 AA; 56522 MW; 5C1E862FEDD5E47C CRC64;

Query Match 38.6%; Score 1017; DB 1; Length 494;
Best Local Similarity 41.3%; Pred. NO. 1.3e-64;
Matches 203; Conservative 76; Mismatches 198; Indels 14; Gaps 5;

QY 2 NCTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKLSQSDN-GYCPYDLY 60
Db 3 NPTLQYFHWYTPDGGKLUWSELAERADGINDIGINMWLWLPACKGASGGYGVGYDYDLP 62
QY 61 DLGEFQKGTVRTKYTKSELQDAIGSLHSRNVQYGDVVLNHRKAGADATEDVTAVEVNP 120
Db 63 DLGEFDQGTIATKYGDKRQLLTALDKKNIAVLDDVVVHKGADAKERIRVQRVQ 122
QY 121 ANRNOETSEYQIKAWTDPRFPGRGNTYSDFKWHWHYHFDGADWDESRKISRIFKPRGE-- 178
Db 123 DDRTOIDNIIIECEGTYTTPPARAGQYSNFIMDYHCFSGIDHIENPDEDGIGFIVNDYT 182
QY 179 GKAMDWEYSSENGNDYLMYADVDYHDPDVAETKKGWIWYANELSLDGFRIIDAKHFK 238
Db 183 GDGWNQVDDEMGDFVLMGENIDFRNHAHVEEIKYARWVWMEQTHCDGFRDLDAVHKHPA 242
QY 239 SFLRDWVQAVQATGKEMFTVAEYQNNAGKLENLNTKTSFNQSVDFVPLHFNLOAASSQ 298
Db 243 WYKXEWIEHVQAVAPKPLFVAEYWSHEVDKQTYIDQVDGKTMFLDAPLQMKPFHASRQ 302
QY 299 GGGYDMERLLDGTGTVSRPEKAVTEVNHDTOPGOSLESTVQTFKPLAYAFILTRSGY 358
Db 303 GAEDMRHIFTGTLVEADPPFAVTLVANHTDQPLQALEAPVPEWPKFLAYAILLRENGV 362
QY 359 PQVFGDMYGTGK-----GTSPEKIPSLKDNIEPILKARKEYAYGQHDYIDHPDVIG 410
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FT METAL 143 143 CALCIUM 2 (BY SIMILARITY).
FT METAL 153 153 CALCIUM 3 (BY SIMILARITY).
FT METAL 164 164 CALCIUM 3 (BY SIMILARITY).
FT METAL 167 167 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 168 168 CALCIUM 1 (BY SIMILARITY).
FT METAL 169 169 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 172 172 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 174 174 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 437 AA; 48637 MW; BD304250B40C7A8B CRC64;

Query Match 12.3%; Score 324; DB 1; Length 437;
Best Local Similarity 24.9%; Pred. No. 1.1e-15;
Matches 108; Conservative 56; Mismatches 140; Indels 130; Gaps 15;

QY 5 LMOYFEWTPNDQHWKR-LQNDAEHLSDIGTAWIPPAVKGLSQSDNGGPGYDLVDLG 63
Db 29 LFOGFNWSWKQGWYNFLSHVDYIAATGVTWVLP--PSHSVAPQGMPCRLDLD 86
QY 64 EFQQGTGVTRTYKTKSELQDAIGSLHSRNVGVYDVVNLNKHAGADATEDVTAVEVNPANR 123
Db 87 -----ASKVGTGAELSLIAAFHSKSIKCVADIINHRC----- 120
QY 124 NQETSEEQIKAWTDPRFPGRGNTVSDPKWHYHFDGADWDESKISRIKFRGEGKAWD 183
Db 121 -----ADYKDSRGYICFEFGGTPDSRLD 143
QY 184 W---EVSENGNY-----DYLMYADVDYDHPDVVAETKKGIGWVANELSLDGR 229
Db 144 WGPDMICDDTYQXNGRHRGTGADFGAPDIDHLNTRVQTSLDNLNWLKSLVDFGWR 203
QY 230 IDAAKHIFSLRDMVQAVRQATKEMFTVAEYQN-----NAGKLENYL 274
Db 204 LDFAKGYSATVAKTYVDNTDPS-----FVVAEISWNWRYDNGEPPSNQDQDRQLVNW 258
QY 275 NKTSPNSQVDFVPLHNLQAASSGGVDMRRLDGT-----VVSHPKAVTFVFNHDT 329
Db 259 QAVGGPASFDFTTKGELOA-VQG---ELWRMKDNGKAPGMIGWLPKAVTFIDNHDT 314
QY 330 QPGQSLESTVOTWFKP-----LAVAFILTRSGVQVFGYDMYGTGKTSKPEIPLSKDNI 384
Db 315 -----GSTQNSWFFPQSDKVMQRYAYILT-HPGVPCIFYDHFVDM-----NLKQEI 358
QY 385 EPILKARKEYAYGP 398
Db 359 STLAAVRSRNGIHP 372

RESULT 10
ID AMYB PAEPO STANDARD; PRT; 1196 AA.
AC P21543;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Beta/alpha-amylase precursor [includes: Beta-amylase (EC 3.2.1.2);
Alpha-amylase (EC 3.2.1.1)].
OS Paenibacillus polymyxa (Bacillus polymyxa).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=1406;
RN [1]
RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=87165765; PubMed=2435707;
RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,
RT Teukagoshi N., Uda S.;
RT "Cloning and nucleotide sequence of the gene coding for enzymatically
active fragments of the Bacillus polymyxa beta-amylase.";
RL J. Bacteriol. 169:1564-1570(1987).
RN [2]
RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.

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RC STRAIN=72;
RX MEDLINE=89123046; PubMed=2464578;
RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
RT Teukagoshi N., Uda S.;
RT "A single gene directs synthesis of a precursor protein with beta-
and alpha-amylase activities in Bacillus polymyxa.";
RL J. Bacteriol. 171:375-382(1989).
RN [3]
RP SEQUENCE OF 1-776 FROM N.A.
RC STRAIN=ATCC 8523;
RX MEDLINE=87231094; PubMed=2438660;
RA Rhodes C., Strasser J., Friedberg F.;
RT "Sequence of an active fragment of B. polymyxa beta amylase.";
RL Nucleic Acids Res. 15:3934-3934(1987).
RN [4]
RP DISULFIDE BOND AND MUTAGENESIS OF CYSTEINE RESIDUES.
RX MEDLINE=91215008; PubMed=1827035;
RA Uozumi N., Matsuoka T., Teukagoshi N., Uda S.;
RT "Structural and functional roles of cysteine residues of Bacillus
polymyxa beta-amylase.";
RL Biochemistry 30:4594-4599(1991).
CC -I- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
PRODUCE MULTIFORM BETA-AMYLASES AND A 48 Kda ALPHA-AMYLASE AFTER
SECRETION.
CC -I- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
polysaccharides so as to remove successive maltose units from the
non-reducing ends of the chains.
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: In the N-terminal section; belongs to family 14 of
glycosyl hydrolases.
CC -I- SIMILARITY: In the C-terminal section; belongs to family 13 of
glycosyl hydrolases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M15817; AAA85446.1; -.
DR EMBL; Y00150; CAA68344.1; -.
DR PIR; A29130; A29130.
DR HSP; P36924; 1B9Z.
DR InterPro; IPR006589; Alp_amyl_cat.sub.
DR InterPro; IPR006048; Alpha_amyl_C.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR005085; CBM 25.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR001554; Glyco_hydro_14.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF03423; CBM 25; 2.
DR Pfam; PF01373; Glyco_hydro_14; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR PRINTS; PR00750; BETAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy_C; 1.
DR PROSITE; PS00506; BETA_AMYLASE 1; 1.
DR PROSITE; PS00679; BETA_AMYLASE 2; 1.
KW Multifunctional enzyme; Hydrolase; Glycosidase; Signal;
KW Polysaccharide degradation; Repeat.
FT SIGNAL 1 35
FT CHAIN 36 1196 BETA/ALPHA-AMYLASE.
FT DOMAIN 36 454 BETA-AMYLASE.
FT REPEAT 455 558
FT REPEAT 565 668
FT DOMAIN 669 1196 ALPHA-AMYLASE.
FT DISULFID 118 126
FT ACT_SITE 198 198 BY SIMILARITY.

```


Best Local Similarity 24.5%; Pred. No. 2.6e-15;
Matches 108; Conservative 54; Mismatches 136; Indels 142; Gaps 16;

QY 5 LMOYFEWTPNDGQHWK-----LQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPY 57
Db 29 LFQGFNW-----ESWKKQGGWYNFLGHVDDIAATGTHVWLP--PSHVAPOGYMPG 80
QY 58 DLYDLGEFOQKGTVRTKYTKSELQDAIGSLHSRNVQVGVVNLNKKAGADATEDVTA 117
Db 81 RLYDL-----ASKYGTGAELSLIAAFHSGIKCVADIVNHC-----120
QY 118 VNPANRNETSEYQIKAWTDFFRPGRGNTYSDFKWHYHFDGADWDSRKSIRIFKRG 177
Db 121 -----ADYKDSRGICYFEGGT 137
QY 178 EKGAWD-----EVSSENGNY-----DYLMAVDYDHPDVVAETKKGWLYANEL 223
Db 138 PDSRLDWPDMICSDDTQSYNGRHRDTGADFGAPDIDLHTRVQVTELSDLNWLKSDV 197
QY 224 SLDFRIDAAKHKFSFLRDWVQAVRQATGKEMFTVAEYQW-----NAG 268
Db 198 GFDGWRDLFAKYSAAVAKTYDNTDPS-----FVVAEISNMYDGNBPSWQDGRQ 252
QY 269 KLENYLNKTSFNQSVDFPLHFNLOAASSQGGYDMRELLDGT-----VVSRRHPEKAVTF 323
Db 253 ELVWQAQVGPASAFDFTTKGELQA-VQG-----ELWMMKDGNGKAPGMIGWLPEKAVTF 308
QY 324 VENHDTQPGQSLSTVQWTFKP-----LAYAFILTRSGYQVQVGYDMYKGTGTSPEIP 378
Db 309 IDNHDT-----GSTQNSWPPSPDKVMQGYAYILT-HPGVPCIFYDHFVDM-----352
QY 379 SIKONIEPILKARKEYAYGP 398
Db 353 LKQEIETLAARSRNEIHP 372

RESULT 12
AM3D_ORYSA
ID AM3D_ORYSA STANDARD; PRT; 435 AA.
AC DT27933;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase).
GN AMY1.3 OR AMY3D.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriactoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etioolated leaf;
RC MEDLINE=91088278; PubMed=2263460;
RA Huang N., Koizumi N., Reini S., Rodriguez R.L.;
RT "Structural organization and differential expression of rice alpha-
amylase genes";
RL Nucleic Acids Res. 18:7007-7014 (1990).
RN [2]
RP SEQUENCE FROM N.A. (CLONE POS137).
RX MEDLINE=90318322; PubMed=2370848;
RA O'Neill S.D., Kumagai M.H., Majumdar A., Huang N., Sutliff T.D.,
RA Rodriguez R.L.;
RT "The alpha-amylase genes in Oryza sativa: characterization of cDNA
clones and mRNA expression during seed germination";
RL Mol. Gen. Genet. 221:235-244 (1990).
CC -1- FUNCTION: Important for breakdown of endosperm starch during
germination.
CC -1- CATABOLIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -1- SUBUNIT: Monomer.

CC -1- TISSUE SPECIFICITY: Is expressed in all tissues, except in
immature seeds. Is the most abundant alpha-amylase isozyme in
callus.
CC -1- DEVELOPMENTAL STAGE: Expressed at a high level during germination
in the aleurones cells under the control of the plant hormone
gibberellic acid and in the developing grains at a low level.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M59351; AAA33895.1; -;
CC EMBL; M24287; AAA33886.1; -;
CC PIR; S12625; S12625.
CC HSP; P04063; IAVA.
CC Gramene; P27933; -;
CC InterPro; IPR006589; Alp_aml_cat_sub.
CC InterPro; IPR006047; Alpha_aml_cat.
CC InterPro; IPR006046; Glyco_hydro_13.
CC Pfam; PF00128; alpha-amylase; 1.
CC PRINTS; PR00110; ALPHAAMYLASE.
CC SMART; SM00642; Amyy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 25
FT CHAIN 26 435
FT ACT_SITE 203 203
FT ACT_SITE 311 311
FT METAL 116 116
FT METAL 133 133
FT METAL 136 136
FT METAL 138 138
FT METAL 141 141
FT METAL 151 151
FT METAL 162 162
FT METAL 167 167
FT METAL 170 170
FT METAL 172 172
FT CONFLICT 73 74
FT CONFLICT 137 137
FT SEQUENCE 435 AA; 47911 MW; 1BBD6AB195BA0D6E CRC64;
Query Match 12.1%; Score 318; DB 1; Length 435;
Best Local Similarity 28.0%; Pred. No. 3e-15;
Matches 111; Conservative 42; Mismatches 134; Indels 110; Gaps 17;
QY 5 LMOYFEWTPNDGQHWK-----LQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPY 57
Db 28 LFQGFNW-----ESWKKQGGWYNFLKHQVDDIAKAGVTHVWLP--PSHVAPOGYMPG 79
QY 58 DLYDLGEFOQKGTVRTKYTKSELQDAIGSLHSRNVQVGVVNLNKKAG--ADATEDVTA 115
Db 80 RLYDL-----ASKYGTGAELSLIAAFHSGVQCVADVNVNHRCAEKDARGVYCV 131
QY 116 VNPANRNETSEYQIKAWTDFFRPGRGNTYSDFKWHYHFDGADWDSRKSIRIFKPF 175
Db 132 FEGGTFPDL-----WPGMICSDDTQYSDGTCH-----RD 162
QY 176 RGEKAWDWEVSSSENGYDLYMADVDYDHPDVVAETKKGWLYANELSDGPFIDAAKH 235
Db 163 TGEQ-----FGAEPDIDLHNPVRQELTDLNWLKSDVDFGFWLDFAKG 207
QY 236 IKFSLRDWQAVQATGKEMFTVAEYQW-----NNAG-----LENYLNKTSFN 280
Db 208 YSTDIAMKYVESC-----KPGFVVAEIVNSLSYNGDGKPAANQDQGRQELVNVNVAVGPP 262


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FT ACT_SITE 204 204 BY SIMILARITY.
FT ACT_SITE 229 229 BY SIMILARITY.
FT ACT_SITE 315 315 BY SIMILARITY.
FT METAL 116 116 CALCIUM 1 (BY SIMILARITY).
FT METAL 133 133 CALCIUM 2 (BY SIMILARITY).
FT METAL 136 136 CALCIUM 2 (BY SIMILARITY).
FT METAL 138 138 CALCIUM 2 (BY SIMILARITY).
FT METAL 142 142 CALCIUM 2 (BY SIMILARITY).
FT METAL 152 152 CALCIUM 3 (BY SIMILARITY).
FT METAL 163 163 CALCIUM 3 (BY SIMILARITY).
FT METAL 166 166 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 167 167 CALCIUM 1 (BY SIMILARITY).
FT METAL 168 168 CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 171 171 CALCIUM 3 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
FT METAL 173 173 CALCIUM 1 AND 3 (BY SIMILARITY).
SQ SEQUENCE 438 AA; 47796 MW; 2393FDAC51E80F51 CRC64;

Query Match 11.7%; Score 307.5; DB 1; Length 438;
Best Local Similarity 25.2%; Pred. No. 1.7e-14;
Matches 110; Conservative 51; Mismatches 131; Indels 145; Gaps 18;

Qy 5 LMQYFEWYTPNDGQHWK-----LQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPY 57
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
28 LFQGFNN-----ESWQSGGWYNNMMGKVDDIAAAGVTHWLP--PSHSVSNEGYMPG 79
Qy 58 DLVDLGBFQKGTVRTKYKYSLEQDAIGSLHSRNQVYGVVNLNKKAGADATEDVTAVE 117
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
80 RLVDID-----ASKYGAELKSLIGALHGKGVQAIADIVINHRC----- 119
Qy 118 VNPANRNQETSEYQIKAWTDFRPPGRGNTYDFKWHYHFDGADWDESRKISRIFKFRG 177
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
120 -----ADYKDSRCIYCFEGGT 136
Qy 178 EGRKADW-----EVSENGY-----DYLMYADVVDHPDVAETKKGWIWYANEL 223
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
137 SDGRLDWGPIMICRDDTKYSDGTANLDTGADFAAAPDIDLNDRVQRELKEWLLWLKSDL 196
Qy 224 SLGDFRIDAAKHKFSFLRDWVQVROATGKEMFTVAEYQNNNA-----GK----- 269
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
197 GFDAWRLDFARGSPENAKVYIDGTSPS-----LAVAEVMDNMATGGDKPNYDQDAHRQ 251
Qy 270 -LENYLNKTSFNOS---VFDVPLHFNLOAASSQGGYDMRRLDGT-----VVSRRHPEKA 320
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
252 NLVNWVDKVGGAASAGWVDFETTKGILNAA-VEG---ELWRLIDPGKAPGVGWGWPAKA 307
Qy 321 VTFVENHDTQPGQSLSTVQTFWFKP-----LAYAFILTRSGYQVYFQVDMYGTGTSFK 375
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
308 ATFVDNHD-----GSTQAMWPPFSKVMQGYAVILT-HPGIPCFYDFHFFNW----- 354
Qy 376 EIPSLKDNIEPIKARK 392
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
355 ---GFKDQIAALVAIRK 368
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Search completed: October 7, 2004, 00:13:23
Job time : 9.47121 secs

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QY 62 LGFEQKGTGRTKTKSELQDAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 121
Db 98 LGFEQKGTGRTKTKSELQDAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 157
QY 122 NRNQETSEYQIKAWTDFFRPPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGKA 181
Db 158 NRNQETSEYQIKAWTDFFRPPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGKA 217
QY 182 WDWVSSSENGNYDYLWYADVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFKSF 241
Db 218 WDWVSSSENGNYDYLWYADVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFKSF 277
QY 242 RDMQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFQSVDFVPLHFNLOAASSOGGG 301
Db 278 RDMQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFQSVDFVPLHFNLOAASSOGGG 337
QY 302 YDMRRLDGTGTVSRHPEKAVTFVFNHDTQPGQSLSTVQTFWPKPLAYAFILTRSSGYPQV 361
Db 338 YDMRRLDGTGTVSRHPEKAVTFVFNHDTQPGQSLSTVQTFWPKPLAYAFILTRSSGYPQV 397
QY 362 FYGDMYGTGTSKPEIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRGDSAAK 421
Db 398 FYGDMYGTGTSKPEIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRGDSAAK 457
QY 422 SGLAALITDGGGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGVSIVY 481
Db 458 SGLAALITDGGGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGVSIVY 517
QY 482 QK 483
Db 518 QQ 519

RESULT 2
Q91AS4 PRELIMINARY; PRT; 513 AA.
ID Q91AS4
AC Q91AS4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Glucan 1,4-alpha-maltohexaosidase (EC 3.2.1.98).
GN BC3482.
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP MEDLINE=22608415; PubMed=12721630;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,
RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haeckel R., Fongstein M., Ehrlich S.D.,
RA Overbeek R., Kyripides N.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis ";
RL Nature 423:87-91(2003).
DR EMBL; AE017009; AAP0417.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
DR KW Glycosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 513 AA; 58306 MW; 05C4611C4BFF9FF6 CRC64;

Query Match 74.2%; Score 1957; DB 16; Length 513;
Best Local Similarity 71.8%; Pred. No. 1.5e-126;
Matches 346; Conservative 48; Mismatches 88; Indels 0; Gaps 0;

QY 2 NGTLMQYFEWYAPNDGNHNRRLTQDAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 121
Db 52 NGTLMQYFEWYAPNDGNHNRRLTQDAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 151
QY 62 LGFEQKGTGRTKTKSELQDAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 121
Db 98 LGFEQKGTGRTKTKSELQDAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 157
QY 122 NRNQETSEYQIKAWTDFFRPPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGKA 181
Db 158 NRNQETSEYQIKAWTDFFRPPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGKA 217
QY 182 WDWVSSSENGNYDYLWYADVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFKSF 241
Db 218 WDWVSSSENGNYDYLWYADVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFKSF 277
QY 242 RDMQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFQSVDFVPLHFNLOAASSOGGG 301
Db 278 RDMQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFQSVDFVPLHFNLOAASSOGGG 337
QY 302 YDMRRLDGTGTVSRHPEKAVTFVFNHDTQPGQSLSTVQTFWPKPLAYAFILTRSSGYPQV 361
Db 338 YDMRRLDGTGTVSRHPEKAVTFVFNHDTQPGQSLSTVQTFWPKPLAYAFILTRSSGYPQV 397
QY 362 FYGDMYGTGTSKPEIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRGDSAAK 421
Db 398 FYGDMYGTGTSKPEIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRGDSAAK 457
QY 422 SGLAALITDGGGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGVSIVY 481
Db 458 SGLAALITDGGGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGVSIVY 517
QY 482 QK 483
Db 518 QQ 519

RESULT 3
Q9AQ54 PRELIMINARY; PRT; 533 AA.
ID Q9AQ54
AC Q9AQ54;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Alpha-amylase.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W.,
RA Park K.-H.;
RT "Cloning of maltopentaose-producing amylase from Bacillus megaterium
RT KSM B-404 ";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220440; AAK00598.1; -.
DR HSSP; P06278; 1VJS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
DR KW Glycosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;

Query Match 74.2%; Score 1957; DB 2; Length 533;
Best Local Similarity 72.0%; Pred. No. 1.6e-156;
Matches 347; Conservative 45; Mismatches 90; Indels 0; Gaps 0;

QY 2 NGTLMQYFEWYAPNDGNHNRRLTQDAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 121
Db 52 NGTLMQYFEWYAPNDGNHNRRLTQDAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 151
QY 62 LGFEQKGTGRTKTKSELQDAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 121
Db 98 LGFEQKGTGRTKTKSELQDAIGSLHSRNVQVYGDVVLNKHAGADATEDVTAVENPA 157
QY 122 NRNQETSEYQIKAWTDFFRPPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGKA 181
Db 158 NRNQETSEYQIKAWTDFFRPPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGKA 217
QY 182 WDWVSSSENGNYDYLWYADVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFKSF 241
Db 218 WDWVSSSENGNYDYLWYADVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFKSF 277
QY 242 RDMQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFQSVDFVPLHFNLOAASSOGGG 301
Db 278 RDMQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFQSVDFVPLHFNLOAASSOGGG 337
QY 302 YDMRRLDGTGTVSRHPEKAVTFVFNHDTQPGQSLSTVQTFWPKPLAYAFILTRSSGYPQV 361
Db 338 YDMRRLDGTGTVSRHPEKAVTFVFNHDTQPGQSLSTVQTFWPKPLAYAFILTRSSGYPQV 397
QY 362 FYGDMYGTGTSKPEIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRGDSAAK 421
Db 398 FYGDMYGTGTSKPEIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRGDSAAK 457
QY 422 SGLAALITDGGGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGVSIVY 481
Db 458 SGLAALITDGGGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWEFHVNDGVSIVY 517
QY 482 QK 483
Db 518 QQ 519

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Db 112 LGFENQKGTVRTKYGKQAQLKSAIDALHKKNIIDVGDVNNHKGADYTTTVAVEVDPS 171
QY 122 NRNQETSEBYQIKAWTDFFPPGRGNTYSDFKWHWYHFDGADWDSRKRISIFKFRGEGKA 181
Db 172 NRNVESGDVEISAWTGFNPFGRGDSYSNFKWKWYHFDGTDWDEGRKLNRIYKFRGIGKA 231
QY 182 WDEVSSENGNYDLYMAYDVYDHPDVVAETKKWGIWYANELSLDGRIDAAKHIFSL 241
Db 232 WDEVSSENGNYDLYMAYDLDFDHPDVANEMKNGTWYANELNDGFRDLDAVKHIDHEYL 291
QY 242 RDWVQAVROATGKEMFTVAEYQWNNACKLENLYNKTSPNQSVDVPLHFNLAQASSQGG 301
Db 292 RDWVNVROQTGKEMFTVAEYQWNNACKLENLYNKTSPNQSVDVPLHFNLAQASSQGG 351
QY 302 YDMRRLDGTWVSRHPEKAVTFVENHDTQPGQSLSTVQWTFKPLAYAFILTRREGDPSV 361
Db 352 YDMRNLKGTWVANHPTLATVLTVENHDSQPGQSLSTVQWTFKPLAYAFILTRREGDPSV 411
QY 362 FYGDMYGTGKTSPEIKSPKONTEPILKARKEYAYGQHDYIDHPDVIGWTRREGDPSAAK 421
Db 412 FYGDMYGTGKTSPEIKSPKONTEPILKARKEYAYGQHDYIDHPDVIGWTRREGDPSV 471
QY 422 SGLAALITDGGGSKMYAGLKNAGETWYDITGNRSSTVTKIGSDGGEFFHNDGVSIVY 481
Db 472 SGLATLISDGGGSKMYAGLKNAGETWYDITGNRSSTVTKIGSDGGEFFHNDGVSIVY 531
QY 482 QK 483
Db 532 QR 533

RESULT 4
ID Q81YJ4 PRELIMINARY; PRT; 513 AA.
AC Q81YJ4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase.
GN AMYS OR BA3551.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;
RN [1]
RP MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasee N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Ostad O.A., Helgason E., Ristone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Niemman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86 (2003).
DR EMBL; AE017035; AAP27311.1; -.
DR TIGR; BA3551; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; Alp_amyl_cat.
DR SMART; SM00642; alpha-amylase; 1.
KW Complete proteome.
SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

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Query Match 72.9%; Score 1924; DB 16; Length 513;
 Best Local Similarity 70.7%; Pred. No. 2.8e-124;

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Matches 341; Conservative 48; Mismatches 93; Indels 0; Gaps 0;
QY 2 NGTLMQYFEWYTPNDQOHKWLQNDABHLSIDIGITAVIPPAYKGLSQSNGYGPVLYD 61
Db 32 NGTLMQYFEWYAPSDRNHNRLRTDAENLAQKIGTSWIPPAYKGTQNDVGYCAYDLYD 91
QY 62 LGFQOKGTVRTKYGKSELODAIGSLHSRNVOYGDVNLHKGADATETDTAVEVNP 121
Db 92 LGFBNQKGTVRTKYGKQAQLKSAIEALHKKNIIDVGDVNNHKGADYTTTVAVEVD 151
QY 122 NRNQETSEBYQIKAWTDFFPPGRGNTYSDFKWHWYHFDGADWDSRKRISIFKFRGEGKA 181
Db 152 NRNVESGDVEISAWTGFNPFGRGDSYSNFKWKWYHFDGTDWDEGRKLNRIYKFRGIGKA 211
QY 182 WDEVSSENGNYDLYMAYDVYDHPDVVAETKKWGIWYANELSLDGRIDAAKHIFSL 241
Db 212 WDEVSSENGNYDLYMAYDLDFDHPDVANEMKNGTWYANELNDGFRDLDAVKHIDHEYL 271
QY 242 RDWVQAVROATGKEMFTVAEYQWNNACKLENLYNKTSPNQSVDVPLHFNLAQASSQGG 301
Db 272 RDWVNVROQTGKEMFTVAEYQWNNACKLENLYNKTSPNQSVDVPLHFNLAQASSQGG 331
QY 302 YDMRRLDGTWVSRHPEKAVTFVENHDTQPGQSLSTVQWTFKPLAYAFILTRREGDPSV 361
Db 332 YDMRNLKGTWVANHPTLATVLTVENHDSQPGQSLSTVQWTFKPLAYAFILTRREGDPSV 391
QY 362 FYGDMYGTGKTSPEIKSPKONTEPILKARKEYAYGQHDYIDHPDVIGWTRREGDPSAAK 421
Db 392 FYGDMYGTGKTSPEIKSPKONTEPILKARKEYAYGQHDYIDHPDVIGWTRREGDPSV 451
QY 422 SGLAALITDGGGSKMYAGLKNAGETWYDITGNRSSTVTKIGSDGGEFFHNDGVSIVY 481
Db 452 SGLATLISDGGGSKMYAGLKNAGETWYDITGNRSSTVTKIGSDGGEFFHNDGVSIVY 511
QY 482 QK 483
Db 512 QQ 513

RESULT 5
ID Q82839 PRELIMINARY; PRT; 516 AA.
AC Q82839;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1409;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KSM-1378;
RX MEDLINE=98342096; PubMed=9675143;
RA Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T.,
RA Ozaki K., Ito S.;
RT "Improved thermostability of a Bacillus alpha-amylase by deletion of
RT an arginine-glycine residue is caused by enhanced calcium binding.";
RL Biochem. Biophys. Res. Commun. 248:372-377 (1998).
DR EMBL; AB008763; BAA32431.1; -.
DR HSPB; P06278; IVD5.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;

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Query Match 69.8%; Score 1842; DB 2; Length 516;
 Best Local Similarity 66.8%; Pred. No. 1.3e-118;

Best Local Similarity 65.1%; Pred. No. 1.1e-112;		Matches 315; Conservative 58; Mismatches 106; Indels 5; Gaps 2;	
Qy	1	VNGTLMQYFEWTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	60
Db	35	INETMWOYFEWLPNDGTLTWKVKNEANLSGLITALLWLPAYKGLSQSDNGYGPYDLY	94
Qy	61	DLGEFOQKGTVRTKTKYKTSKSELODAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVEVNP	120
Db	95	DLGEFNQKGTIRTKYTKTQYIQALQAAGQVYADVFNHKAAGADGTETFDVAVEVDP	154
Qy	121	ANRNETSEYQIKAWTDFRPPGRGNTYSDPKWHYHFDGADWDESRKISRIKFRGEGK	180
Db	155	SNRNETSGTQIQAWTDFRPPGRGNTYSSPKWRWYHFDGTDWDESRKLNRIYKFRSTGK	214
Qy	181	AWDWEVSENGNYDLYMADVDDHDPVVAETKKGWIYANELSLDGRIDDAKHKFSF	240
Db	215	AWDEVDTEGNYDLYMADLDMHPEVVTTELKNGTWYVNTTIDGRLDAVKHIKYSF	274
Qy	241	LRDWQVAVRQATKEMFTVAEYQNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASQGG	300
Db	275	FPDMLTVVRNQTGNLPAVGFWSDVNVKLNHYITKINGSLSLFDAPLHNNFYTASKSG	334
Qy	301	GYDMRELLDGTVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAYAFILTRREGYPQ	360
Db	335	YFDMRYLLNNTLMKDPQSLAVTLVDNHDTPQGSQSWPEWFKPLAYAFILTRQEGYPC	394
Qy	361	VFYGDYGTGKTSK-ETPSLKDNIEPILKARKEYAGPOHDYIDHPDVIQWTRREGDSSA	419
Db	395	VFYGDYGI----PKYNIPLGSKIDPLLIARRDYAIGTQRDYIDHQDIIGWTRREGIDTK	450
Qy	420	AKSGLAALITDGPQSGKMYAGLKNAGETWYDITGNRSRTVKIGSDGSGWGFHVDGVSVI	479
Db	451	PNSGLAALITDGPQSGKMYVYKKGHAGKVFYDLTGNESDVTINADGWGFEKNGGVSVI	510
Qy	480	YVQK 483	
Db	511	WVAK 514	
RESULT 10			
ID	Q93148	PRELIMINARY; PRT; 501 AA.	
AC	Q93148;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Amylase.		
GN	AMYK38.		
OS	Bacillus sp. KSM-K38.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=129736;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=KSM-K38;		
RA	Hayashi Y.;		
RT	"Isolation of a new Bacillus alpha-amylase.";		
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AB051102; BAB71820.1; -		
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	InterPro; IPR006047; Alpha_amyl_cat.		
DR	Pfam; PF00128; alpha-amylase; 1.		
SQ	SEQUENCE 501 AA; 57485 MW; 1240F46739A5CC11 CRC64;		
Query Match 61.4%; Score 1619.5; DB 2; Length 501;			
Best Local Similarity 59.6%; Pred. No. 2.6e-103;			
Matches 288; Conservative 68; Mismatches 122; Indels 5; Gaps 2;			
Qy	1	VNGTLMQYFEWTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	60
Db	24	LANGTMQYFEWHLNDGQHWRLHDDAALSDAGITAIWIPPAYKGSQADVGYGAYDLY	83
RESULT 11			
ID	Q87HG6	PRELIMINARY; PRT; 507 AA.	
AC	Q87HG6;		
DT	01-JUN-2003 (TrEMBLrel. 24, Created)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Alpha-amylase.		
GN	VPA0999.		
OS	Vibrio parahaemolyticus.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;		
OC	Vibrionaceae; Vibrio.		
OX	NCBI_TaxID=670;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=RIMD 2210633 / Serotype O3:K6;		
RX	MEDLINE=22508454; PubMed=12620739;		
RA	Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,		
RA	Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,		
RA	Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;		
RT	"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism		
RT	distinct from that of V. cholerae.";		
RL	Lancet 361:743-749(2003).		
DR	EMBL; AP005087; BAC62342.1; -		
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	InterPro; IPR006047; Alpha_amyl_cat.		
DR	Pfam; PF00128; alpha-amylase; 1.		
DR	Complete proteome.		
SQ	SEQUENCE 507 AA; 58428 MW; 91B549E2BE0700BD CRC64;		
Query Match 56.0%; Score 1478.5; DB 16; Length 507;			
Best Local Similarity 55.0%; Pred. No. 1.4e-93;			
Matches 268; Conservative 76; Mismatches 128; Indels 15; Gaps 6;			
Qy	2	NGTLMQYFEWTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	60
Db	26	NGTMQYFEWTPNDGALWTVQVESNAPALAEAGTALWLPAYKAGGSDVGVGVDYMY	85
Qy	61	DLGEFOQKGTVRTKTKYKTSKSELODAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVEVNP	120

Db 86 DLGEFDQKGTIRTKYGTAKQYISAINAAHNNI QIYGDVVFVHRRGGADGKSWVDTKRVDW 145
QY 121 ANRQETSEEEYQIKAWTDFFRPPGRGNTYSDFKWHWHYHFDGADWDSRKSIRIFKFRGEGKA 180
Db 146 DNRNIELGDKW-IEAWVEFNPPGRNDKYSNPHWTWYHFDGVDWDDAGKKAIFKFRGEGK 204
QY 181 ADWEVSSSENGNDYLMYADVDYDHPDVVAETKKGWGIWYANELSLDGFRIDAAKHIFSF 240
Db 205 ADWEVSSSENGNDYLMYADLDMDHPEVKQELKDWGEWYINMTGVGDFRMDAVGHIKYQY 264
QY 241 LRDWQAVROATGKEMFTVAEYQWONNAGKLENYLNKTSFNQSVFDPVPLHFNLOAASSQGG 300
Db 265 LQEWIDHLRWKTKGELFTVGEYWNVDVNLHNFITKTSGMSLSLDPALHWNFNASKSGG 324
QY 301 GYDMLRLDGTWVSRHPEKAVTFVENHDTQPGSLESTVQWTFKPLAYAFILTRSGYVQ 360
Db 325 NYDMRQIMNGTLMKDNPKVAVTLVENHDTQPLQALESTVDMWFKPLAYAFILTRSGYVQ 384
QY 361 VFYCDMYGTGK-----GTSPEKIPSLKDNIEPILKARKEYAYGQPHDYIDHPDVIGWTR 414
Db 385 VFYADYGAQYSDKYNINAKVP-----YIEELVTLKEVAYGQNSYLDHWDVIGWTR 440
QY 415 GDSAAKSGLAALITDGGSGKRMVAGLKNAGETWYDITGNRSPTVKIGSDGWEFHVND 474
Db 441 GDAEHFNS-NAVIMSDGFGGTGMVYTG--KPSTRYVDKLGIRTEVWTDANGMAEFVNG 497
QY 475 GSVSIYV 481
Db 498 GSVSVVW 504

RESULT 12

Q89YPI PRELIMINARY; PRT; 481 AA.
AC Q89YPI
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Alpha-amylase precursor.
GN B74690.
OS Bacteroides thetaiotaomicron.
OC Bacterioidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550850; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076 (2003).
DR EMBL; AE016946; AA079795.1; .
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5EE1A CRC64;

Query Match 51.9%; Score 1369; DB 16; Length 481;
Best Local Similarity 51.0%; Pred. No. 4.4e-86;
Matches 246; Conservative 83; Mismatches 149; Indels 4; Gaps 2;
QY 2 NGTLMQYFEWYTNPDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSNGYGYDLYD 61
Db 3 NGVMQYFEWHLNDGKLMQIKEDALHLHDIGITAVWIPPAYKADQEGYATYDLYD 62
QY 62 LGFEQKGTGRTYKTKSELQDAIGSLHSRNQVQYGDVNLNHHKAGADATEDVTAVERNPA 121

Db 63 LGFEQKGTGRTYKTKDELKMKMIDELHKYHIAVYLDVNLNHHKAGDGFTEKFMVVEVDPK 122
QY 122 NRQETSEEEYQIKAWTDFFRPPGRGNTYSDFKWHWHYHFDGADWDSRKSIRIFKFRGEGKA 181
Db 123 ERYKALGEPPEIQWGTGYSFHGRKXKHSDFKWHYHFSGTGDDAQKRSQVFOQEGKA 182
QY 182 WDWEVSSSENGNDYLMYADVDYDHPDVVAETKKGWGIWYANELSLDGFRIDAAKHIFSF 241
Db 183 WSEGVSDSENGNDYLLCNDIDLQHPVEVSELNRWKVSNELNLDGRLDAIKMKQDFV 242
QY 242 RDWQAVROATGKEMFTVAEYQWONNAGKLENYLNKTSFNQSVFDPVPLHFNLOAASSQGG 301
Db 243 AQFLDAVRSRGNDFYAVGEYWNGLDALDAYIEAVGHKVNLFDPVPLHYNMFQASQSGKD 302
QY 302 YDMLRLDGTWVSRHPEKAVTFVENHDTQPGSLESTVQWTFKPLAYAFILTRSGYVQ 361
Db 303 YDRLDILKOTLVEHHPDLAVTI VDNHDTQSGSSLESNVEDWFKPLAYGLILLMKEGYPC 362
QY 362 FYGDMYGTGTSPEKIPSLKDNIEPILKARKEYAYGQPHDYIDHPDVIGWTRGDSAAK 421
Db 363 FYGDYGIKG--EKSPHTR-IIDILLDARRKAYAGQIEYFDHPSTIGTIRTCDEEHNG 418
QY 422 SGLAALITDGGSGKRMVAGLKNAGETWYDITGNRSPTVKIGSDGWEFHVNDGVSIVY 481
Db 419 SGLVFLMSNDEAGSKIMSLGKHKGEVWHBITGSISEITLDERGNGEFSVESRNLA 478
QY 482 QK 483
Db 479 KK 480

RESULT 13

Q03657 PRELIMINARY; PRT; 493 AA.
AC Q03657
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylase.
GN AMYE.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RA Marcel T.;
RL Nucleic Acids Res. 0:0-0(0).
DR EMBL; X60779; CAA43194.1; .
DR PIR; S15713; S15713.
DR HSP; P06278; IVS.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_I3.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 493 AA; 56537 MW; FECCD2F805BB4694 CRC64;

Query Match 47.5%; Score 1253; DB 2; Length 493;
Best Local Similarity 47.2%; Pred. No. 4.5e-76;
Matches 226; Conservative 74; Mismatches 177; Indels 2; Gaps 1;
QY 2 NGTLMQYFEWYTNPDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSNGYGYDLYD 61
Db 4 NHTMQYFEWHLNADGDHWRKLAEMAPELAKAGIDTWWPPVTVKVAEDTGYGYDLYD 63
QY 62 LGFEQKGTGRTYKTKSELQDAIGSLHSRNQVQYGDVNLNHHKAGADATEDVTAVERNPA 121
Db 64 LGFEQKGTGRTYKTKQELIEAIEACQKNGIAVYVDLVMNHHKAGADETEVFKVIEVDPN 123
QY 122 NRQETSEEEYQIKAWTDFFRPPGRGNTYSDFKWHWHYHFDGADWDSRKSIRIFKFRGEGKA 181

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Db 124 DRTKEISEPPEIGBWTFTFPGRGQDYSSFKWNSSEHFNFGDFDARBEERTGVFRIAGENKK 183
QY 182 WDMEVSSSENGNYDLYMADVDYDHPDVVAETKKWGIWYANELSUDGFRIDAAXHKIFSFL 241
Db 184 WNNVDDDFGNFYDLYMFANIDYDHPDVVRREMDWGWKLIDTLCGGFRDLAIKIHNEFI 243
QY 242 RDWQVAVQATGKEMFTVAEYQWQNNAGKLENYLNKTSFNQSVFDPVPLHFNLAQASSQGGG 301
Db 244 KEFAAEAMIRKRGQDFYIVGFWNSLNDACREFLDVDYQIDLDVDSLHYKLEASLGRD 303
QY 302 YDMRLLDGTVSRHPEKATVFVNHDTQPGQSLSTVQWTFPPLAYAFILITRESGYPQV 361
Db 304 FDLISKIFDDTLVQTHPTAVTFVDNHDSPHEALESIGWDFKPSAYALTLLRDGYPV 363
QY 362 FYGDMYGTGTSPEKIPSLKDNTEPILKARKEYAGPQHDYIDHPDVIGWTRGDSAAK 421
Db 364 FYGDIYGIGG--PEPDGKKEIILJLSARCNKAYGEQEDYFPHANTIGWRVGRVEIEG 421
QY 422 SGLAALITDGPFGSKRMVAGLNAGETWYDITGNRSDTVKIGSDGGEFHVNDGSVSIY 480
Db 422 SGCVAVISNGDDGKRMFGEHRAGEVWDLTKSCDDQITIEEDGWATFVCGGVSVM 480

RESULT 14
Q97Q49 ID Q97Q49 PRELIMINARY; PRT; 484 AA.
AC Q97Q49;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-amylase.
GN SPI382.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzaple E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Lofcus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae.";
RL Science 293:498-506(2001).
DR ENBL; AE007435; AAK75480.1; -.
DR FIK; G95160; G95160.
DR TIGR; SPI382; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 484 AA; 55918 MW; 4E90A450A90EFB8C CRC64;
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Query Match 46.1%; Score 1217; DB 16; Length 484;
Best Local Similarity 47.0%; Pred. No. 1.3e-75;
Matches 226; Conservative 81; Mismatches 168; Indels 6; Gaps 3;
QY 2 NGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIPPPAYKGLSQSDNGYGPVDLYD 61
Db 3 NQTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIPPPAYKGLSQSDNGYGPVDLYD 62
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QY 62 LGEEFOOKGTVRTKYGTKSLEQDAIGSLHSRNVQVYGVVVLNHHKAGADATEDVTAVENPA 121
Db 63 LGEEFNQKGTVRTKYGTGPKEDYLOAIQALKAAQGIQPMADVVVLNHHKAAADHREAFQVIEVDPV 122
QY 122 NRNQETSEYQIKAMTDFRPGRGWYSDPKWHWHYHFDGADWDESKISRIKFRCEGKA 181
Db 123 DRTVELGEBFTINGWTSFTFDGRQDTYNGFHHWHYHFTGTDYDAKRSKSGIYLIQDNGK 182
QY 182 MWWE--VSSSENGNYDLYMADVDYDHPDVVAETKKWGIWYANELSUDGFRIDAAXHKIFS 239
Db 183 WANEELVDNENGNLYMADLDKHEPVIQNIYDADWFMETTVAGFRDLDAVKHIDSF 242
QY 240 FLRDWQAVQATGKEMFTVAEYQWQNNAGKLENYLNKTSFNQSVFDPVPLHFNLAQASSQG 299
Db 243 FMRNFTRDMKEKYGDFFYVGFGEFNPDKKANLDYLEKTEHEHFDLVVRLHQLNFEASQAG 302
QY 300 GGYDMRLLDGTVSRHPEKATVFVNHDTQPGQSLSTVQWTFKPLAYAFILITRESGYP 359
Db 303 ANYDLRGIFTDSLVELLKPDKATVFDNHDTRQGALESTVEEFKPAAYALILLRQOGLP 362
QY 360 QVFGDMYGTGTSPEKIPSLKDNTEPILKARKEYAGPQHDYIDHPDVIGWTRGDSAA 419
Db 363 CVFYGDYIGISQYAG--DFKEILLDRLLAIRKOLAYGEQNDYFDHANCIGWYRSGAEN- 419
QY 420 AKSGLAALITDGPFGSKRMVAGLNAGETWYDITGNRSDTVKIGSDGGEFHVNDGSVSI 479
Db 420 -QSPIAVLISNDQENSKSMFVGQEWNTQTFVLLGNHQGVTTIDEEGYGQFPVSARSVS 478
QY 480 Y 480
Db 479 W 479

RESULT 15
Q8DT08 ID Q8DT08 PRELIMINARY; PRT; 486 AA.
AC Q8DT08;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Intracellular alpha-amylase (EC 3.2.1.1).
GN AMYA OR SMU.1590.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savić G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RT pathogen.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
DR EMBL; AB014990; AAN59233.1; -.
DR GO; GO:0004556; F:alpha-amylase activity; IEA.
DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Glycosidase; Hydrolase; Complete proteome.
SQ SEQUENCE 486 AA; 56457 MW; EF482B92FB37C4D8 CRC64;
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Query Match 46.0%; Score 1214.5; DB 16; Length 486;
Best Local Similarity 44.6%; Pred. No. 2e-75;
Matches 216; Conservative 88; Mismatches 175; Indels 5; Gaps 3;
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Db 3 NETMOMYFEWLPNDGKHQHLAEDASHLKNIGISKVMPAPFKGTGSDNDVGYGYDLYD 62
Qy 62 LGEPFOQKGTVRTKYGTSELSQDAIGSLHSRNQVYGVWLNHKGADATEDVTAVEVNP 121
Db 63 LGFENQGTVRTKYGSREDYLNALKEQEIPIISDIVLNHKGADAKERFQVVKVNP 122
Qy 122 NRQETSEYQIKAWTDPRFPGRGNTYSDFKWHYHFDGADWDSRKISRIFKPRGEGKA 181
Db 123 NRQEKISEPYEIEGTQFNFPGRQDNYSDFKWHYHFTGVYDALHNENGIYMLGDNKG 182
Qy 182 W--DWEVSSNGNVDYLMYADVDYDHPDVAETKKWGIWYANELSLDGFRIDAAKHIKS 239
Db 183 WASQENIDQNGNYDYLMDYDDIDFKHPEVQEHLDWVAFLETSGVGGRDLDAIKHDKT 242
Qy 240 FLRDWQAVQATCKENFTVAEYQNNAGKLENYLNKTSFNQSVFDPVPLHFNQAASSQG 299
Db 243 FMAQFIRYIIEHLKADLYVFEYWKDSHFDTIDYLSHSDLOFDLIDVNLHMSLFEACQKG 302
Qy 300 GGYDMRLLDGTVVSRHPEKAVTFVENHDTQPQGSLESTVQTFKPLAYAFILTRSGYP 359
Db 303 SDFDLSTILDSLMKSHDPFAVTFVDNHSQRGQALESTVAENFKPLAYGLILLRQEGIP 362
Qy 360 QVFGDMYKTSKPKIPLSKONIEPILKARKEYAYGQPDHYIDHPDVIQWTRGDSOA 419
Db 363 CVFYGDYIGISGEPAQE--SFQTVLDKLLYIRQVHYVQSQEDYPDYANCIGWTCIGDEE- 419
Qy 420 AKSGLAALITDGGGSKRMVAGLKNAGETWVDITGNESDVTKIGSDGMBEHVNDGVSII 479
Db 420 HPDGVAVIISNGEANCRRMMNGEFNRNKVFVDYLNCTTEVILDDQGWGDFPVQEASLSA 479
Qy 480 YVQK 483
Db 480 WVNK 483
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Search completed: October 7, 2004, 00:19:00
Job time : 47.3093 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2004, 00:12:34 ; Search time 14.9658 Seconds
(without alignments)
1666.155 Million cell updates/sec

Title: US-09-925-576C-10
Perfect score: 2638
Sequence: 1 VNGTLMQYFEWYTPNDGQHW.....SDGWGEFHVNDGVSIVYQK 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2638	100.0	483	4	US-09-291-023A-16
2	2638	100.0	483	4	US-09-537-168-6
3	2638	100.0	483	4	US-09-381-687-6
4	2638	100.0	483	4	US-09-540-715A-16
5	2638	100.0	514	1	US-08-720-899-4
6	2638	100.0	514	1	US-08-459-610-4
7	2638	100.0	514	2	US-08-343-804-4
8	2638	100.0	514	2	US-08-687-399-4
9	2638	100.0	514	2	US-08-600-908A-4
10	2638	100.0	514	3	US-08-683-838A-4
11	2638	100.0	514	3	US-09-264-097-4
12	2638	100.0	514	4	US-09-636-252A-4
13	2638	100.0	520	1	US-08-468-700-36
14	2638	100.0	520	1	US-08-645-971-4
15	2638	100.0	520	2	US-08-468-220-34
16	2638	100.0	520	2	US-08-468-698-34
17	2638	100.0	520	2	US-08-704-706A-36
18	2638	100.0	520	3	US-08-890-383-5
19	2638	100.0	520	3	US-08-914-679A-5
20	2638	100.0	520	3	US-08-985-859-37
21	2638	100.0	520	3	US-08-194-664A-34
22	2638	100.0	520	5	PCT-US94-01553A-34
23	2638	100.0	520	5	PCT-US95-10426-34
24	2624	99.5	480	3	US-09-182-859-4
25	2624	99.5	480	3	US-09-170-670-5
26	2624	99.5	480	3	US-09-193-068-5
27	2624	99.5	480	3	US-09-183-412-5

ALIGNMENTS

RESULT 1
US-09-291-023A-16
; Sequence 16, Application US/09291023A
; Patent No. 6309871
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic Acid
; FILE OF INVENTION: Encoding Same
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/291,023A
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: DK 1999 00438
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 16
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus
US-09-291-023A-16

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Best Local Similarity		100.0%;	Pred. No. 2.1e-231;		
Matches 483;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	1	VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVTWPYPAYKGLSQSDNGVGPYDLY	60		
Qy	61	DLGEFQKGVTRTKYGTGKSELDQAIQSLHSERNVQVYGDVVLNHNKAGADATEDVTAVENVP	120		
Db	61	DLGEFQKGVTRTKYGTGKSELDQAIQSLHSERNVQVYGDVVLNHNKAGADATEDVTAVENVP	120		
Qy	121	ANRQETSEYQIKAWTDFRPPGRGNTYSDPKWHWHFDGADWDESKIRIPIKFRGEGK	180		
Db	121	ANRQETSEYQIKAWTDFRPPGRGNTYSDPKWHWHFDGADWDESKIRIPIKFRGEGK	180		
Qy	181	ADWEVSSSENGYDYLMDYADVDYDHPVVAETKKGWYANELSLDGFRIIDAAKHKFSF	240		
Db	181	ADWEVSSSENGYDYLMDYADVDYDHPVVAETKKGWYANELSLDGFRIIDAAKHKFSF	240		
Qy	241	LRDWQAVRQATGKEMFTVAEYQNNAGKLENTKTSFNQSVDFVPLHFNLAQSSQGG	300		
Db	241	LRDWQAVRQATGKEMFTVAEYQNNAGKLENTKTSFNQSVDFVPLHFNLAQSSQGG	300		
Qy	301	GYDMRRLLDGTVTVSRHPEKAVTFVENHDTOPGOSLSTVQTVTFKFLAYAFILTRSGYPQ	360		
Db	301	GYDMRRLLDGTVTVSRHPEKAVTFVENHDTOPGOSLSTVQTVTFKFLAYAFILTRSGYPQ	360		

Sequence 5, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 2, Appli
Sequence 34, Appli
Sequence 2, Appli
Sequence 32, Appli
Sequence 32, Appli
Sequence 34, Appli
Sequence 3, Appli
Sequence 35, Appli
Sequence 32, Appli

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Db 301 GYDMRLDGTVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILITRESGYPQ 360
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Db 361 VFYGDYMGTKGTSPEKPSLKNIEPILKARKEYAYGPOHDYIDHPDVIWGTREGDSSAA 420
QY 421 KSLAALITDGPGRKMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
Db 421 KSLAALITDGPGRKMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
QY 481 VQK 483
Db 481 VQK 483

RESULT 2
US-09-537-168-6
; Sequence 6, Application US/09537168
; Patent No. 6410295
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/09/537,168
; CURRENT FILING DATE: 2000-03-29
; EARLIER APPLICATION NUMBER: PA 1999 00437
; EARLIER FILING DATE: 1999-03-30
; EARLIER APPLICATION NUMBER: 60/127,427
; EARLIER FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-09-537-168-6
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Query Match 100.0%; Score 2638; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.1e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
QY 61 DLGEFQOKGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNHNKAGADATEDVTAVERN 120
Db 61 DLGEFQOKGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNHNKAGADATEDVTAVERN 120
QY 121 ANRNOETSEEQIKAWTDFFPGRGNTYSDPKWHWHFDCADWDESKRSIRIFKPRGEGK 180
Db 121 ANRNOETSEEQIKAWTDFFPGRGNTYSDPKWHWHFDCADWDESKRSIRIFKPRGEGK 180
QY 181 AWDWEVSSNGNYDLYMADVVDYDHPDVVAETKKGWIWYANELSLDGFRIIDAAKHIFSF 240
Db 181 AWDWEVSSNGNYDLYMADVVDYDHPDVVAETKKGWIWYANELSLDGFRIIDAAKHIFSF 240
QY 241 LRDWVQAVRQATGKEMFTVAEYQNNAGKLENLYNLTSTFNQSVDFVPLHFNLAQASSQGG 300
Db 241 LRDWVQAVRQATGKEMFTVAEYQNNAGKLENLYNLTSTFNQSVDFVPLHFNLAQASSQGG 300
QY 301 GYDMRLDGTVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILITRESGYPQ 360
Db 301 GYDMRLDGTVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILITRESGYPQ 360
QY 361 VFYGDYMGTKGTSPEKPSLKNIEPILKARKEYAYGPOHDYIDHPDVIWGTREGDSSAA 420
Db 361 VFYGDYMGTKGTSPEKPSLKNIEPILKARKEYAYGPOHDYIDHPDVIWGTREGDSSAA 420
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QY 421 KSLAALITDGPGRKMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
Db 421 KSLAALITDGPGRKMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
QY 481 VQK 483
Db 481 VQK 483

RESULT 3
US-09-381-687-6
; Sequence 6, Application US/09381687
; Patent No. 6486113
; GENERAL INFORMATION:
; APPLICANT: HATADA, Yuji
; APPLICANT: IKAWA, Kaori
; APPLICANT: ITO, Susumu
; APPLICANT: IGARASHI, Kazuaki
; APPLICANT: HAGIHARA, Hiroshi
; APPLICANT: HAYASHI, Yasuhiro
; APPLICANT: ABAKI, Hiroyuki
; APPLICANT: OZAKI, Katsuya
; TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
; FILE REFERENCE: 2173-0115P
; CURRENT APPLICATION NUMBER: US/09/381,687
; CURRENT FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 483
; TYPE: PRT
; ORGANISM: B. amyloliquefaciens
US-09-381-687-6
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Query Match 100.0%; Score 2638; DB 4; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.1e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
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QY 61 DLGEFQOKGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNHNKAGADATEDVTAVERN 120
Db 61 DLGEFQOKGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNHNKAGADATEDVTAVERN 120
QY 121 ANRNOETSEEQIKAWTDFFPGRGNTYSDPKWHWHFDCADWDESKRSIRIFKPRGEGK 180
Db 121 ANRNOETSEEQIKAWTDFFPGRGNTYSDPKWHWHFDCADWDESKRSIRIFKPRGEGK 180
QY 181 AWDWEVSSNGNYDLYMADVVDYDHPDVVAETKKGWIWYANELSLDGFRIIDAAKHIFSF 240
Db 181 AWDWEVSSNGNYDLYMADVVDYDHPDVVAETKKGWIWYANELSLDGFRIIDAAKHIFSF 240
QY 241 LRDWVQAVRQATGKEMFTVAEYQNNAGKLENLYNLTSTFNQSVDFVPLHFNLAQASSQGG 300
Db 241 LRDWVQAVRQATGKEMFTVAEYQNNAGKLENLYNLTSTFNQSVDFVPLHFNLAQASSQGG 300
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Db 301 GYDMRLDGTVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILITRESGYPQ 360
QY 361 VFYGDYMGTKGTSPEKPSLKNIEPILKARKEYAYGPOHDYIDHPDVIWGTREGDSSAA 420
Db 361 VFYGDYMGTKGTSPEKPSLKNIEPILKARKEYAYGPOHDYIDHPDVIWGTREGDSSAA 420
QY 421 KSLAALITDGPGRKMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
Db 421 KSLAALITDGPGRKMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGSVSIY 480
QY 481 VQK 483
Db 481 VQK 483
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Db 481 VQK 483

RESULT 4

US-09-540-715A-16
; Sequence 16, Application US/09540715A

; Patent No. 6623948

; GENERAL INFORMATION:

; APPLICANT: Outtrup, Helle

; APPLICANT: Borchart, Torben

; APPLICANT: Nielsen, Bjarne

; APPLICANT: Hoeck, Lisbeth

; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic A

; FILE REFERENCE: 5821.010-US

; CURRENT APPLICATION NUMBER: US/09/540,715A

; CURRENT FILING DATE: 2000-03-31

; PRIOR FILING DATE: 2001-08-14

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 16

; LENGTH: 483

; TYPE: PRT

; ORGANISM: Bacillus

US-09-540-715A-16

Query Match 100.0%; Score 2638; DB 4; Length 483;

Best Local Similarity 100.0%; Pred. No. 2.1e-231;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHAGADATEDVTAVERN	120
Db	61	DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHAGADATEDVTAVERN	120
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Db	121	ARNQETSEBYQIKAWTDFFPGRGNTYSDFKWHYHFDGADWDESKISRIKFRGEGK	180
Qy	181	ADWEVSSSENGNDYLMYADVDPDVAETKKGWYANELSLDGFRIIDAAKHIFSF	240
Db	181	ADWEVSSSENGNDYLMYADVDPDVAETKKGWYANELSLDGFRIIDAAKHIFSF	240
Qy	241	LRDWQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASQGG	300
Db	241	LRDWQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASQGG	300
Qy	301	GYDMRRLDGTWVSRHPEKAVTFVENHDTQPGQSLSTVQTFWPKLAYAFILITRESGYPQ	360
Db	301	GYDMRRLDGTWVSRHPEKAVTFVENHDTQPGQSLSTVQTFWPKLAYAFILITRESGYPQ	360
Qy	361	VFYGDMYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPDHYIDHPDVIWGTREGDSSAA	420
Db	361	VFYGDMYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPDHYIDHPDVIWGTREGDSSAA	420
Qy	421	KSGLAALITDGPGGSKRMAYAGLNAGETWYDITGNRSDTVKIGSDGGEFHVNDGSYSIY	480
Db	421	KSGLAALITDGPGGSKRMAYAGLNAGETWYDITGNRSDTVKIGSDGGEFHVNDGSYSIY	480
Qy	481	VQK 483	
Db	481	VQK 483	

RESULT 5

US-08-720-899-4

; Sequence 4, Application US/08720899

; Patent No. 5753460

GENERAL INFORMATION:

; APPLICANT: Bisgaard-Frantzen, Henrik

; APPLICANT: Borchart, Torben Vedel

; APPLICANT: Svendsen, Allan

; APPLICANT: Thellersen, Marianne

; APPLICANT: Van der Zee, Pia

; TITLE OF INVENTION: AMYLASE VARIANTS

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 5753460o No. 5753460disk of No. 5753460th America, Inc.

; STREET: 405 Lexington Avenue, 64th Floor

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10174-6401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/720,899

; FILING DATE: 10-OCT-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/343,804

; FILING DATE: 22-NOV-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lowney Dr. Karen A.

; REGISTRATION NUMBER: 31,274

; REFERENCE/DOCKET NUMBER: 4054.214-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-867-0123

; TELEFAX: 212-878-9655

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 514 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-720-899-4

Query Match

100.0%; Score 2638; DB 1; Length 514;

Best Local Similarity 100.0%; Pred. No. 2.3e-231;

Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VNGTLMQYFEWYTPNDQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	60
Db	32	VNGTLMQYFEWYTPNDQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY	91
Qy	61	DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHAGADATEDVTAVERN	120
Db	92	DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHAGADATEDVTAVERN	151
Qy	121	ARNQETSEBYQIKAWTDFFPGRGNTYSDFKWHYHFDGADWDESKISRIKFRGEGK	180
Db	152	ARNQETSEBYQIKAWTDFFPGRGNTYSDFKWHYHFDGADWDESKISRIKFRGEGK	211
Qy	181	ADWEVSSSENGNDYLMYADVDPDVAETKKGWYANELSLDGFRIIDAAKHIFSF	240
Db	212	ADWEVSSSENGNDYLMYADVDPDVAETKKGWYANELSLDGFRIIDAAKHIFSF	271
Qy	241	LRDWQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASQGG	300
Db	272	LRDWQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASQGG	331
Qy	301	GYDMRRLDGTWVSRHPEKAVTFVENHDTQPGQSLSTVQTFWPKLAYAFILITRESGYPQ	360
Db	332	GYDMRRLDGTWVSRHPEKAVTFVENHDTQPGQSLSTVQTFWPKLAYAFILITRESGYPQ	391
Qy	361	VFYGDMYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPDHYIDHPDVIWGTREGDSSAA	420
Db	392	VFYGDMYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPDHYIDHPDVIWGTREGDSSAA	451

Qy 421 KSLAALITDGGSKMYAGLKNAGETWYDITGNRSDTVKIGDQGWGFHNDGVSIV 480
 Db 452 KSLAALITDGGSKMYAGLKNAGETWYDITGNRSDTVKIGDQGWGFHNDGVSIV 511
 Qy 481 VQK 483
 Db 512 VQK 514

RESULT 6
 US-08-459-610-4
 ; Sequence 4, Application US/08459610
 ; Patent No. 5801043
 ; GENERAL INFORMATION:
 ; APPLICANT: Bisgaard-Frantzen, Henrik
 ; APPLICANT: Borchert, Torben Vedel
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Thellersen, Marianne
 ; APPLICANT: Van der Zee, Pia
 ; TITLE OF INVENTION: AMYLASE VARIANTS
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 5801043o No. 5801043disk of No. 5801043th America, Inc.
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/459,610
 ; FILING DATE: 02-JUN-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/343,804
 ; FILING DATE: 22-NOV-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lowney Dr., Karen A.
 ; REGISTRATION NUMBER: 31,274
 ; REFERENCE/DOCKET NUMBER: 4054.214-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 514 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-459-610-4

Query Match 100.0%; Score 2638; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 2.3e-231;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEWYTPNDQGHKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGYDLY 60
 Db 32 VNGTLMQYFEWYTPNDQGHKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGYDLY 91
 Qy 61 DLGEFOQKGVTRKYGTGKSLQDAISGLHSRNVQVYGDVVLNKHGADATEDVTAVERN 120
 Db 92 DLGEFOQKGVTRKYGTGKSLQDAISGLHSRNVQVYGDVVLNKHGADATEDVTAVERN 151
 Qy 121 ANRNETSEYQIKAWTDFFPQGNNTYSDFKWHWHYFDGADWDSRKISRIFKRGSGK 180
 Db 152 ANRNETSEYQIKAWTDFFPQGNNTYSDFKWHWHYFDGADWDSRKISRIFKRGSGK 211
 Qy 181 ANDWEVSSSENGNYDYLMIADVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHKFSF 240

Db 212 ANDWEVSSSENGNYDYLMIADVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHKFSF 271
 Qy 241 LRDWQAVRQATGKEMFTVAEYQNNAGKLENLYNKTSTFQSVDFVPLHFNLAQASQGG 300
 Db 272 LRDWQAVRQATGKEMFTVAEYQNNAGKLENLYNKTSTFQSVDFVPLHFNLAQASQGG 331
 Qy 301 GYDMRLLDGTVVSRRHPEKAVTFVENHDTQPGOSLESTVQTPKPLAYAFILTRGSGYPQ 360
 Db 332 GYDMRLLDGTVVSRRHPEKAVTFVENHDTQPGOSLESTVQTPKPLAYAFILTRGSGYPQ 391
 Qy 361 VFYGDMYGTGTSKPSKIPSLKONIEPILKARKEYAYGPOHDIYDHPDVVIGWTRGSSAA 420
 Db 392 VFYGDMYGTGTSKPSKIPSLKONIEPILKARKEYAYGPOHDIYDHPDVVIGWTRGSSAA 451
 Qy 421 KSLAALITDGGSKMYAGLKNAGETWYDITGNRSDTVKIGDQGWGFHNDGVSIV 480
 Db 452 KSLAALITDGGSKMYAGLKNAGETWYDITGNRSDTVKIGDQGWGFHNDGVSIV 511
 Qy 481 VQK 483
 Db 512 VQK 514

RESULT 7
 US-08-343-804-4
 ; Sequence 4, Application US/08343804
 ; Patent No. 5830837
 ; GENERAL INFORMATION:
 ; APPLICANT: Bisgaard-Frantzen, Henrik
 ; APPLICANT: Borchert, Torben Vedel
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Thellersen, Marianne
 ; APPLICANT: Van der Zee, Pia
 ; TITLE OF INVENTION: AMYLASE VARIANTS
 ; NUMBER OF SEQUENCES: 38
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 5830837o No. 5830837disk of No. 5830837th America, Inc.
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10174-6401
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/343,804
 ; FILING DATE: 22-NOV-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lowney Dr., Karen A.
 ; REGISTRATION NUMBER: 31,274
 ; REFERENCE/DOCKET NUMBER: 4054.214-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 514 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-343-804-4

Query Match 100.0%; Score 2638; DB 2; Length 514;
 Best Local Similarity 100.0%; Pred. No. 2.3e-231;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEWYTPNDQGHKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGYDLY 60

Db 32 VNGTLMQYFEWYTPNDQGHKRLQNDAEHLSDIGITAVWIPPPAYKGLSQSDNGVGPVDLY 91
Qy 61 DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHKAGADATEDVTAVEVNP 120
Db 92 DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHKAGADATEDVTAVEVNP 151
Qy 121 ANRNETSEBYQIKAWTDFFPPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGK 180
Db 152 ANRNETSEBYQIKAWTDFFPPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGK 211
Qy 181 ADWEVSSSENGNDYLMYADVDYDHPDVAETKKWGIWYANELSLDGFRIIDAAKHIFSF 240
Db 212 ADWEVSSSENGNDYLMYADVDYDHPDVAETKKWGIWYANELSLDGFRIIDAAKHIFSF 271
Qy 241 LRDWQAVROATKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNLOAASQGG 300
Db 272 LRDWQAVROATKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNLOAASQGG 331
Qy 301 GYDMRLLDGTVVSRRHPEKAVTFVNHDTOPGQSLSTVQTFWPKLAYAFILTRGSGYPQ 360
Db 332 GYDMRLLDGTVVSRRHPEKAVTFVNHDTOPGQSLSTVQTFWPKLAYAFILTRGSGYPQ 391
Qy 361 VFYGDYMTGKTSPEKPSLKNIEPILKARKEYAYGPQHDYIDHPDVIWGTREGDSSAA 420
Db 392 VFYGDYMTGKTSPEKPSLKNIEPILKARKEYAYGPQHDYIDHPDVIWGTREGDSSAA 451
Qy 421 KSGLAALITDGPQSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 480
Db 452 KSGLAALITDGPQSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 511
Qy 481 VQK 483
Db 512 VQK 514

RESULT 8

US-08-687-399-4
; Sequence 4, Application US/08687399
; Patent No. 5928381
; GENERAL INFORMATION:
; APPLICANT: Toft, Annette H.
; APPLICANT: Marcher, Dorte
; APPLICANT: Pedersen, Hanne H.
; APPLICANT: Nilsen, Thomas E.
; TITLE OF INVENTION: A Combined Desizing and Bleaching
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59283810 No. 59283810disk of No. 59283810th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/687,399
; CLASSIFICATION: 008
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4127.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-687-399-4
Query Match 100.0%; Score 2638; DB 2; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VNGTLMQYFEWYTPNDQGHKRLQNDAEHLSDIGITAVWIPPPAYKGLSQSDNGVGPVDLY 60
Db 32 VNGTLMQYFEWYTPNDQGHKRLQNDAEHLSDIGITAVWIPPPAYKGLSQSDNGVGPVDLY 91
Qy 61 DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHKAGADATEDVTAVEVNP 120
Db 92 DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHKAGADATEDVTAVEVNP 151
Qy 121 ANRNETSEBYQIKAWTDFFPPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGK 180
Db 152 ANRNETSEBYQIKAWTDFFPPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGK 211
Qy 181 ADWEVSSSENGNDYLMYADVDYDHPDVAETKKWGIWYANELSLDGFRIIDAAKHIFSF 240
Db 212 ADWEVSSSENGNDYLMYADVDYDHPDVAETKKWGIWYANELSLDGFRIIDAAKHIFSF 271
Qy 241 LRDWQAVROATKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNLOAASQGG 300
Db 272 LRDWQAVROATKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNLOAASQGG 331
Qy 301 GYDMRLLDGTVVSRRHPEKAVTFVNHDTOPGQSLSTVQTFWPKLAYAFILTRGSGYPQ 360
Db 332 GYDMRLLDGTVVSRRHPEKAVTFVNHDTOPGQSLSTVQTFWPKLAYAFILTRGSGYPQ 391
Qy 361 VFYGDYMTGKTSPEKPSLKNIEPILKARKEYAYGPQHDYIDHPDVIWGTREGDSSAA 420
Db 392 VFYGDYMTGKTSPEKPSLKNIEPILKARKEYAYGPQHDYIDHPDVIWGTREGDSSAA 451
Qy 421 KSGLAALITDGPQSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 480
Db 452 KSGLAALITDGPQSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 511
Qy 481 VQK 483
Db 512 VQK 514
RESULT 9
US-08-600-908A-4
; Sequence 4, Application US/08600908A
; Patent No. 5989169
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisg rd-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: -Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 59891690 No. 59891690disk of No. 59891690th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,908A
; FILING DATE: 13-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-600-908A-4

Query Match 100.0%; Score 2638; DB 2; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Db 32 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 91
QY 61 DLGEFQOQGTVRTKYGTKSELQDAIGSLHSRNVQYGDVVLNKHAGADATEDVTAVERN 120
Db 92 DLGEFQOQGTVRTKYGTKSELQDAIGSLHSRNVQYGDVVLNKHAGADATEDVTAVERN 151
QY 121 ANRNETSEYQIKAWTDFFRPGRGNTYSDPKWHYHFDGADWDESRKISRIFKFRGEGK 180
Db 152 ANRNETSEYQIKAWTDFFRPGRGNTYSDPKWHYHFDGADWDESRKISRIFKFRGEGK 211
QY 181 AMDWEVSSNGNYDLYMADVDPVAVETKKGWIWYANELSLDGFRIIDAAKHIFKSF 240
Db 212 AMDWEVSSNGNYDLYMADVDPVAVETKKGWIWYANELSLDGFRIIDAAKHIFKSF 271
QY 241 LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVDFVPLHFNLAQASSQG 300
Db 272 LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVDFVPLHFNLAQASSQG 331
QY 301 GYDMRRLDGTVVSRRHPEKAVTFVENHDTOPGQSLSTVQWPKPLAYAFILTRREGYPQ 360
Db 332 GYDMRRLDGTVVSRRHPEKAVTFVENHDTOPGQSLSTVQWPKPLAYAFILTRREGYPQ 391
QY 361 VFYGDYGTGTSPEIKONIEPILKARKEYAYGQHDYIDHPDVIGTWREGDSSAA 420
Db 392 VFYGDYGTGTSPEIKONIEPILKARKEYAYGQHDYIDHPDVIGTWREGDSSAA 451
QY 421 KSLAALITDGPQSGKEMVAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 480
Db 452 KSLAALITDGPQSGKEMVAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 511
QY 481 VQK 483
Db 512 VQK 514

RESULT 10
US-08-683-838A-4
; Sequence 4, Application US/08683838A
; Patent No. 6022724
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Big rd-Frantzen, Henrik
; APPLICANT: Borchart, Torben Vedel
; TITLE OF INVENTION: '-Amylase Mutants
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6022724o No. 6022724disk of No. 6022724th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/683,838A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 08/600,908
; FILING DATE: 13-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4394.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-683-838A-4

Query Match 100.0%; Score 2638; DB 3; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Db 32 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 91
QY 61 DLGEFQOQGTVRTKYGTKSELQDAIGSLHSRNVQYGDVVLNKHAGADATEDVTAVERN 120
Db 92 DLGEFQOQGTVRTKYGTKSELQDAIGSLHSRNVQYGDVVLNKHAGADATEDVTAVERN 151
QY 121 ANRNETSEYQIKAWTDFFRPGRGNTYSDPKWHYHFDGADWDESRKISRIFKFRGEGK 180
Db 152 ANRNETSEYQIKAWTDFFRPGRGNTYSDPKWHYHFDGADWDESRKISRIFKFRGEGK 211
QY 181 AMDWEVSSNGNYDLYMADVDPVAVETKKGWIWYANELSLDGFRIIDAAKHIFKSF 240
Db 212 AMDWEVSSNGNYDLYMADVDPVAVETKKGWIWYANELSLDGFRIIDAAKHIFKSF 271
QY 241 LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVDFVPLHFNLAQASSQG 300
Db 272 LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSTFNQSVDFVPLHFNLAQASSQG 331
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Db 332 GYDMRRLDGTVVSRRHPEKAVTFVENHDTOPGQSLSTVQWPKPLAYAFILTRREGYPQ 391
QY 361 VFYGDYGTGTSPEIKONIEPILKARKEYAYGQHDYIDHPDVIGTWREGDSSAA 420
Db 392 VFYGDYGTGTSPEIKONIEPILKARKEYAYGQHDYIDHPDVIGTWREGDSSAA 451
QY 421 KSLAALITDGPQSGKEMVAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 480
Db 452 KSLAALITDGPQSGKEMVAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 511
QY 481 VQK 483
Db 512 VQK 514

RESULT 11
US-09-264-097-4
; Sequence 4, Application US/09264097
; Patent No. 6287826
; GENERAL INFORMATION:
; APPLICANT: No. 6287826man, Barrie Edmund
```

APPLICANT: Hendriksen, Hanne Vang
TITLE OF INVENTION: Enzymatic Preparation of Glucose Syrup
FILE OF INVENTION: From Starch
FILE REFERENCE: 5278.200-US
CURRENT APPLICATION NUMBER: US/09/264,097
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: PA 0321/98
EARLIER FILING DATE: 1998-03-09
EARLIER APPLICATION NUMBER: 60/079,209
EARLIER FILING DATE: 1998-03-24
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 514
TYPE: PRT
ORGANISM: Bacillus amyloliquefaciens
US-09-264-097-4

Query Match 100.0%; Score 2638; DB 3; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
DB 32 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 91
QY 61 DLGEFOQKGTVRTKYGTGKSELODAIGSLHSRNVOVYGDVVLNKHAGADATEDVTAVEVNP 120
DB 92 DLGEFOQKGTVRTKYGTGKSELODAIGSLHSRNVOVYGDVVLNKHAGADATEDVTAVEVNP 151
QY 121 ANRNETSEYQIKAWTDFFRPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGK 180
DB 152 ANRNETSEYQIKAWTDFFRPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGK 211
QY 181 AWDWEVSSNGNYDYLWADVDYDHPDVAETKKGWYANELSLDGFRIIDAAKHIFSF 240
DB 212 AWDWEVSSNGNYDYLWADVDYDHPDVAETKKGWYANELSLDGFRIIDAAKHIFSF 271
QY 241 LRDMQVAVRQATGKEMFTVAEYWNQAGKLENLYNKTSTFNQSVDFVPLHFNLAQSSQGG 300
DB 272 LRDMQVAVRQATGKEMFTVAEYWNQAGKLENLYNKTSTFNQSVDFVPLHFNLAQSSQGG 331
QY 301 GYDMRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRGSGYPQ 360
DB 332 GYDMRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRGSGYPQ 391
QY 361 VFYGDYMGTKGTSPEKIPSLKONIEPILKARKEYAYGQHDYIDHPDVIGWTRGDSAA 420
DB 392 VFYGDYMGTKGTSPEKIPSLKONIEPILKARKEYAYGQHDYIDHPDVIGWTRGDSAA 451
QY 421 KSGLAALITDGPQSGKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 480
DB 452 KSGLAALITDGPQSGKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 511
QY 481 VQK 483
DB 512 VQK 514

RESULT 12
US-09-636-252A-4
Sequence 4, Application US/09636252A
Patent No. 6440716
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisgaard-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: Alpha-Amylase Mutants
FILE REFERENCE: 0776/1F216-US2
CURRENT APPLICATION NUMBER: US/09/636,252A
CURRENT FILING DATE: 2000-08-10
PRIOR APPLICATION NUMBER: 08/683,838
PRIOR FILING DATE: 1996-07-18

NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 514
TYPE: PRT
ORGANISM: B. amyloliquefaciens
US-09-636-252A-4

Query Match 100.0%; Score 2638; DB 4; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.3e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
DB 32 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 91
QY 61 DLGEFOQKGTVRTKYGTGKSELODAIGSLHSRNVOVYGDVVLNKHAGADATEDVTAVEVNP 120
DB 92 DLGEFOQKGTVRTKYGTGKSELODAIGSLHSRNVOVYGDVVLNKHAGADATEDVTAVEVNP 151
QY 121 ANRNETSEYQIKAWTDFFRPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGK 180
DB 152 ANRNETSEYQIKAWTDFFRPGRGNTYSDFKWHWHYHFDGADWDESKISRIKFRGEGK 211
QY 181 AWDWEVSSNGNYDYLWADVDYDHPDVAETKKGWYANELSLDGFRIIDAAKHIFSF 240
DB 212 AWDWEVSSNGNYDYLWADVDYDHPDVAETKKGWYANELSLDGFRIIDAAKHIFSF 271
QY 241 LRDMQVAVRQATGKEMFTVAEYWNQAGKLENLYNKTSTFNQSVDFVPLHFNLAQSSQGG 300
DB 272 LRDMQVAVRQATGKEMFTVAEYWNQAGKLENLYNKTSTFNQSVDFVPLHFNLAQSSQGG 331
QY 301 GYDMRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRGSGYPQ 360
DB 332 GYDMRLLDGTVVSRHPEKAVTFVENHDTQPGQSLESTVQTWFKPLAYAFILTRGSGYPQ 391
QY 361 VFYGDYMGTKGTSPEKIPSLKONIEPILKARKEYAYGQHDYIDHPDVIGWTRGDSAA 420
DB 392 VFYGDYMGTKGTSPEKIPSLKONIEPILKARKEYAYGQHDYIDHPDVIGWTRGDSAA 451
QY 421 KSGLAALITDGPQSGKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 480
DB 452 KSGLAALITDGPQSGKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWFHNDGVSIIY 511
QY 481 VQK 483
DB 512 VQK 514

RESULT 13
US-08-468-700-36
Sequence 36, Application US/08468700
Patent No. 5736499
GENERAL INFORMATION:
APPLICANT: COLIN MITCHINSON
APPLICANT: CAROL A. REQUADT
APPLICANT: TRACI H. ROPP
APPLICANT: LEIF P. SOLHEIM
TITLE OF INVENTION: MUTANT ALPHA-AMYLASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 180 Kimball Way
CITY: South San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,700
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 252
; ATTORNEY/AGENT INFORMATION:
; NAME: Stone, Christopher
; REGISTRATION NUMBER: 35,696
; REFERENCE/DOCKET NUMBER: GC275
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 742-7555
; TELEFAX: (415) 742-7217
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 520 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-468-700-36

Query Match 100.0%; Score 2638; DB 1; Length 520;
Best Local Similarity 100.0%; Pred. No. 2.4e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
DB 38 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 97

QY 61 DLGEFOQKGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNKHAGADATEDVAVEVNP 120
DB 98 DLGEFOQKGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNKHAGADATEDVAVEVNP 157

QY 121 ANRQETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYDFDAGDWDESKISRIFKFRGEGK 180
DB 158 ANRQETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYDFDAGDWDESKISRIFKFRGEGK 217

QY 181 AWDWEVSSNGNDYLMYADVDDHPDVVAETKKGWYANIELSLDGFRIIDAAKHIFKFSF 240
DB 218 AWDWEVSSNGNDYLMYADVDDHPDVVAETKKGWYANIELSLDGFRIIDAAKHIFKFSF 277

QY 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASSQGG 300
DB 278 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASSQGG 337

QY 301 GYDMRRLDGTGTVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAYAFILITRESGYQP 360
DB 338 GYDMRRLDGTGTVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAYAFILITRESGYQP 397

QY 361 VFYGDWYGTGTSRHPKAVTFVENHDTQPGQSLSTVQTFWFKPLAYAFILITRESGYQP 420
DB 398 GYDMRRLDGTGTVSRHPEKAVTFVENHDTQPGQSLSTVQTFWFKPLAYAFILITRESGYQP 457

QY 361 VFYGDWYGTGTSRHPKAVTFVENHDTQPGQSLSTVQTFWFKPLAYAFILITRESGYQP 420
DB 398 VFYGDWYGTGTSRHPKAVTFVENHDTQPGQSLSTVQTFWFKPLAYAFILITRESGYQP 457

QY 421 KSLGALALITDGGGSKRMVAGLKNAGETWYDITGNRSDTVKGISDQGWGEFHVNDGVSIVY 480
DB 458 KSLGALALITDGGGSKRMVAGLKNAGETWYDITGNRSDTVKGISDQGWGEFHVNDGVSIVY 517

QY 481 VQK 483
DB 518 VQK 520

RESULT 14
US-08-645-971-4
; Sequence 4, Application US/08645971
; Patent No. 5763385
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Modified Alpha-Amylases Having Altered
; TITLE OF INVENTION: Calcium Binding Properties
; NUMBER OF SEQUENCES: 5
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,971
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 520 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Bacillus amyloliquefaciens
; US-08-645-971-4

Query Match 100.0%; Score 2638; DB 1; Length 520;
Best Local Similarity 100.0%; Pred. No. 2.4e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
DB 38 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 97

QY 61 DLGEFOQKGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNKHAGADATEDVAVEVNP 120
DB 98 DLGEFOQKGTVRTKYGTSKSELQDAIGSLHSRNQVYGDVVLNKHAGADATEDVAVEVNP 157

QY 121 ANRQETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYDFDAGDWDESKISRIFKFRGEGK 180
DB 158 ANRQETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYDFDAGDWDESKISRIFKFRGEGK 217

QY 181 AWDWEVSSNGNDYLMYADVDDHPDVVAETKKGWYANIELSLDGFRIIDAAKHIFKFSF 240
DB 218 AWDWEVSSNGNDYLMYADVDDHPDVVAETKKGWYANIELSLDGFRIIDAAKHIFKFSF 277

QY 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASSQGG 300
DB 278 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASSQGG 337

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QY 361 VFYGDWYGTGTSRHPKAVTFVENHDTQPGQSLSTVQTFWFKPLAYAFILITRESGYQP 420
DB 398 VFYGDWYGTGTSRHPKAVTFVENHDTQPGQSLSTVQTFWFKPLAYAFILITRESGYQP 457

QY 421 KSLGALALITDGGGSKRMVAGLKNAGETWYDITGNRSDTVKGISDQGWGEFHVNDGVSIVY 480
DB 458 KSLGALALITDGGGSKRMVAGLKNAGETWYDITGNRSDTVKGISDQGWGEFHVNDGVSIVY 517

QY 481 VQK 483
DB 518 VQK 520

RESULT 15
US-08-468-220-34
; Sequence 34, Application US/08468220
; Patent No. 5824532
; GENERAL INFORMATION:
; APPLICANT: Antrim, Richard L.
; APPLICANT: Barnett, Christopher
; APPLICANT: Mitchinson, Colin
; APPLICANT: Power, Scott D.
; APPLICANT: Requaft, Carol
; APPLICANT: Solheim, Leif P.
; TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International, Inc.
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA

/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/468,220
/ FILING DATE: 06-JUN-95
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/194,664
/ FILING DATE: 10-FEB-94
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/016,395
/ FILING DATE: 11-FEB-93
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stone, Christopher L.
/ REGISTRATION NUMBER: 35,696
/ REFERENCE/DOCKET NUMBER: GC220D1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 742-7555
/ TELEFAX: (415) 742-7217
/ INFORMATION FOR SEQ ID NO: 34:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 520 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-468-220-34

Query Match 100.0%; Score 2638; DB 2; Length 520;
Best Local Similarity 100.0%; Pred. No. 2.4e-231;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKYGLSQSDNGYGPYDLY 60
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QY 61 DLGEFQKQGTVRTKYGTSELSQDAIGSLHSRNQVYGDVVLNKHKAGADATEDVTAVEVNP 120
Db 98 DLGEFQKQGTVRTKYGTSELSQDAIGSLHSRNQVYGDVVLNKHKAGADATEDVTAVEVNP 157
QY 121 ANRQETSEYQIKAWTDPRPGRGNTYSDFKWHYHFDGADWDESRKISRIFKFRGEGK 180
Db 158 ANRQETSEYQIKAWTDPRPGRGNTYSDFKWHYHFDGADWDESRKISRIFKFRGEGK 217
QY 181 AWDWEVSSENGNDYLMYADVVDYDHPDVVAETKKWGIWYANELSLDGFRIIDAAKHKPSF 240
Db 218 AWDWEVSSENGNDYLMYADVVDYDHPDVVAETKKWGIWYANELSLDGFRIIDAAKHKPSF 277
QY 241 LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSEFQSVFDPVLFHFNLAASSQGG 300
Db 278 LRDWVQAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSEFQSVFDPVLFHFNLAASSQGG 337
QY 301 GYDMRRLDGTGVSRHPEKAVTFVENHDTOPGQSESTVQTFWPKPLAYAFILITRESGYPQ 360
Db 338 GYDMRRLDGTGVSRHPEKAVTFVENHDTOPGQSESTVQTFWPKPLAYAFILITRESGYPQ 397
QY 361 VFYGDMTGKTGTSPEKIPSLKDNTEPILKARKEYAYGPQHDYIDHPDVIGWTRREGDSSAA 420
Db 398 VFYGDMTGKTGTSPEKIPSLKDNTEPILKARKEYAYGPQHDYIDHPDVIGWTRREGDSSAA 457
QY 421 KSGLAALITDGPGGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
Db 458 KSGLAALITDGPGGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 517
QY 481 VQK 483
Db 518 VQK 520

Search completed: October 7, 2004, 00:47:12
Job time : 16.9658 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:19:14 ; Search time 53.2274 Seconds
(without alignments)
2920.093 Million cell updates/sec

Title: US-09-925-576C-10
Perfect score: 2638
Sequence: 1 VNGTLMQYFEWYTPNDGQHW.....SDGWBGFHVDGVSIVYQK 483

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications AA:
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 - 2: /cgn2_6/ptodata/2/pubppaa/PTCT_NEW_PUB.pep.*
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 - 6: /cgn2_6/ptodata/2/pubppaa/PTCTUS_PUBCOMB.pep.*
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 - 9: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep.*
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 - 13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep.*
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 - 17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2638	100.0	483	9	US-09-854-346-10
2	2638	100.0	483	9	US-09-918-543-10
3	2638	100.0	483	10	US-09-925-576C-10
4	2638	100.0	483	14	US-10-146-327-6
5	2638	100.0	483	16	US-10-477-725-10
6	2638	100.0	514	14	US-10-184-771-4
7	2624	99.5	480	9	US-09-854-346-5
8	2624	99.5	480	12	US-10-665-667-5
9	2624	99.5	480	12	US-10-644-187-4
10	2624	99.5	480	12	US-10-327-837-5
11	2624	99.5	480	14	US-10-186-042-4
12	2486	94.2	483	14	US-10-184-771-13
13	2201	83.4	481	14	US-10-146-327-2
14	2193	83.1	512	14	US-10-081-872-114
15	2193	83.1	512	14	US-10-105-733-8

16	2193	83.1	512	14	US-10-081-739A-8	Sequence 8, Appli
17	2193	83.1	512	15	US-10-385-305-114	Sequence 114, App
18	2187	82.9	512	14	US-10-199-922-2	Sequence 2, Appli
19	2184	82.8	483	9	US-09-769-864-4	Sequence 4, Appli
20	2184	82.8	483	9	US-09-854-346-8	Sequence 8, Appli
21	2184	82.8	483	9	US-09-918-543-8	Sequence 8, Appli
22	2184	82.8	483	9	US-09-918-543-30	Sequence 30, Appli
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24	2184	82.8	483	12	US-10-665-667-4	Sequence 4, Appli
25	2184	82.8	483	12	US-10-644-187-2	Sequence 2, Appli
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27	2184	82.8	483	14	US-10-146-327-4	Sequence 4, Appli
28	2184	82.8	483	14	US-10-186-042-2	Sequence 2, Appli
29	2184	82.8	483	16	US-10-399-161-6	Sequence 6, Appli
30	2184	82.8	483	16	US-10-477-725-8	Sequence 8, Appli
31	2184	82.8	512	14	US-10-184-771-2	Sequence 2, Appli
32	1931	73.2	513	14	US-10-081-872-146	Sequence 146, App
33	1931	73.2	513	15	US-10-385-305-146	Sequence 146, App
34	1930	73.2	513	14	US-10-081-872-70	Sequence 70, Appli
35	1930	73.2	513	15	US-10-385-305-70	Sequence 70, Appli
36	1925	73.0	478	14	US-10-081-872-166	Sequence 166, App
37	1925	73.0	478	15	US-10-385-305-166	Sequence 166, App
38	1870	70.9	485	9	US-09-769-864-2	Sequence 2, Appli
39	1870	70.9	485	9	US-09-769-864-8	Sequence 8, Appli
40	1870	70.9	485	9	US-09-854-346-4	Sequence 4, Appli
41	1870	70.9	485	9	US-09-902-188A-2	Sequence 2, Appli
42	1870	70.9	485	9	US-09-918-543-4	Sequence 4, Appli
43	1870	70.9	485	9	US-09-795-211-2	Sequence 2, Appli
44	1870	70.9	485	10	US-09-925-576C-4	Sequence 4, Appli
45	1870	70.9	485	12	US-10-665-667-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-854-346-10
; Sequence 10, Application US/09854346
; Patent No. US20020068352A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020068352A1ozymes A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Jorgensen, Christel Thea
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Alpha-amylase variants with altered 1.6 activity
; FILE REFERENCE: 6140.200-US
; CURRENT APPLICATION NUMBER: US/09/854.346
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-09-854-346-10

Query Match	100.0%;	Score 2638;	DB 9;	Length 483;
Best Local Similarity	100.0%;	Pred. No. 2.5e-238;		
Matches	483;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
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Qy	61	DLGSEFOQKGVTRTKYKTKSLODAIGSLHNRNVQYGVGVNLHKGAGADATDVAVEVNP	120	
Db	61	DLGSEFOQKGVTRTKYKTKSLODAIGSLHNRNVQYGVGVNLHKGAGADATDVAVEVNP	120	
Qy	121	ANRQNETSEEVQIKAWTDFFRPGKNTYSPFKWHYHFDGADWDESRKISIFKFRGEGK	180	
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Qy 421 KSGLAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
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Db 421 KSGLAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
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Qy 481 VQK 483
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RESULT 2
US-09-918-543-10
; Sequence 10, Application US/09918543
; Patent No. US20020155574A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020155574Alozymes A/S
; APPLICANT: Thisted, Thomas
; APPLICANT: Kjaerulff, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Fuglsang, Claus Crone
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062.200-US
; CURRENT APPLICATION NUMBER: US/09/918.543
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-09-918-543-10

Query Match 100.0%; Score 2638; DB 9; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.5e-238;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
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Qy 61 DLGEFOQKGTVRTKYGTKSELQDAIGSLHSRNVQVGDVVLNKHAGADATEDVTAVERN 120
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Db 61 DLGEFOQKGTVRTKYGTKSELQDAIGSLHSRNVQVGDVVLNKHAGADATEDVTAVERN 120
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Qy 121 ANRNQETSEYQIKAWTDFFPGRGNTYSDPKWHWHYFDGADWDESRKISRIFKFRGEGK 180
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Db 361 VFYGDYMTGKTSPEKIPSLKDNTEPILKARKEYAYGPOHDYIDHPDVIGWTRGDSAA 420
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Db 421 KSGLAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
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Qy 481 VQK 483
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Db 481 VQK 483
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Qy 361 VFYGDYMTGKTSPEKIPSLKDNTEPILKARKEYAYGPOHDYIDHPDVIGWTRGDSAA 420
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Db 421 KSGLAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
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Qy 481 VQK 483
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Db 481 VQK 483
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RESULT 3
US-09-925-576C-10
; Sequence 10, Application US/09925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004.204-US
; CURRENT APPLICATION NUMBER: US/09/925.576C
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-09-925-576C-10

Query Match 100.0%; Score 2638; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.5e-238;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
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Qy 61 DLGEFOQKGTVRTKYGTKSELQDAIGSLHSRNVQVGDVVLNKHAGADATEDVTAVERN 120
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Db 61 DLGEFOQKGTVRTKYGTKSELQDAIGSLHSRNVQVGDVVLNKHAGADATEDVTAVERN 120
|
Qy 121 ANRNQETSEYQIKAWTDFFPGRGNTYSDPKWHWHYFDGADWDESRKISRIFKFRGEGK 180
|
Db 121 ANRNQETSEYQIKAWTDFFPGRGNTYSDPKWHWHYFDGADWDESRKISRIFKFRGEGK 180
|
Qy 181 AWDWEVSSNGNYDYLMTADVDDYDHPDVVAETKKWGIWYANELSLDGFPRIDAACHIKFSF 240
|
Db 181 AWDWEVSSNGNYDYLMTADVDDYDHPDVVAETKKWGIWYANELSLDGFPRIDAACHIKFSF 240
|
Qy 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASSQGG 300
|
Db 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVDFVPLHFNLAQASSQGG 300
|
Qy 301 GYDMRRLDGTGTVSRHPKAVTFVENHDTQPGSLSTVQWTFKPLAYAFILITRESGYPO 360
|
Db 301 GYDMRRLDGTGTVSRHPKAVTFVENHDTQPGSLSTVQWTFKPLAYAFILITRESGYPO 360
|
Qy 361 VFYGDYMTGKTSPEKIPSLKDNTEPILKARKEYAYGPOHDYIDHPDVIGWTRGDSAA 420
|
Db 361 VFYGDYMTGKTSPEKIPSLKDNTEPILKARKEYAYGPOHDYIDHPDVIGWTRGDSAA 420
|
Qy 421 KSGLAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
|
Db 421 KSGLAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
|
Qy 481 VQK 483
|
Db 481 VQK 483
|
```

```
RESULT 4
US-10-146-327-6
; Sequence 6, Application US/10146327
; Publication No. US20030044954A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kiaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/10/146,327
; PRIOR FILING DATE: 2002-05-15
; PRIOR FILING DATE: 2002-05-15
; PRIOR FILING DATE: US/09/537,168
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PA 1999 00437
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/127,427
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-10-146-327-6

Query Match      100.0%; Score 2638; DB 14; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.5e-238;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGLSQSDNGYGPYDLY 60
Qy 61 DLGEFOQKGTVRTKYGTSELDQALGSLHSRNQVYGDVVLNHNKAGADATEDVTAVERN 120
Db 61 DLGEFOQKGTVRTKYGTSELDQALGSLHSRNQVYGDVVLNHNKAGADATEDVTAVERN 120
Qy 121 ANRNETSEBYQIKAWTDFFPPGRGNTYSDPKWHWHYHFDGADWDESKISRIFKFRGEGK 180
Db 121 ANRNETSEBYQIKAWTDFFPPGRGNTYSDPKWHWHYHFDGADWDESKISRIFKFRGEGK 180
Qy 181 AWDWEVSSENGNDYLMYADVVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFSP 240
Db 181 AWDWEVSSENGNDYLMYADVVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFSP 240
Qy 241 LRWDVQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVFDPVPLHFNLAASSQGG 300
Db 241 LRWDVQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVFDPVPLHFNLAASSQGG 300
Qy 301 GYDMRRLDGTWVSRHPEKAVTFVENHDTOPGQSLSTVQTFWPKPLAYAFILITRESGYPQ 360
Db 301 GYDMRRLDGTWVSRHPEKAVTFVENHDTOPGQSLSTVQTFWPKPLAYAFILITRESGYPQ 360
Qy 361 VFYGDYMTGKTSPEKIPSLKDNIEPIILKARKEYAYGQHDYIDHPDVIGWTRGDSAA 420
Db 361 VFYGDYMTGKTSPEKIPSLKDNIEPIILKARKEYAYGQHDYIDHPDVIGWTRGDSAA 420
Qy 421 KSGLAALITDPPGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGGEFHVNDGVSIIY 480
Db 421 KSGLAALITDPPGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGGEFHVNDGVSIIY 480
Qy 481 VQK 483
Db 481 VQK 483

RESULT 5
US-10-146-327-6
; Sequence 6, Application US/10146327
; Publication No. US20030044954A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Jorgensen, Christel T.
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Kiaerulff, Soren
; TITLE OF INVENTION: Alpha-Amylase Variants
; FILE REFERENCE: 5886.200-US
; CURRENT APPLICATION NUMBER: US/10/146,327
; PRIOR FILING DATE: 2002-05-15
; PRIOR FILING DATE: 2002-05-15
; PRIOR FILING DATE: US/09/537,168
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: PA 1999 00437
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 60/127,427
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-10-146-327-6

Query Match      100.0%; Score 2638; DB 14; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.5e-238;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGLSQSDNGYGPYDLY 60
Qy 61 DLGEFOQKGTVRTKYGTSELDQALGSLHSRNQVYGDVVLNHNKAGADATEDVTAVERN 120
Db 61 DLGEFOQKGTVRTKYGTSELDQALGSLHSRNQVYGDVVLNHNKAGADATEDVTAVERN 120
Qy 121 ANRNETSEBYQIKAWTDFFPPGRGNTYSDPKWHWHYHFDGADWDESKISRIFKFRGEGK 180
Db 121 ANRNETSEBYQIKAWTDFFPPGRGNTYSDPKWHWHYHFDGADWDESKISRIFKFRGEGK 180
Qy 181 AWDWEVSSENGNDYLMYADVVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFSP 240
Db 181 AWDWEVSSENGNDYLMYADVVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFSP 240
Qy 241 LRWDVQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVFDPVPLHFNLAASSQGG 300
Db 241 LRWDVQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVFDPVPLHFNLAASSQGG 300
Qy 301 GYDMRRLDGTWVSRHPEKAVTFVENHDTOPGQSLSTVQTFWPKPLAYAFILITRESGYPQ 360
Db 301 GYDMRRLDGTWVSRHPEKAVTFVENHDTOPGQSLSTVQTFWPKPLAYAFILITRESGYPQ 360
Qy 361 VFYGDYMTGKTSPEKIPSLKDNIEPIILKARKEYAYGQHDYIDHPDVIGWTRGDSAA 420
Db 361 VFYGDYMTGKTSPEKIPSLKDNIEPIILKARKEYAYGQHDYIDHPDVIGWTRGDSAA 420
Qy 421 KSGLAALITDPPGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGGEFHVNDGVSIIY 480
Db 421 KSGLAALITDPPGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGGEFHVNDGVSIIY 480
Qy 481 VQK 483
Db 481 VQK 483

RESULT 6
US-10-184-771-4
; Sequence 4, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borcherdt, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
```

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; Sequence 10, Application US/10477725
; Publication No. US20040096952A1
; GENERAL INFORMATION:
; APPLICANT: NOVOZYMES A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Thisted, Thomas
; APPLICANT: von der Osten, Claus
; TITLE OF INVENTION: Alpha-amylase variant with altered properties
; FILE REFERENCE: 10182.204-US
; CURRENT APPLICATION NUMBER: US/10/477,725
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 10
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-10-477-725-10
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Query Match      100.0%; Score 2638; DB 16; Length 483;
Best Local Similarity 100.0%; Pred. No. 2.5e-238;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGLSQSDNGYGPYDLY 60
Qy 61 DLGEFOQKGTVRTKYGTSELDQALGSLHSRNQVYGDVVLNHNKAGADATEDVTAVERN 120
Db 61 DLGEFOQKGTVRTKYGTSELDQALGSLHSRNQVYGDVVLNHNKAGADATEDVTAVERN 120
Qy 121 ANRNETSEBYQIKAWTDFFPPGRGNTYSDPKWHWHYHFDGADWDESKISRIFKFRGEGK 180
Db 121 ANRNETSEBYQIKAWTDFFPPGRGNTYSDPKWHWHYHFDGADWDESKISRIFKFRGEGK 180
Qy 181 AWDWEVSSENGNDYLMYADVVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFSP 240
Db 181 AWDWEVSSENGNDYLMYADVVDYDHPDVVAETKKGWIYANELSLDGFRIIDAAKHIFSP 240
Qy 241 LRWDVQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVFDPVPLHFNLAASSQGG 300
Db 241 LRWDVQAVRQATGKEMFTVAEYQNNAGKLENYLNKTSFNQSVFDPVPLHFNLAASSQGG 300
Qy 301 GYDMRRLDGTWVSRHPEKAVTFVENHDTOPGQSLSTVQTFWPKPLAYAFILITRESGYPQ 360
Db 301 GYDMRRLDGTWVSRHPEKAVTFVENHDTOPGQSLSTVQTFWPKPLAYAFILITRESGYPQ 360
Qy 361 VFYGDYMTGKTSPEKIPSLKDNIEPIILKARKEYAYGQHDYIDHPDVIGWTRGDSAA 420
Db 361 VFYGDYMTGKTSPEKIPSLKDNIEPIILKARKEYAYGQHDYIDHPDVIGWTRGDSAA 420
Qy 421 KSGLAALITDPPGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGGEFHVNDGVSIIY 480
Db 421 KSGLAALITDPPGSKMYAGLKNAGETWYDITGNRSDTVKIGSDGGEFHVNDGVSIIY 480
Qy 481 VQK 483
Db 481 VQK 483
```

```
RESULT 6
US-10-184-771-4
; Sequence 4, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borcherdt, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; CURRENT FILING DATE: 2002-06-28
```

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; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 514
; TYPE: PRT
; ORGANISM: B. amyloliquefaciens
US-10-184-771-4

Query Match          100.0%; Score 2638; DB 14; Length 514;
Best Local Similarity 100.0%; Pred. No. 2.7e-238;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Db 32 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 91
Qy 61 DLGEFQOKGTVRTKYGTGKSELQDAIGSLHSRNVQVGDVVLNKHAGADATEDVTAVEVNP 120
Db 92 DLGEFQOKGTVRTKYGTGKSELQDAIGSLHSRNVQVGDVVLNKHAGADATEDVTAVEVNP 151
Qy 121 ANRQETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYFDGADWDESRKISRIFKFRGEGK 180
Db 152 ANRQETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYFDGADWDESRKISRIFKFRGEGK 211
Qy 181 AWDWEVSSNGNYDYLKADVDYDHPDVVAETKKGWGWYANELSLDGFPRIDAAKHIFKFSF 240
Db 212 AWDWEVSSNGNYDYLKADVDYDHPDVVAETKKGWGWYANELSLDGFPRIDAAKHIFKFSF 271
Qy 241 LRDWQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSPNQSVDFVPLHFNLAQASSQGG 300
Db 272 LRDWQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSPNQSVDFVPLHFNLAQASSQGG 331
Qy 301 GYDMRRLLDGTVVRSHPEKAVTFVENHDTQPGQSLESTVQTFKPLAYAFILTRREGSYPQ 360
Db 332 GYDMRRLLDGTVVRSHPEKAVTFVENHDTQPGQSLESTVQTFKPLAYAFILTRREGSYPQ 391
Qy 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRREGDSSAA 420
Db 392 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRREGDSSAA 451
Qy 421 KSGLAALITDGGSKRMVAGLKNAGETWYDITGNRSNTVKIGSDGWGEFHVNDGVSIIY 480
Db 452 KSGLAALITDGGSKRMVAGLKNAGETWYDITGNRSNTVKIGSDGWGEFHVNDGVSIIY 511
Qy 481 VQK 483
Db 512 VQK 514

RESULT 7
US-09-769-864-5
; Sequence 5, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5

Query Match          99.5%; Score 2624; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 5.1e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Qy 61 DLGEFQOKGTVRTKYGTGKSELQDAIGSLHSRNVQVGDVVLNKHAGADATEDVTAVEVNP 120
Db 61 DLGEFQOKGTVRTKYGTGKSELQDAIGSLHSRNVQVGDVVLNKHAGADATEDVTAVEVNP 120
Qy 121 ANRQETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYFDGADWDESRKISRIFKFRGEGK 180
Db 121 ANRQETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYFDGADWDESRKISRIFKFRGEGK 180
Qy 181 AWDWEVSSNGNYDYLKADVDYDHPDVVAETKKGWGWYANELSLDGFPRIDAAKHIFKFSF 240
Db 181 AWDWEVSSNGNYDYLKADVDYDHPDVVAETKKGWGWYANELSLDGFPRIDAAKHIFKFSF 240
Qy 241 LRDWQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSPNQSVDFVPLHFNLAQASSQGG 300
Db 241 LRDWQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSPNQSVDFVPLHFNLAQASSQGG 300
Qy 301 GYDMRRLLDGTVVRSHPEKAVTFVENHDTQPGQSLESTVQTFKPLAYAFILTRREGSYPQ 360
Db 301 GYDMRRLLDGTVVRSHPEKAVTFVENHDTQPGQSLESTVQTFKPLAYAFILTRREGSYPQ 360
Qy 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRREGDSSAA 420
Db 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRREGDSSAA 420
Qy 421 KSGLAALITDGGSKRMVAGLKNAGETWYDITGNRSNTVKIGSDGWGEFHVNDGVSIIY 480
Db 421 KSGLAALITDGGSKRMVAGLKNAGETWYDITGNRSNTVKIGSDGWGEFHVNDGVSIIY 480

RESULT 8
US-10-665-667-5
; Sequence 5, Application US/10665667
; Publication No. US20040038368A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/10/665,667
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/769,864
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5

Query Match          99.5%; Score 2624; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 5.1e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLY 60
Qy 61 DLGEFQOKGTVRTKYGTGKSELQDAIGSLHSRNVQVGDVVLNKHAGADATEDVTAVEVNP 120
Db 61 DLGEFQOKGTVRTKYGTGKSELQDAIGSLHSRNVQVGDVVLNKHAGADATEDVTAVEVNP 120
Qy 121 ANRQETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYFDGADWDESRKISRIFKFRGEGK 180
Db 121 ANRQETSEBYQIKAWTDFRPPGRGNTYSDFKWHWHYFDGADWDESRKISRIFKFRGEGK 180
Qy 181 AWDWEVSSNGNYDYLKADVDYDHPDVVAETKKGWGWYANELSLDGFPRIDAAKHIFKFSF 240
Db 181 AWDWEVSSNGNYDYLKADVDYDHPDVVAETKKGWGWYANELSLDGFPRIDAAKHIFKFSF 240
Qy 241 LRDWQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSPNQSVDFVPLHFNLAQASSQGG 300
Db 241 LRDWQVAVRQATGKEMFTVAEYQWNNAGKLENLYNKTSPNQSVDFVPLHFNLAQASSQGG 300
Qy 301 GYDMRRLLDGTVVRSHPEKAVTFVENHDTQPGQSLESTVQTFKPLAYAFILTRREGSYPQ 360
Db 301 GYDMRRLLDGTVVRSHPEKAVTFVENHDTQPGQSLESTVQTFKPLAYAFILTRREGSYPQ 360
Qy 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRREGDSSAA 420
Db 361 VFYGDWYGTGTSPEKIPSLKDNIEPILKARKEYAYGPOHDYIDHPDVIGWTRREGDSSAA 420
Qy 421 KSGLAALITDGGSKRMVAGLKNAGETWYDITGNRSNTVKIGSDGWGEFHVNDGVSIIY 480
Db 421 KSGLAALITDGGSKRMVAGLKNAGETWYDITGNRSNTVKIGSDGWGEFHVNDGVSIIY 480
```

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QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIIPPAYKGLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIIPPAYKGLSQSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRTKYGTGKSELQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVEVNP 120
Db 61 DLGEFOQKGTVRTKYGTGKSELQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVEVNP 120
QY 121 ANRNETSEBYQIKAWTDFRPPGRGNTYSDPKWHWHYHFDGADWDESKIRIFKFRGEGK 180
Db 121 ANRNETSEBYQIKAWTDFRPPGRGNTYSDPKWHWHYHFDGADWDESKIRIFKFRGEGK 180
QY 181 AWDWEVSSSENGNDYLMYADVDDHDPVVAETKKGWIWYANELSLDGFRIIDAAKHKFSF 240
Db 181 AWDWEVSSSENGNDYLMYADVDDHDPVVAETKKGWIWYANELSLDGFRIIDAAKHKFSF 240
QY 241 LRDWQAVRQATCKEMFTVAEYQNNAGKLENLYNKTSTFNQSVDFVPLHFNLAASQGG 300
Db 241 LRDWQAVRQATCKEMFTVAEYQNNAGKLENLYNKTSTFNQSVDFVPLHFNLAASQGG 300
QY 301 GYDMRLDGTVVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAYAFILTRSGYPQ 360
Db 301 GYDMRLDGTVVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAYAFILTRSGYPQ 360
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPQHDYIDHPDVIWGTREGDSAA 420
Db 361 VFYGDWYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPQHDYIDHPDVIWGTREGDSAA 420
QY 421 KSGLAALITDPCGSKRMVAGLKNAGETWYDITGNRSDDTVKIGSDGWFHVDGVSIIY 480
Db 421 KSGLAALITDPCGSKRMVAGLKNAGETWYDITGNRSDDTVKIGSDGWFHVDGVSIIY 480
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RESULT 9

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US-10-644-187-4
; Sequence 4, Application US/10644187
; Publication No. US20040048351A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Bisgard-Prantzen, Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/644,187
; PRIOR FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-10-644-187-4
```

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Query Match 99.5%; Score 2624; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 5.1e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIIPPAYKGLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIIPPAYKGLSQSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRTKYGTGKSELQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVEVNP 120
```

```
Db 61 DLGEFOQKGTVRTKYGTGKSELQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVEVNP 120
QY 121 ANRNETSEBYQIKAWTDFRPPGRGNTYSDPKWHWHYHFDGADWDESKIRIFKFRGEGK 180
Db 121 ANRNETSEBYQIKAWTDFRPPGRGNTYSDPKWHWHYHFDGADWDESKIRIFKFRGEGK 180
QY 181 AWDWEVSSSENGNDYLMYADVDDHDPVVAETKKGWIWYANELSLDGFRIIDAAKHKFSF 240
Db 181 AWDWEVSSSENGNDYLMYADVDDHDPVVAETKKGWIWYANELSLDGFRIIDAAKHKFSF 240
QY 241 LRDWQAVRQATCKEMFTVAEYQNNAGKLENLYNKTSTFNQSVDFVPLHFNLAASQGG 300
Db 241 LRDWQAVRQATCKEMFTVAEYQNNAGKLENLYNKTSTFNQSVDFVPLHFNLAASQGG 300
QY 301 GYDMRLDGTVVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAYAFILTRSGYPQ 360
Db 301 GYDMRLDGTVVSRHPEKAVTFVENHDTQPGQSLSTVQTFKPLAYAFILTRSGYPQ 360
QY 361 VFYGDWYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPQHDYIDHPDVIWGTREGDSAA 420
Db 361 VFYGDWYGTGTSPEKIPSLKDNIEPIILKARKEYAYGPQHDYIDHPDVIWGTREGDSAA 420
QY 421 KSGLAALITDPCGSKRMVAGLKNAGETWYDITGNRSDDTVKIGSDGWFHVDGVSIIY 480
Db 421 KSGLAALITDPCGSKRMVAGLKNAGETWYDITGNRSDDTVKIGSDGWFHVDGVSIIY 480
```

RESULT 10

```
US-10-327-837-5
; Sequence 5, Application US/10327837
; Publication No. US20030211958A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Prantzen, Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10/327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 480
; TYPE: PRT
; ORGANISM: B. amyloliquefaciens
US-10-327-837-5
```

```
Query Match 99.5%; Score 2624; DB 12; Length 480;
Best Local Similarity 100.0%; Pred. No. 5.1e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIIPPAYKGLSQSDNGYGPYDLY 60
Db 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVIIPPAYKGLSQSDNGYGPYDLY 60
QY 61 DLGEFOQKGTVRTKYGTGKSELQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVEVNP 120
Db 61 DLGEFOQKGTVRTKYGTGKSELQDAIGSLHSRNVQVYGDVVLNHNKAGADATEDVTAVEVNP 120
QY 121 ANRNETSEBYQIKAWTDFRPPGRGNTYSDPKWHWHYHFDGADWDESKIRIFKFRGEGK 180
Db 121 ANRNETSEBYQIKAWTDFRPPGRGNTYSDPKWHWHYHFDGADWDESKIRIFKFRGEGK 180
QY 181 AWDWEVSSSENGNDYLMYADVDDHDPVVAETKKGWIWYANELSLDGFRIIDAAKHKFSF 240
Db 181 AWDWEVSSSENGNDYLMYADVDDHDPVVAETKKGWIWYANELSLDGFRIIDAAKHKFSF 240
```

QY 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFVPLHFNLOAASSQGG 300
DB 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFVPLHFNLOAASSQGG 300
QY 301 GYDMRRLDGTVVSRHPEKAVTFVFNHDTQPGQSLESTVQWFKPLAYAFILITRESGYPO 360
DB 301 GYDMRRLDGTVVSRHPEKAVTFVFNHDTQPGQSLESTVQWFKPLAYAFILITRESGYPO 360
QY 361 VFYGDYMTGKTSPEIKSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTRGDSAA 420
DB 361 VFYGDYMTGKTSPEIKSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTRGDSAA 420
QY 421 KSLGAAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
DB 421 KSLGAAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480

RESULT 11

US-10-186-042-4
; Sequence 4, Application US/10186042
; Publication No. US20030171236A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 4796.204-US
; CURRENT APPLICATION NUMBER: US/10/186.042
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/672,459
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 09/182,859
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: 0515/96
; PRIOR FILING DATE: 1996-04-30
; PRIOR APPLICATION NUMBER: 0712/96
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 0775/96
; PRIOR FILING DATE: 1996-07-11
; PRIOR APPLICATION NUMBER: 1263/96
; PRIOR FILING DATE: 1996-11-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Bacillus amyloliquefaciens
US-10-186-042-4

Query Match 99.5%; Score 2624; DB 14; Length 480;
Best Local Similarity 100.0%; Pred. No. 5.1e-237;
Matches 480; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVMIPPAYKGLSQSDNGYGYDLY 60
DB 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVMIPPAYKGLSQSDNGYGYDLY 60
QY 61 DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHAGADATEDVTAVERN 120
DB 61 DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHAGADATEDVTAVERN 120
QY 121 ANRNETSEYQIKAWTDFFRPGRGNTYSDFKWHYHFDGADWDESRKISRIFKFRGEGK 180
DB 121 ANRNETSEYQIKAWTDFFRPGRGNTYSDFKWHYHFDGADWDESRKISRIFKFRGEGK 180
QY 181 AWDWEVSSSENGNYDLYMAYADVDDHPDVVAETKKGIWYANELSLDGFPRIDAAKHKPSF 240
DB 181 AWDWEVSSSENGNYDLYMAYADVDDHPDVVAETKKGIWYANELSLDGFPRIDAAKHKPSF 240
QY 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFVPLHFNLOAASSQGG 300
DB 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFVPLHFNLOAASSQGG 300

QY 301 GYDMRRLDGTVVSRHPEKAVTFVFNHDTQPGQSLESTVQWFKPLAYAFILITRESGYPO 360
DB 301 GYDMRRLDGTVVSRHPEKAVTFVFNHDTQPGQSLESTVQWFKPLAYAFILITRESGYPO 360
QY 361 VFYGDYMTGKTSPEIKSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTRGDSAA 420
DB 361 VFYGDYMTGKTSPEIKSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTRGDSAA 420
QY 421 KSLGAAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
DB 421 KSLGAAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480

RESULT 12

US-10-184-771-13
; Sequence 13, Application US/10184771
; Publication No. US20030170769A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 0776/1F216-US2
; CURRENT APPLICATION NUMBER: US/10/184,771
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US/09/636,252
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 08/683,838
; PRIOR FILING DATE: 1996-07-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Bacillus
US-10-184-771-13

Query Match 94.2%; Score 2486; DB 14; Length 483;
Best Local Similarity 93.4%; Pred. No. 4.5e-224;
Matches 451; Conservative 16; Mismatches 16; Indels 0; Gaps 0;
QY 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVMIPPAYKGLSQSDNGYGYDLY 60
DB 1 VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVMIPPAYKGLSQSDNGYGYDLY 60
QY 61 DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHAGADATEDVTAVERN 120
DB 61 DLGEFOQKGTVRTKYGTSELODAIGSLHSRNQVYGDVVLNKHAGADATEDVTAVERN 120
QY 121 ANRNETSEYQIKAWTDFFRPGRGNTYSDFKWHYHFDGADWDESRKISRIFKFRGEGK 180
DB 121 ANRNETSEYQIKAWTDFFRPGRGNTYSDFKWHYHFDGADWDESRKISRIFKFRGEGK 180
QY 181 AWDWEVSSSENGNYDLYMAYADVDDHPDVVAETKKGIWYANELSLDGFPRIDAAKHKPSF 240
DB 181 AWDWEVSSSENGNYDLYMAYADVDDHPDVVAETKKGIWYANELSLDGFPRIDAAKHKPSF 240
QY 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFVPLHFNLOAASSQGG 300
DB 241 LRDWQAVRQATGKEMFTVAEYQWNNAGKLENYLNKTSFNQSVFVPLHFNLOAASSQGG 300
QY 301 GYDMRRLDGTVVSRHPEKAVTFVFNHDTQPGQSLESTVQWFKPLAYAFILITRESGYPO 360
DB 301 GYDMRRLDGTVVSRHPEKAVTFVFNHDTQPGQSLESTVQWFKPLAYAFILITRESGYPO 360
QY 361 VFYGDYMTGKTSPEIKSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTRGDSAA 420
DB 361 VFYGDYMTGKTSPEIKSLKDNIEPILKARKEYAYGPQHDYIDHPDVIGWTRGDSAA 420
QY 421 KSLGAAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480
DB 421 KSLGAAALITDGPGGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWGEFHVNDGVSIIY 480

QY 481 VQK 483
 Db 481 VQR 483

RESULT 13

US-10-146-327-2
 ; Sequence 2, Application US/10146327
 ; Publication No. US20030044954A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Andersen, Carsten
 ; APPLICANT: Jorgensen, Christel T.
 ; APPLICANT: Biegaard-Prantzen, Henrik
 ; APPLICANT: Svendsen, Allan
 ; APPLICANT: Kjaerulf, Soren
 ; FILE REFERENCE: 5886.200-US
 ; CURRENT APPLICATION NUMBER: US/10/146,327
 ; CURRENT FILING DATE: 2002-05-15
 ; PRIOR APPLICATION NUMBER: US/09/537,168
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: PA 1999 00437
 ; PRIOR FILING DATE: 1999-03-30
 ; PRIOR APPLICATION NUMBER: 60/127,427
 ; PRIOR FILING DATE: 1999-04-01
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 481
 ; TYPE: PRT
 ; ORGANISM: Bacillus amyloliquefaciens
 US-10-146-327-2

Query Match 83.4%; Score 2201; DB 14; Length 481;
 Best Local Similarity 81.6%; Pred. No. 2.4e-197;
 Matches 394; Conservative 38; Mismatches 49; Indels 2; Gaps 1;

QY	1	VNGLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGLSQSDNGYGPYDLY	60
Db	1	VNGLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGLSQSDNGYGPYDLY	60
QY	61	DLGEFOQKGTVRTKYGTSGELQDAIGSLHNRNVQVGDVVLNKHAGADATEDVAVENP	120
Db	61	DLGEFHQKGTVRTKYGTSGELQDAIGSLHNRNVQVGDVVLNKHAGADATEDVAVENP	120
QY	121	ANRNOETSEYQIKAWTDREPPGRGNTYSDPKWYHFDGADWDESKISRIEKFGEK	180
Db	121	ADNRVIGSHLLIKAWTHFHPGRGSTYSDPKWYHFDGADWDESKISRIEKFGEK	178
QY	181	AWDWEVSSENGNDYLMYADVDYDHPDVAETKKWGIWYANELSLDGFRIIDAAKHKFSF	240
Db	179	TWDEVSNEFNGNDYLMYADVDYDHPDVAETKKWGIWYANELSLDGFRIIDAAKHKFSF	238
QY	241	LRDWQAVRQATGKEMFTVAEYQNNAGKLENLYNKTSPNQSVDFVPLHFNLAQASQGG	300
Db	239	LROWNVHREKTKEMFTVAEYQNNAGKLENLYNKTSPNQSVDFVPLHFNLAQASQGG	298
QY	301	GYDMRLLDGTVVSRHPEKAVTFVENHDTOPGQSLESTVQTPKPLAYAFILITRESGYPQ	360
Db	299	GYDMRLLDGTVVSRHPEKAVTFVENHDTOPGQSLESTVQTPKPLAYAFILITRESGYPQ	358
QY	361	VFYGDMYGTGKSPKEIPSLKDNIEPIILKARKEVAYGPDHYDHPDVIQWTRGDSAA	420
Db	359	VFYGDMYGTGKSDQREIPALKHKEIPIILKARKEVAYGPDHYDHPDVIQWTRGDSAA	418
QY	421	KSGLAALITDPGSKEMVYAGLNAGETWYDITGNRSDTVKIGSDGWEHFVNDGVSIIY	480
Db	419	NSGLAALITDPGSKEMVYVGRQNAAGETWHDITGNRSEPPVINSEGEHFVNGGVSIIY	478
QY	481	VQK 483	
Db	479	VQR 481	

RESULT 14

US-10-081-872-114
 ; Sequence 114, Application US/10081872
 ; Publication No. US2003012534A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Callen, Walter
 ; APPLICANT: Richardson, Toby
 ; APPLICANT: Frey, Gerhard
 ; APPLICANT: Short, Jay M.
 ; APPLICANT: Mathur, Eric J.
 ; APPLICANT: Gray, Kevin A.
 ; APPLICANT: Kerovuo, Janne S.
 ; APPLICANT: Slupeksa, Malgorzata
 ; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
 ; FILE REFERENCE: 09010-108001
 ; CURRENT APPLICATION NUMBER: US/10/081,872
 ; CURRENT FILING DATE: 2002-02-21
 ; PRIOR APPLICATION NUMBER: US 60/270,495
 ; PRIOR FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: US 60/270,496
 ; PRIOR FILING DATE: 2001-02-21
 ; PRIOR APPLICATION NUMBER: US 60/291,122
 ; PRIOR FILING DATE: 2001-05-14
 ; NUMBER OF SEQ ID NOS: 321
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 114
 ; LENGTH: 512
 ; TYPE: PRT
 ; ORGANISM: Environmental
 US-10-081-872-114

Query Match 83.1%; Score 2193; DB 14; Length 512;
 Best Local Similarity 80.7%; Pred. No. 1.5e-196;
 Matches 390; Conservative 43; Mismatches 48; Indels 2; Gaps 1;

QY	1	VNGLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGLSQSDNGYGPYDLY	60
Db	32	LNGLMQYFEWYTPNDGQHWKRLQNDASAYLAEGITAVWIPPAKGLSQSDNGYGPYDLY	91
QY	61	DLGEFOQKGTVRTKYGTSGELQDAIGSLHNRNVQVGDVVLNKHAGADATEDVAVENP	120
Db	92	DLGEFHQKGTVRTKYGTSGELQDAIGSLHNRNVQVGDVVLNKHAGADATEDVAVENP	151
QY	121	ANRNOETSEYQIKAWTDREPPGRGNTYSDPKWYHFDGADWDESKISRIEKFGEK	180
Db	152	ADNRVIGSHRLIKAWTHFHPGRGSTYSDPKWYHFDGADWDESKISRIEKFGEK	209
QY	181	AWDWEVSSENGNDYLMYADVDYDHPDVAETKKWGIWYANELSLDGFRIIDAAKHKFSF	240
Db	210	AWDWEVSNEFNGNDYLMYADVDYDHPDVAETKKWGIWYANELSLDGFRIIDAAKHKFSF	269
QY	241	LRDWQAVRQATGKEMFTVAEYQNNAGKLENLYNKTSPNQSVDFVPLHFNLAQASQGG	300
Db	270	LROWNVHREKTKEMFTVAEYQNNAGKLENLYNKTSPNQSVDFVPLHFNLAQASQGG	329
QY	301	GYDMRLLDGTVVSRHPEKAVTFVENHDTOPGQSLESTVQTPKPLAYAFILITRESGYPQ	360
Db	330	GYDMRLLDGTVVSRHPEKAVTFVENHDTOPGQSLESTVQTPKPLAYAFILITRESGYPQ	389
QY	361	VFYGDMYGTGKSPKEIPSLKDNIEPIILKARKEVAYGPDHYDHPDVIQWTRGDSAA	420
Db	390	VFYGDMYGTGKSDQREIPALKHKEIPIILKARKEVAYGPDHYDHPDVIQWTRGDSAA	449
QY	421	KSGLAALITDPGSKEMVYAGLNAGETWYDITGNRSDTVKIGSDGWEHFVNDGVSIIY	480
Db	450	NSGLAALITDPGSKEMVYVGRQNAAGETWHDITGNRSEPPVINSEGEHFVNGGVSIIY	509
QY	481	VQK 483	
Db	510	VQR 512	

Search completed: October 7, 2004, 00:57:30
Job time : 54.2274 secs

```
RESULT 15
US-10-105-733-8
; Sequence 8, Application US/10105733
; Publication No. US20030138786A1
; GENERAL INFORMATION:
; APPLICANT: Callen, Walter
; APPLICANT: Richardson, Toby
; APPLICANT: Frey, Gerhard
; APPLICANT: Miller, Carl
; APPLICANT: Kazaoka, Martin
; APPLICANT: Short, Jay
; APPLICANT: Mathur, Eric
; TITLE OF INVENTION: ENZYMES HAVING ALPHA AMYLASE ACTIVITY
; FILE REFERENCE: 09010-107002
; CURRENT APPLICATION NUMBER: US/10/105,733
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 10/081,739
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,495
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/270,496
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/291,122
; PRIOR FILING DATE: 2001-05-14
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 512
; TYPE: PRT
; ORGANISM: Environmental
US-10-105-733-8

Query Match      83.1%; Score 2193; DB 14; Length 512;
Best Local Similarity 80.7%; Pred. No. 1.5e-196;
Matches 390; Conservative 43; Mismatches 48; Indels 2; Gaps 1;

QY 1 VNGTLQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAKGLSQSDNGYGPYDLY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 32 LNGTHQYFEWYTPNDGQHWKRLQNDASAYLAHGITAVWIPPAKGTQADVGYGAYDLY 91
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 DLGEPQOKGTVRTKYGTKELODAIGSLHSRNQVYGDVVLNKHAGADATEDVAVEVNP 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 92 DLGEPHQKGTVRTKYGTKELOSAIKLSHSRDINNVYGDVVINHKGADATEDVAVEVDP 151
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 ANRNQETSEYQIKAWTDFFPGRGNTYSDFKWHWHYHFDGADWDSRKLSRIKFKRGECK 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 152 ADRNRVISGHRIRKAWTHFFPGRGSTYSDFKWHWHYHFDGTDWDSRKLNRIRYKF--QOK 209
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 AWDVEYSSNGNDYDLYMADVDYDHPDVVAETKKGIWYANELSLDGFRIIDAAKHKFSF 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 210 AWDVEYSSNGNDYDLYMADVDYDHPDVVAETKKGIWYANELSLDGFRIIDAAKHKFSF 269
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 LRDWQAVQATQKEMFTVAEYQNNAGKLENLYNKTSPNQSVDFVPLHPNLQAASSQGG 300
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 270 LRDWVNVHREKTKEMFTVAEYQNDLGALENLYNKTSPNQSVDFVPLHPNLQAASSQGG 329
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 301 GYDMRLLDGTWVSRPEKAVTVENHDTQPGQSLESTVQTFWFKPLAYAFILTRSGYPQ 360
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 330 GYDMRLLDGTWVSRPEKAVTVENHDTQPGQSLESTVQTFWFKPLAYAFILTRSGYPQ 389
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 361 VFYGDWYGTGTPKPSIKNDIEPIILKARKEYAGPQHDYIDHPDVIQWTRREGDSSAA 420
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 390 VFYGDWYGTGTPKPSIKNDIEPIILKARKEYAGPQHDYIDHPDVIQWTRREGDSSAA 449
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 421 KSGLAALITDGPQGSKRMVAGLKNAGETWYDITGNRSDTVKIGSDGWFHVNDSVSIY 480
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 450 NSGLAALITDGPQGAARVYVGRQAGETWYDITGNRSDTVKIGSDGWFHVNDSVSIY 509
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 481 VQK 483
Db :|||:|
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:46:32 ; Search time 8.50628 Seconds
(without alignments)
2968.867 Million cell updates/sec

Title: US-09-925-576C-12

Perfect score: 2708

Sequence: 1 HHNGTGTWQYFEWYLPND.....ADGNGFVNGSGSVIWNK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2613	96.5	518	1 AMT6_BACS7	P19571 bacillus sp
2	1887	69.7	512	1 AMY_BACLI	P06278 bacillus li
3	1859.5	68.7	549	1 AMY_BACST	P06279 bacillus st
4	1847	68.2	514	1 AMY_BACAM	P00692 bacillus am
5	1105	40.8	494	1 AMY2_SALTY	P26613 salmonella
6	1075	39.7	495	1 AMY2_ECOLI	P26612 escherichia
7	320	11.8	1196	1 AMYB_PAEPO	P21543 paenibacill
8	283.5	10.5	421	1 AMYA_VIGMU	P17859 vigna mungo
9	270.5	10.0	551	1 AMT4_PBSA	P22963 pseudomonas
10	270	10.0	440	1 AM3A_ORYSA	P27932 oryza sativ
11	267	9.9	548	1 AMT4_PSEST	P33507 pseudomonas
12	264	9.7	368	1 AMY3_HORVU	P04747 hordeum vul
13	263.5	9.7	435	1 AM3D_ORYSA	P27933 oryza sativ
14	262	9.7	427	1 AMY2_HORVU	P04063 hordeum vul
15	259	9.6	719	1 AMYM_BACST	P19531 bacillus st
16	256.5	9.5	428	1 AMY1_ORYSA	P17654 oryza sativ
17	256.5	9.5	438	1 AMY1_HORVU	P00693 hordeum vul
18	254	9.4	429	1 AMY6_HORVU	P04750 hordeum vul
19	253	9.3	437	1 AM3C_ORYSA	P27939 oryza sativ
20	253	9.3	438	1 AM3B_ORYSA	P27937 oryza sativ
21	252.5	9.3	710	1 CDGT_THETU	P26827 thermoanaer
22	250.5	9.3	413	1 AMY3_WHEAT	P08117 triticum ae
23	247.5	9.1	713	1 CDGT_PAEWA	P31835 paenibacill
24	246.5	9.1	498	1 AMYA_ASAPW	Q02905 aspergillus
25	246.5	9.1	499	1 AMYB_ASAPW	Q02906 aspergillus
26	243.5	9.0	499	1 AMYA_ASPOP	P10529 aspergillus
27	243	9.0	437	1 AM3E_ORYSA	P27934 oryza sativ
28	243	9.0	713	1 CDGT_BACSP	P30921 bacillus sp
29	242.5	9.0	442	1 MGTA_THENA	O86956 thermotoga
30	241.5	8.9	718	1 CDGT_BACCI	P30920 bacillus ci
31	240.5	8.9	499	1 AMY ASPSH	P30292 aspergillus
32	240	8.9	528	1 AMY_BACCI	P08137 bacillus ci
33	234	8.6	712	1 CDGT_BACS3	P09121 bacillus sp

RESULT 1
AMT6_BACS7
ID AMT6_BACS7 STANDARD; PRT; 518 AA.
AC P19571;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glucan 1,4-alpha-maltohexaosidase precursor (EC 3.2.1.98) (G6-amylase)
DE (Maltotetraose-producing amylase) (Exo-maltohexaosidase).
OS Bacillus sp. (strain 707).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1416;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-36.
RX MEDLINE=88162814; PubMed=3258152;
RA Takamoto A., Kimura K., Ishii Y., Takano T., Yamane K.;
RT "Nucleotide sequence of the maltotetraose-producing amylase gene from
an alkalophilic Bacillus sp. #707 and structural similarity to
liquefying type alpha-amylases.";
RL Biochem. Biophys. Res. Commun. 151:25-31(1988).
CC -|- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
in amylaceous polysaccharides so as to remove successive
maltotetraose residues from the non-reducing chain ends.
CC -|- COFACTOR: Binds 2 calcium ions and 1 sodium ion per subunit (By
similarity).
CC -|- PATHWAY: Starch degradation.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
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CC -----
CC EMBL: M18862; AAA22231.1; ;
CC PIR: A27705; A27705.
CC HSP: P06278; 1VJS.
CC InterPro: IPR006589; Alp_amy1_cat_sub.
CC InterPro: IPR006047; Alpha_amy1_cat.
CC InterPro: IPR006046; Glyco_hydro_13.
CC Pfam: PF00128; alpha-amylase; 1.
CC PRINTS: PR00110; ALPHAMYLASE.
CC SMART: SM00642; Amy; 1.
CC HydroLase; Glycosidase; Carbohydrate metabolism; Signal.
CC SIGNAL 1 33
CC CHAIN 34 518
CC ACT_SITE 269 269
CC ACT_SITE 273 273
CC ACT_SITE 366 366
CC METAL 139 139
CC METAL 196 196
CC METAL 219 219
CC GLUCAN 1,4-ALPHA-MALTOHEXAOSIDASE.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC CALCIUM 1 (BY SIMILARITY).
CC CALCIUM 2 AND SODIUM (BY SIMILARITY).
CC CALCIUM 2 (VIA CARBONYL OXYGEN) (BY
SIMILARITY).

ALIGNMENTS

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FT METAL          221      221      CALCIUM 2 AND SODIUM (BY SIMILARITY) .
FT METAL          232      232      CALCIUM 1 AND SODIUM (BY SIMILARITY) .
FT METAL          238      238      CALCIUM 1 AND SODIUM (BY SIMILARITY) .
FT METAL          240      240      CALCIUM 2 (BY SIMILARITY) .
FT METAL          242      242      CALCIUM 2 (BY SIMILARITY) .
FT METAL          273      273      CALCIUM 1 (VIA CARBONYL OXYGEN) (BY
SQ SEQUENCE      518 AA; 59009 MW; 3A961E21612682C4 CRC64;

Query Match      96.5%; Score 2613; DB 1; Length 518;
Best Local Similarity 95.5%; Pred. No. 3.9e-168;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDGISAVWTPPPAWKGASQNDVGGA 60
Db 34 HHNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKSGITAVWTPPPAWKGASQNDVGGA 93
Qy 61 YDLVLDGFENKGTIRTKYGTENLOQAVALNALKSGIQVYGDVVMNHKGGADATEMVR 120
Db 94 YDLVLDGFENKGTIRTKYGTENLOQAVALNALKSGIQVYGDVVMNHKGGADATEMVR 153
Qy 121 EVNPNRRNQVSGEYTTIEAWTKFDPGRGNTHSNFKRWYHFDGVDWDQSKLNNRIYKF 180
Db 154 EVNPNRRNQVSGEYTTIEAWTRFDPGRGNTHSNFKRWYHFDGVDWDQSKLNNRIYKF 213
Qy 181 RGDGKGWDWEVDTEGNYDYLIMYADIDMDHPEVNVNLRNNGWVYNTLGLDGFRI 240
Db 214 RGHGKAWDWEVDTEGNYDYLIMYADIDMDHPEVNVNLRNNGWVYNTLGLDGFRI 273
Qy 241 IKYSFTDWINHVRSATGKNWAEVAFKNDLGAENLYNKTWNHSHVDFVPLHLYN 300
Db 274 IKYSFTDWINHVRSATGKNWAEVAFKNDLGAENLYNKTWNHSHVDFVPLHLYN 333
Qy 301 SKSGNGYDMRQIFNGTIVVQHPHMAVTFVDNHDSDPEALESFVEWFKPLAVALTLTRE 360
Db 334 SKSGNGYDMRQIFNGTIVVQHPHMAVTFVDNHDSDPEALESFVEWFKPLAVALTLTRE 393
Qy 361 QGTPSPVGYGYGIPTHGVPAKSKIDPILAEARQKAYGQNDYLDHNNIIGWTREGNTA 420
Db 394 QGTPSPVGYGYGIPTHGVPAKSKIDPILAEARQKAYGQNDYLDHNNIIGWTREGNTA 453
Qy 421 HPNSGLATIMSDGAGGKMWFGVGRNKGQVWTDITGNRAGTGTINADGWNFSVNGSV 480
Db 454 HPNSGLATIMSDGAGGKMWFGVGRNKGQVWTDITGNRAGTGTINADGWNFSVNGSV 513
Qy 481 IWVWK 485
Db 514 IWVWK 518

RESULT 2
ID AMY_BACLI STANDARD; PRT; 512 AA.
AC P06278; O84171.
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase) (BLA).
GN AMYS OR AMYL
OS Bacillus licheniformis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1402;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27811;
RX MEDLINE=86111694; PubMed=2418011;
RA Yuuki T., Nomura T., Tezuka H., Tsuboi A., Yamagata H.,
RA Tsukagoshi N., Uda S.;
RT "Complete nucleotide sequence of a gene coding for heat- and
RT pH-stable alpha-amylase of Bacillus licheniformis: comparison of the
RT amino acid sequences of three bacterial liquefying alpha-amylases
RT deduced from the DNA sequences.";
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RL J. Biochem. 98:1147-1156(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=861195857; PubMed=3009417;
RA Gray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
RA Carmona C., Requadt C.;
RT "Structural genes encoding the thermophilic alpha-amylases of
RT Bacillus stearothermophilus and Bacillus licheniformis.";
RL J. Bacteriol. 166:635-643(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX Shahhosseini M., Ziaei A.A., Ghaemi N., Pourbabeai A.A.;
RT "An unusual DNA sequence encoded a hyperthermostable alpha-amylase.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-104 FROM N.A.
RX MEDLINE=84185455; PubMed=6609154;
RA Stephens M.A., Orlepp S.A., Ollington J.F., McConnell D.J.;
RT "Nucleotide sequence of the 5' region of the Bacillus licheniformis
RT alpha-amylase gene: comparison with the B. amyloliquefaciens gene.";
RL J. Bacteriol. 158:369-372(1984).
RN [5]
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=89213924; PubMed=2540150;
RA Laoide B.M., Chambliss G.H., McConnell D.J.;
RT "Bacillus licheniformis alpha-amylase gene, amyl, is subject to
RT promoter-independent catabolite repression in Bacillus subtilis.";
RL J. Bacteriol. 171:2435-2442(1989).
RN [6]
RP SEQUENCE OF 30-47.
RX MEDLINE=82098050; PubMed=6172418;
RA Kuhn H., Fietzek P.P., Lampen J.O.;
RT "N-terminal amino acid sequence of Bacillus licheniformis
RT alpha-amylase: comparison with Bacillus amyloliquefaciens and
RT Bacillus subtilis enzymes.";
RL J. Bacteriol. 149:372-373(1982).
RN [7]
RP MAPPING OF SUBSTRATE-BINDING SITE.
RX MEDLINE=2192788; PubMed=11997021;
RA Kandra L., Gyemant G., Remenyik J., Hovanszki G., Liptak A.;
RT "Action pattern and subsite mapping of Bacillus licheniformis
RT alpha-amylase (BLA) with modified maltooligosaccharide substrates.";
RL FEBS Lett. 518:79-82(2002).
RN [8]
RP MUTAGENESIS OF HIS-64; HIS-162; HIS-276; HIS-322; HIS-435 AND HIS-479.
RC STRAIN=ATCC 6598;
RX MEDLINE=90368748; PubMed=2394736;
RA Declerck N., Joyet P., Gaillardin C., Masson J.M.;
RT "Use of amber suppressors to investigate the thermostability of
RT Bacillus licheniformis alpha-amylase. Amino acid replacements at 6
RT histidine residues reveal a critical position at His-133.";
RL J. Biol. Chem. 265:15481-15488(1990).
RN [9]
RP MUTAGENESIS OF ALA-238.
RC STRAIN=ATCC 6598;
RX MEDLINE=96367070; PubMed=8771184;
RA Declerck N., Joyet P., Trosset J.Y., Garnier J., Gaillardin C.;
RT "Hyperthermostable mutants of Bacillus licheniformis alpha-amylase:
RT multiple amino acid replacements and molecular modelling.";
RL Protein Eng. 8:1029-1037(1995).
RN [10]
RP MUTAGENESIS OF ASP-150; ASN-155; ARG-175; ASP-193; ASN-201; GLN-207;
RX ASN-217; ASN-219; ASN-221; ASP-229; ASP-233; ALA-298; GLN-300; GLN-359
RN AND GLU-365.
RC STRAIN=ATCC 6598;
RX MEDLINE=20425100; PubMed=10966804;
RA Declerck N., Machius M., Wiegand G., Huber R., Gaillardin C.;
RT "Probing structural determinants specifying high thermostability in
RT Bacillus licheniformis alpha-amylase.";
RL J. Mol. Biol. 301:1041-1057(2000).
RN [11]
RP MUTAGENESIS OF GLN-293 AND ASN-294.
RC STRAIN=ATCC 6598;
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RX MEDLINE=22622182; PubMed=12736372;
RA Declerck N., Machius M., Joyet P., Wiegand G., Huber R.,
RA Gaillardin C.;
RT "Hyperthermostabilization of Bacillus licheniformis alpha-amylase and
RL modulation of its stability over a 50 degrees C temperature range.";
RL Protein Eng. 16:287-293(2003).
RN [12]
RP MUTAGENESIS OF TRP-292 AND VAL-315.
RC STRAIN=ATCC 27811;
RX MEDLINE=22797417; PubMed=12915728;
RA Rivera M.H., Lopez-Munguia A., Soberon X., Saab-Rincon G.;
RT "Alpha-amylase from Bacillus licheniformis mutants near to the
RT catalytic site: effects on hydrolytic and transglycosylation
RT activity";
RL Protein Eng. 16:505-514(2003).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RC STRAIN=ATCC 27811;
RX MEDLINE=95182462; PubMed=7877175;
RA Machius M., Wiegand G., Huber R.;
RT "Crystal structure of calcium-depleted Bacillus licheniformis alpha-
RT amylase at 2.2-A resolution.";
RL J. Mol. Biol. 246:545-559(1995).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=98212915; PubMed=9551551;
RA Machius M., Declerck N., Huber R., Wiegand G.;
RT "Activation of Bacillus licheniformis alpha-amylase through a
RT disorder-->order transition of the substrate-binding site mediated
RT by a calcium-sodium-calcium metal triad.";
RL Structure 6:281-292(1998).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 330-512.
RX MEDLINE=20384196; PubMed=10924103;
RA Brzozowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,
RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
RT "Structural analysis of a chimeric bacterial alpha-amylase.
RT High-resolution analysis of native and ligand complexes.";
RL Biochemistry 39:9099-9107(2000).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF MUTANT
RH162V/N219F/A238V/Q293S/N294Y.
RC STRAIN=ATCC 6598;
RX MEDLINE=22538505; PubMed=12540849;
RA Machius M., Declerck N., Huber R., Wiegand G.;
RT "Kinetic stabilization of Bacillus licheniformis alpha-amylase through
RT introduction of hydrophobic residues at the surface.";
RL J. Biol. Chem. 278:11546-11553(2003).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- BIOTECHNOLOGY: Used in the food industry for high temperature
CC liquefaction of starch-containing mashes and in the detergent
CC industry to remove starch. Sold under the name Termamyl by
CC Novozymes.
CC -1- MISCELLANEOUS: Able to work at relatively high (alkaline) pH
CC values (up to pH 11) and at high temperatures (up to 100 degrees
CC Celsius).
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC EMBL; X03236; CAA26981.1; -;
CC EMBL; M38570; AAA22226.1; -;
CC EMBL; M13256; AAA22240.1; -;
CC EMBL; K01984; AAA22193.1; -;

DR EMBL; AF438149; AAO26743.1; -;
DR EMBL; M26412; AAA22237.1; -;
DR EMBL; A17930; CAA01355.1; -;
DR PIR; A91997; ALBSL.
DR PDB; 1BL1; 23-MAR-99.
DR PDB; 1BPL; 17-AUG-96.
DR PDB; 1E3X; 21-JUN-01.
DR PDB; 1E3Z; 24-JUN-03.
DR PDB; 1E40; 24-JUN-03.
DR PDB; 1E43; 21-JUN-01.
DR PDB; 1E44; 03-APR-03.
DR PDB; 1VJ5; 12-MAR-97.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Aamy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
FT SIGNAL; 1 29
FT CHAIN; 30 512
FT ACT_SITE; 260 260
FT ACT_SITE; 264 264
FT ACT_SITE; 357 357
FT METAL; 133 133
FT METAL; 190 190
FT METAL; 210 210
FT METAL; 212 212
FT METAL; 223 223
FT METAL; 229 229
FT METAL; 231 231
FT METAL; 233 233
Query Match 69.7%; Score 1887; DB 1; Length 512;
Best Local Similarity 68.0%; Pred. No. 1.9e-119;
Matches 330; Conservative 69; Mismatches 76; Indels 10; Gaps 4;
QY 6 NGTMQYFEWYLPDNGNHNRLSDASNLKDGISAVIPPAWKGASQNDVGYGAYDLYD 65
DB 33 NGTLMQYFEWYMPDNGQHWKRLQND SAYLAEGHGTAVWIPPAWKGTSQADVGYGAYDLYD 92
QY 66 LGFENQKGIIRTKYGTNRNQLQAAVNAKNSGIQVGVVNVHKGSGADATEVPAVEVNP 125
DB 93 LGFHHQKGTVRTKYGTKEGLOSAIKSLHSDINNVYGVVNVHKGSGADATEDVTAVEVDP 152
QY 126 NRNOEVSGETTIEATWTKFDPGGRNTHSNFKRWYHFDGVVDQSRKLNRIYKFRGDGK 185
DB 153 DRNRVSGEHRKAWTHFFPGRGSTYSDFKWHYHFDGTDWDESKL-NRIYKFO--GK 209
QY 186 GWDVEYDTENGNDYLYMYADIDMDHPEVNVNELRNWGVYNTTGLDGFRIIDAVKHKYSF 245
DB 210 AWDWEVSNENGNDYLYMYADIDYDHPDVAAEIKRWGTWYANELLQDGFRLDAVKHKFSF 269
QY 246 TRWINHVRSATGNMPFAVAFWKNLDGALNTYLNKTNWHSVDFVPLHNLNASKSGG 305
DB 270 LRDWVAHVREKTKEMFTVAEYQWQNDLGALNTYLNKTNHNSVDFVPLHYQFHAASQGG 329
QY 306 NYDMRQIFNGTVVQRHPMHAFTFVDNHDSDPERALESFVEEWFKPLAYALTLTREOGYPS 365
DB 330 GYDMRKLNTSVVSKHKLKAVTFVDNHDTPQGSLSTVQTWPKPLAYAILFTRESGPQ 389
QY 366 VFYGDYVGIPTHG-----VPAMSKIDPILAEARKYAYGRQNDYLDHNNIIGTREGNTA 420
DB 390 VFYGDYWG--TKGDSQREIPALAKHIEPILKARKQYAGYQHDYFDHHDVGVGTREGDSS 447
QY 421 HPNSGLATINSDGAGGNKMFVGRNKGQVWTDITGNRAGTGTINADGWGNFVNGSGVS 480
DB 448 VANSGLAALITDGPGGAKRMVYGRQNAGETWHDITGNRSPVNVINSGEGFHVNGSGVS 507
QY 481 IWNK 485
DB 508 IYVQR 512

Db 159 DRNOEISGTYQIQAWTKDFPGNGTYSYFKRWYHFDGVDWDESRKL-SRIYKFRGIGK 217
 Qy 186 GWDEWEDTENGNDYLYADIDMDHPEVNNELNNGWVYNTLGLDGRIDAVKHKIKYSP 245
 Db 218 AWDWEVDTEGNDYLYADIDMDHPEVNNELNNGWVYNTLGLDGRIDAVKHKIKYSP 277
 Qy 246 TRDWINHVRATGKNNPFAVAFKNDLGAENYLNKTNWHSVDFVPLHNLNASKSGG 305
 Db 278 FPDWLSDRVSQTKPLFTVGEYWSYDINKLHNTKMTNGTMSLFDAPLHKNKFTASKSGG 337
 Qy 306 NYDMROIFENGTVVQRHPHMAVTVDNHDSDPEBALESFVEWFKPLAYALTLTREQGYPS 365
 Db 338 TFDRLTMTLWKDQPTLAVTFVDNHDTEPGQALQSWDFWFKPLAYALTLTREQGYPC 397
 Qy 366 VFYGDYVIGTHGVPAWKSKIDPILKARQYAGRQNDYLDHNNIIGTREGNTAHNSG 425
 Db 398 VFYGDYVIGTHGVPAWKSKIDPILKARQYAGRQNDYLDHNNIIGTREGNTAHNSG 457
 Qy 426 LATIMSDGAGNKMVGRNKAQGVWTDITGNRAGVTINADGKNFVNGSGSVSIWV 483
 Db 458 LAALITDGPCKSMYVKGQHAGKFYDLTCNRSDDTITNSDQWGEKVGNGSGSVSVWV 515

RESULT 4

AMY BACAM STANDARD; PRT; 514 AA.
 ID AMY BACAM
 AC P00692;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
 DE glucanohydrolase).
 OS Bacillus amyloliquefaciens.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1390;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IH;
 RX MEDLINE=83108808; PubMed=6185474;
 RA Takkinen K., Pettersson R.F., Kalkkinen N., Palva I., Soederlund H.,
 RA Kaeeriaeinen L.;
 RT "Amino acid sequence of alpha-amylase from Bacillus amyloliquefaciens
 RT deduced from the nucleotide sequence of the cloned gene.";
 RL J. Biol. Chem. 258:1007-1013(1983).
 RN [2]
 RP SEQUENCE OF 32-222.
 RX MEDLINE=80241725; PubMed=6156671;
 RA Chung H.S., Friedberg F.;
 RT "Sequence of the N-terminal half of Bacillus amyloliquefaciens alpha-
 RT amylase.";
 RL Biochem. J. 185:387-395(1980).
 RN [3]
 RP SEQUENCE OF 1-96 FROM N.A.
 RX MEDLINE=82051296; PubMed=6170539;
 RA Palva I., Pettersson R.F., Kalkkinen N., Lehtovaara P., Sarvas M.,
 RA Soederlund H., Takkinen K., Kaeeriaeinen L.;
 RT "Nucleotide sequence of the promoter and NH2-terminal signal peptide
 RT region of the alpha-amylase gene from Bacillus amyloliquefaciens.";
 RL Gene 15:43-51(1981).
 RN [4]
 RP SEQUENCE OF 1-39 FROM N.A.
 RX MEDLINE=88137952; PubMed=2830166;
 RA Ruchonen L., Hackman P., Lehtovaara P., Knowles J.K.C., Karaenen S.;
 RT "Efficient secretion of Bacillus amyloliquefaciens alpha-amylase by
 RT its own signal peptide from Saccharomyces cerevisiae host cells.";
 RL Gene 59:161-170(1987).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-331.
 RX MEDLINE=20384196; PubMed=10924103;
 RA Brzozowski A.M., Lawson D.M., Turkenburg J.P., Bisgaard-Frantzen H.,
 RA Svendsen A., Borchert T.V., Dauter Z., Wilson K.S., Davies G.J.;
 RT "Structural analysis of a chimeric bacterial alpha-amylase."

RT High-resolution analysis of native and ligand complexes.";
 RL Biochemistry 39:9099-9107(2000).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC -1- COFACTOR: Binds 3 calcium ions and 1 sodium ion per subunit.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC
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 CC EMBL; J01542; AAA22191.1; -;
 CC EMBL; V00092; CAA23430.1; -;
 CC EMBL; A20154; CAA01489.1; -;
 CC EMBL; M18424; AAA22192.1; -;
 CC PIR; A92389; ALESN.
 CC PDB; 1E3X; 21-JUN-01.
 CC PDB; 1E3Z; 24-JUN-03.
 CC PDB; 1E40; 24-JUN-03.
 CC PDB; 1E43; 21-JUN-01.
 CC InterPro; IPR006589; Alp_aml_cat_sub.
 CC InterPro; IPR006047; Alpha_aml_cat.
 CC InterPro; IPR006046; Glyco_hydro_13.
 CC Pfam; PF00128; alpha-amylase; 1.
 CC PRINTS; PR00110; ALPHAAMYLASE.
 CC SMART; SM00842; Aamy; 1.
 CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 CC Signal; 3D-structure.
 FT SIGNAL 1 31
 FT CHAIN 32 514 ALPHA-AMYLASE.
 FT ACT_SITE 262 262
 FT ACT_SITE 292 292
 FT ACT_SITE 359 359
 FT METAL 133 133
 FT METAL 190 190
 FT METAL 212 212
 FT METAL 214 214
 FT METAL 225 225
 FT METAL 231 231
 FT METAL 233 233
 FT METAL 235 235
 FT METAL 266 266
 FT METAL 331 331
 FT METAL 438 438
 FT METAL 461 461
 FT CONFLICT 54 54 L -> I (IN REF. 2).
 FT CONFLICT 64 64 I -> L (IN REF. 2).
 FT CONFLICT 79 79 S -> D (IN REF. 2).
 FT CONFLICT 84 84 G -> S (IN REF. 2).
 SQ SEQUENCE 514 AA; 58403 MW; 3DE66B3FB5CCDE7E CRC64;
 Query Match 68.2%; Score 1847; DB 1; Length 514;
 Best Local Similarity 66.2%; Pred. No. 9.2e-117;
 Matches 323; Conservative 69; Mismatches 88; Indels 8; Gaps 3;
 Qy 3 NGTNGTMMQYFEWYLPNDGNHNNRLRSADSNLKDGI SAVWIPPAWKASQNDVGYGAYD 62
 Db 30 SAVNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAWIPPAWKGLSQNDVGYGAYD 89
 Qy 63 LYDLGFNQKGTIRTKYGRNQLQAAVNAKLSNGIQVYGVGVNHNKGGADATEWRAVEV 122
 Db 90 LYDLGFQKGTIRTKYGRNQLQAAVNAKLSNGIQVYGVGVNHNKGGADATEWRAVEV 149
 Qy 123 NPNNRQVSGEYTIENATWTKDFPGRGNTNHSNFKRWYHFDGVDWDSRKLNNRYKFRG 182
 Db 150 NPNNRQVSGEYTIENATWTKDFPGRGNTNHSNFKRWYHFDGVDWDSRKLNNRYKFRG 208

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QY 183 DKGWDEVDTEGNGYDLYMADIMDHPEVNVNLRNKGWVWYTYTLGLDGFRIIDAVKHK 242
Db 209 EGKAWDEVSSENGYDLYMADYDHPDVAETKKWGIWYANELSDGFRIDAAKHK 268
QY 243 YSFTRDWNHVRSATGKMPAVAFWKNLDLGAENLYNKTNNHNSVDFDPLHLYNASK 302
Db 269 FSLRDLVQVQATGEMFTVAEYQNNACKJENLYNKTNSFNQSVDFDPLHFLQASS 328
QY 303 SGGNYDRQIFNGTVQVRPHMAVTFVDNHDSPQEEALESFVEEWFKPLAYALTLTREQ 362
Db 329 QGGYDMLRLDGTVSRHPEKAVTFVENHDTQPGQSLESTVQVTFKPLAYALTLTREQ 388
QY 363 YPSVFYGDYGIPTHG-----VPAMKSKIDIPLEARKOYAYGRQNDYLDHNNIIGWTREG 417
Db 389 YPOVFYGDYMG--TKGTSPEKIPSLKDNIEILKARKEYAYGPOHDYIDHPVIGWTREG 446
QY 418 NTAHPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGVTNINADGWNFSVNGG 477
Db 447 DSSAAKSGLAALITDGPQSGKRYTAGLNAGETWYDITGNRSDTVKTGSDGWFHVNNDG 506
QY 478 SVSIWVKNK 485
Db 507 SVSIYVQK 514

RESULT 5
AMY2_SALTY
ID _AMY2_SALTY STANDARD; PRT; 494 AA.
AC P26613;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amyase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE glucanohydrolase).
GN AMYA OR STM1963
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=SW1103;
RX MEDLINE=93015717; PubMed=1400215;
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amyase, AmyA.";
RL J. Bacteriol. 174:6644-6652(1992).
[2]
RN SEQUENCE FROM N.A.
RC STRAIN=L72 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT L72.";
RL Nature 413:852-856(2001).
[3]
RN SEQUENCE OF 1-6 FROM N.A.
RC STRAIN=SW1103;
RX MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes.";
RL J. Gen. Microbiol. 138:1051-1065(1992).
[4]
RN SEQUENCE OF 476-494 FROM N.A.
RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIa and IIib, including a
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RT large non-coding region.";
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -I- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -I- SUBUNIT: Monomer (By similarity).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
-----
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CC
DR EMBL; L01643; AAA27110.1; -.
DR EMBL; AB008787; AAL20875.1; -.
DR EMBL; M85241; AAA27079.1; -.
DR EMBL; L13280; AAA1970.1; -.
DR PIR; B45738; B45738.
DR KSSP; P06278; 1VJS.
DR StyGene; SGI0011; amyA.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR Pfam; PF00128; alpha-amyase; 1.
DR SMART; SM00642; Aamy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Complete proteome.
FT ACT_SITE 235 235 BY SIMILARITY.
FT ACT_SITE 265 265 BY SIMILARITY.
FT ACT_SITE 332 332 BY SIMILARITY.
FT METAL 104 104 CALCIUM (BY SIMILARITY).
FT METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
FT SIMILARITY).
FT CONFLICT 462 462 L -> S (IN REF. 1).
SQ SEQUENCE 494 AA; 56522 MW; 5C1E862FEDD5E47C CRC64;
Query Match 40.8%; Score 1105; DB 1; Length 494;
Best Local Similarity 44.1%; Pred. No. 5.1e-67;
Matches 217; Conservative 77; Mismatches 180; Indels 18; Gaps 6;
QY 6 NCTMQLQYFEWYLPNDGNHNRLRSDASNLKDKGISAVMIPPAWKASQNDVYGYAYDIY 64
Db 3 NPTLLQYFHWYYPDGGKLSWSELAERADGLNDIGINMWLPPACKGASGGYSGYDYDILF 62
QY 65 DLGEFNQKGTIRTKYGTNRNQLQAANVALKSNQIQYGVDMVNMHKGADATMVAVEVNP 124
Db 63 DLGEFDQKGTATKYGDKRQLLTALDAKKNIAVLDDVVVNMHKGADAKERIRVQRVNO 122
QY 125 NNRNDEVSGEYTIKAWTKFDPGRGNTHSNKRWYHFGVDVMDOSRKLNNRIYKFRGD- 183
Db 123 DRTQIDNNIIECEGWTRTFPARAGQSNFVWDHCFSGDHIENPD-EDGIFKIVNDY 181
QY 184 -GKGWDEVDTEGNGYDLYMADIMDHPEVNVNLRNKGWVWYTYTLGLDGFRIIDAVKHK 242
Db 182 TGDGNNDQVDDMGNFYDLNGENIDFRNHAVTTEIKYWARWVMEQTHCDGFLDAVKHIP 241
QY 243 YSFTRDWNHVRSATGKMPAVAFWKNLDLGAENLYNKTNNHNSVDFDPLHLYNASK 302
Db 242 AMFYKEWIEHVAQVAPKPLFIVAETWSHEVDKLTQYIDQVKGKTLWFLDAPLQMKFEASR 301
QY 303 SGGNYDRQIFNGTVQVRPHMAVTFVDNHDSPQEEALESFVEEWFKPLAYALTLTREQ 362
Db 302 QGAETDMRHIFFTGLVLEADPFHATLVANHDTPQALQALQALQALQALQALQALQAL 361
QY 363 YPSVFYGDYGIPTH-----GVPAMKSKIDIPLEARKOYAYGRQNDYLDHNNI 411
Db 362 VPSVFYDLYGASVEDSGENGETCRDMPVI-NQLDLILARQFAHGIQTLFFDHPNCI 420
QY 412 GWTREGNTAHPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGVTNINADGWN 471
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Db 421 AFSRSGTEENP--GCVVVLSNGDDGKTKLLGLDGNVANKTWDRDFLGNRDEYVVVWTDQGEAT 478
Qy 472 FSVNGGVSIVW 483
Db 479 FFCNAGSVSVW 490

RESULT 6
ID AMY2 ECOLI STANDARD; PRT; 495 AA.
AC P26612; P78072;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytoplasmic alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
DE Glucanohydrolase).
GN AMYA OR B1927.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JALL;
RX MEDLINE=93015717; PubMed=1400215;
RA Raha M., Kawagishi I., Mueller V., Kihara M., Macnab R.M.;
RT "Escherichia coli produces a cytoplasmic alpha-amylase, AmyA."
RL J. Bacteriol. 174:6644-6652(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayaishi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitagawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampaio G., Seki Y., Sivasubramanian S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-Kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map."
RL DNA Res. 3:379-392(1996).
RN [4]
RP SEQUENCE OF 1-5 FROM N.A.
RC STRAIN=JALL;
RX MEDLINE=92407478; PubMed=1527488;
RA Kawagishi I., Mueller V., Williams A.W., Irikura V.M., Macnab R.M.;
RT "Subdivision of flagellar region III of the Escherichia coli and
RT Salmonella typhimurium chromosomes and identification of two
RT additional flagellar genes."
RL J. Gen. Microbiol. 138:1051-1065(1992).
RN [5]
RP SEQUENCE OF 475-495 FROM N.A.
RC STRAIN=JALL;
RX MEDLINE=93381452; PubMed=8371104;
RA Raha M., Kihara M., Kawagishi I., Macnab R.M.;
RT "Organization of the Escherichia coli and Salmonella typhimurium
RT chromosomes between flagellar regions IIIa and IIIb, including a
RT large non-coding region."
RL J. Gen. Microbiol. 139:1401-1407(1993).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).

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CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC EMBL; L01642; AAA23810.1; --
CC EMBL; AE000285; AAC74994.1; --
CC EMBL; D90833; BAA15755.1; --
CC EMBL; M85240; -- NOT ANNOTATED_CDS.
CC EMBL; L13279; AAA82575.1; --
CC PIR; D64956; AA45738.
CC HSP; P06278; 1VJS.
CC EcoGene; EG11387; amyA.
CC InterPro; IPR006589; Alp_amy1_cat_sub.
CC InterPro; IPR006047; Alpha_amy1_cat.
CC Pfam; PF001128; alpha-amylase; 1.
CC SMART; SM00642; Amy; 1.
CC Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
CC Complete proteome.
CC ACT_SITE 235 235 BY SIMILARITY.
CC ACT_SITE 265 265 BY SIMILARITY.
CC ACT_SITE 332 332 BY SIMILARITY.
CC METAL 104 104 CALCIUM (BY SIMILARITY).
CC METAL 239 239 CALCIUM (VIA CARBONYL OXYGEN) (BY
CC SIMILARITY).
CC CONFLICT 19 20 KL -> SS (IN REF. 1).
CC CONFLICT 109 109 A -> V (IN REF. 1).
CC CONFLICT 149 149 Q -> E (IN REF. 1).
CC CONFLICT 234 234 L -> I (IN REF. 1).
CC SEQUENCE 495 AA; 56639 MW; 26AF6797DDA54D6 CRC64;

Query Match 39.7%; Score 1075; DB 1; Length 495;
Best Local Similarity 43.7%; Pred. No. 5.3e-65;
Matches 215; Conservative 76; Mismatches 183; Indels 18; Gaps 6;

Qy 6 NGTMMQYFEWYLPNDGNHNNRLSDASNLKDKGISAVWIPAMKGSQN-DVGVGVDLY 64
Db 3 NPTLLQCFHWYEGGKLPPELAERADGFDIGINMVLPPAYKAGSGVSGVSYDLF 62
Qy 65 DLGEFNOKGIRTKYGRNQLQAVALKSGNGIQVYGDVVMNHKGADATAMVRAVWNP 124
Db 63 DLGEFDQKSGIPKYGDKAQLLAIDALKRNDIAVLDDVVVNHKGADAKEAIRVQRVA 122
Qy 125 NNRNQVSGEYTIETATKFPDPPGGRNTHSNFKRWYHFDGVDWDQSKLNRIYKFRGD- 183
Db 123 DDRQTDEIEICEGWTRYTFPARAGQYSQFIWDFKCFSGIDHNPED-EDGIFKIVNDY 181
Qy 184 -GKGWDEVDTEGNYDYLNAVADIMDHPVVELRNWGVYNTLGLDGRIDAVKHK 242
Db 182 TGEWMDQDDDELGNFDYLMGENIDFRNHAFTBEIKYWARWVMEQTCDCGFRLDVAVHIP 241
Qy 243 YSFTRDWINHVRSGATGNMFAVAFKNDLGAENLKNKNHNSVDFDVLHVNLYNASK 302
Db 242 AWFYKEWIEHVQVAPKPLFIVAEYWSHEVDKLTQYIDQVEGKTMLEFAPLQMKFHEASR 301
Qy 303 SGNGYDMRQIFNGTVQVRPHMAVTFVDNHDSPPEALESFVEWFKPLAYALTLTREQ 362
Db 302 MGRDYDMTQIFTGTLEADPFHATVTLVANHDTPQLALEAPVEPWFKPLAYALTLLRENG 361
Qy 363 YPSVFYGDYGIPTGV-----PAMSKIDIPLEARKQYACRQNDYLDHNNII 411
Db 362 VPSVFYDLYGAHYEDVGGDQYTPIDMPTIIB-QLDELILARQRFARHGVQTLFDFHNPNCI 420
Qy 412 GWTREGNTAHPSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGVTVINADGWN 471
Db 421 AFSRSGTDEFP--GCVVVNSNGDDGKTKLLGLDGNVANKTWDRDFLGNRDEYVVVWTDQGEAT 478

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QY 472 ESVNGGVSIVW 483
Db 479 FFCNGGVSIVW 490

RESULT 7
AMVB PAEPO
ID AMVB PAEPO STANDARD; PRT; 1196 AA.
AC F21543;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 15-MAY-2004 (Rel. 43, Last annotation update)
DE Beta/alpha-amylase precursor [includes: Beta-amylase (EC 3.2.1.2);
Alpha-amylase (EC 3.2.1.1)].
OS Paenibacillus polymyxa (Bacillus polymyxa).
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
OX NCBI_TaxID=1406;
RN [1]
RP SEQUENCE OF 1-936 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=87165765; PubMed=2435707;
RA Kawazu T., Nakanishi Y., Uozumi N., Sasaki T., Yamagata H.,
TSukagoshi N., Uda S.;
RT "Cloning and nucleotide sequence of the gene coding for enzymatically
active fragments of the Bacillus polymyxa beta-amylase.";
RL J. Bacteriol. 169:1564-1570(1987).
RN [2]
RP SEQUENCE OF 689-1196 FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=72;
RX MEDLINE=89123046; PubMed=2464578;
RA Uozumi N., Sakurai K., Sasaki T., Takekawa S., Yamagata H.,
TSukagoshi N., Uda S.;
RT "A single gene directs synthesis of a precursor protein with beta-
and alpha-amylase activities in Bacillus polymyxa.";
RL J. Bacteriol. 171:375-382(1989).
RN [3]
RP SEQUENCE OF 1-776 FROM N.A.
RC STRAIN=ATCC 8523;
RX MEDLINE=87231094; PubMed=2438660;
RA Rhodes C., Strasser J., Friedberg F.;
RT "Sequence of an active fragment of B. polymyxa beta amylase.";
RL Nucleic Acids Res. 15:3934-3934(1987).
RN [4]
RP DISULFIDE BOND, AND MUTAGENESIS OF CYSTEINE RESIDUES.
RX MEDLINE=91215008; PubMed=1827035;
RA Uozumi N., Matsuda T., Tsukagoshi N., Uda S.;
RT "Structural and functional roles of cysteine residues of Bacillus
polymyxa beta-amylase.";
RL Biochemistry 30:4594-4599(1991).
CC -!- FUNCTION: THE PRECURSOR PROTEIN IS PROTEOLYTICALLY CLEAVED TO
PRODUCE MULTIFORM BETA-AMYLASES AND A 48 Kda ALPHA-AMYLASE AFTER
SECRETION.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-glucosidic linkages in
polysaccharides so as to remove successive maltose units from the
non-reducing ends of the chains.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
linkages in oligosaccharides and polysaccharides.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: In the N-terminal section; belongs to family 14 of
glycosyl hydrolases.
CC -!- SIMILARITY: In the C-terminal section; belongs to family 13 of
glycosyl hydrolases.
CC
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CC
CC EMBL; M15817; AAA85446.1; -.
CC EMBL; Y00150; CAA68344.1; -.

DR PIR; A29130; A29130.
DR HSPP; P36924; 1B9Z.
DR InterPro; IPR006589; Alp_amyl_cat_sub.
DR InterPro; IPR006048; Alpha_amyl_C.
DR InterPro; IPR006047; Alpha_amyl_cat.
DR InterPro; IPR005085; CBM_25.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR001554; Glyco_hydro_14.
DR Pfam; PF00128; alpha-amylase_1_1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF03423; CBM_25; 2.
DR Pfam; PF01373; Glyco_hydro_14; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR PRINTS; PR00750; BETAAMYLASE.
DR SMART; SM00642; Amy; 1.
DR SMART; SM00632; Amy_C; 1.
DR PROSITE; PS00506; BETA_AMYLASE_1; 1.
DR PROSITE; PS00679; BETA_AMYLASE_2; 1.
DR KW Multifunctional enzyme; Hydrolase; Glycosidase; Signal;
KW Polysaccharide degradation; Repeat.
FT SIGNAL 1 35
FT CHAIN 36 1196 BETA/ALPHA-AMYLASE.
FT DOMAIN 36 454 BETA-AMYLASE.
FT REPEAT 455 558
FT REPEAT 565 668
FT DOMAIN 669 1196 ALPHA-AMYLASE.
FT DISULFID 118 126
FT ACT_SITE 198 198 BY SIMILARITY.
FT ACT_SITE 394 394 BY SIMILARITY.
FT MUTAGEN 118 118 C->S: 5-FOLD DECREASE IN ACTIVITY.
FT MUTAGEN 126 126 C->V: 20-FOLD DECREASE IN ACTIVITY.
FT MUTAGEN 358 358 C->S: 60-FOLD DECREASE IN ACTIVITY.
FT CONFLICT 1 1 M -> MGL (IN REF. 3).
FT CONFLICT 67 67 N -> S (IN REF. 3).
FT CONFLICT 100 100 N -> D (IN REF. 3).
FT CONFLICT 154 154 S -> N (IN REF. 3).
FT CONFLICT 177 177 E -> Q (IN REF. 3).
FT CONFLICT 227 228 NA -> KS (IN REF. 3).
FT CONFLICT 330 330 G -> S (IN REF. 3).
FT CONFLICT 425 425 N -> S (IN REF. 3).
FT CONFLICT 493 493 D -> A (IN REF. 3).
FT CONFLICT 532 532 S -> L (IN REF. 3).
FT CONFLICT 559 559 A -> T (IN REF. 3).
FT CONFLICT 665 665 A -> T (IN REF. 3).
FT CONFLICT 681 681 T -> A (IN REF. 3).
FT CONFLICT 686 686 T -> A (IN REF. 3).
FT CONFLICT 725 728 APTS -> VFSP (IN REF. 3).
FT CONFLICT 736 736 N -> K (IN REF. 3).
FT CONFLICT 741 741 N -> S (IN REF. 3).
FT CONFLICT 758 758 S -> N (IN REF. 3).
SQ SEQUENCE 1196 AA; 130893 MW; A41EA6B70F257064 CRC64;
Query Match 11.8%; Score 320; DB 1; Length 1196;
Best Local Similarity 23.3%; Pred. No. 6.5e-14;
Matches 121; Conservative 71; Mismatches 189; Indels 138; Gaps 24;
QY 1 HHNGTNGTMQVFFWYLPNDGNHNRSLRSASNLKDGISAVWTPPAWKGSQNDV-CYG 59
Db 766 NYGFNSNNSQDKWH-----GGDQGIINKLDYIKNGGFTAIWITPTVMQKSEYAHGYH 821
QY 60 AYLDYDLGEFNQKGTIRTKYQTRNLQQAVALNKSNGIQVYGVVMMHKGGADEMTMVA 119
Db 822 TYDFY-----AVDGHGLTKMDKLQELVRKAHDKNIAMVMDVVVNHGT----- 862
QY 120 VEVNPNNEQSVSEYITEAWTKEDF-PGRGNTHSNF-KRWYHFDGVDWDQSKLNRI 177
Db 863 -----DFQPGNGFAKAPFDKADWYHHNGDITDGDYNSNNQ- 897
QY 178 YKFRGDKGWDWEYDTENGNYDLYMADIDMDHPEVVNLRNMGVWVTNTLGLDGFIDA 237
Db 898 -----WKI--ENG--DVAGLDLHNENPATANELKNWIKWLLNETGIDGLDIT 942
QY 238 VKHIKYSFTRDWINHVSATCKMFAVEFWNDLGAIEVNLKTNKNNHVSFVDFPLHNL 297


```

RL FEBS Lett. 255:37-41(1989).
CC -|- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
CC in amylose polyaccharides so as to remove successive
CC maltotetraose residues from the non-reducing chain ends.
CC -|- COPACTOR: Binds 2 calcium ions per subunit (By similarity).
CC -|- PATHWAY: Starch degradation.
CC -|- SUBUNIT: Monomer (By similarity).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC
CC -----
CC EMBL; X16732; CAA34708.1; -.
DR PIR; S05667; S05667.
DR HSP; P13507; 2AMG.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amy1ase; 1.
DR Pfam; PF00686; CBM 20; 1.
DR PRINTS; PR00110; ALPHAMYLASE.
DR ProDom; PD001568; CBD 4; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal.
FT CHAIN 1 21
FT SIGNAL 2 21
FT ACT_SITE 214 214
FT ACT_SITE 240 240
FT ACT_SITE 315 315
FT METAL 22 22
FT METAL 23 23
FT METAL 34 34
FT METAL 37 37
FT METAL 38 38
FT METAL 137 137
FT METAL 172 172
FT METAL 175 175
FT METAL 183 183
FT METAL 218 218
FT DISULFID 161 171
FT DISULFID 237 272
SQ SEQUENCE 551 AA; 59898 MW; F6D67D0BB235EA35 CRC64;

Query Match 10.08; Score 270.5; DB 1; Length 551;
Best Local Similarity 23.48; Pred. No. 5.5e-11;
Matches 128; Conservative 66; Mismatches 165; Indels 187; Gaps 28;

QY 2 HNGTNGTMYQFFEWYL-----PNDGNHNRSLRSDASNLKDKGISAVMTPPAWK----- 49
Db 33 YHGGDEILLOGFHNNVREAPND--WYNIILRQASITAAAGFSAIWMVPVPRDFSSWTDG 90
QY 50 GASQNDVGYGAYLDLGFENQKQITRTKYTRNQLQAANALKSNGIQYGVGVNHNKG 109
Db 91 GKSGGGEGYFWDH-----FNKNG---RYGSDAQLRQAAGALGGAGVKVLYDWPVNH-- 138
QY 110 GADATMVRAVEVNPNNRNEVSGEYIEATWTFPGRGNTHSNFKRWYHFDGVDWDQ 169
Db 139 -----MNRGVPDKEL-----NLPA----- 152
QY 170 SRKLNNRYKFRDGGKGDWEVD--TENGNY-----DYLM--YADIDMDHPWV----N 215
Db 153 -----GQGF-WRNCADGPNYVNDCCDGRFVGESDLNTHGPHQYMGFRD 197
QY 216 ELRNGWVWYNTLGLDGRIDAVKHIKYSPTRDWINHVRSATGKNFVAFAFWKNDLGAI 275

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Db 198 ELANLSGY----GAGGFRDFVRGAPERVDSWM-----SDSADSSFCVGLWK---GPS 246
QY 276 E-----NYLANKTNWH-----SVFDPVPLHYNLYNASKSGGNYDMRQIFNGTIVQOR 320
Db 247 EYPSWDRNTASWQOIKWSDRAKCPVDFALKERQNGSVA-----DWKHGLNGNDPDR 302
QY 321 HPMHVTVDNHDSDQPEALESFEEW-----PKLAYALTLTREQGYPSVF----- 367
Db 303 WREVAVTVDNHDGTGSPGQNGGQHWAQDGLIRQAYAVILT--SPGTVPVYWSHMYDMG 361
QY 368 YGDIYGIPTGVPAMKSKIDPILEARQKAYGRQNDYLDHNNIIGWTREGNTAHPNSGLA 427
Db 362 YGDF-----IRQLIQR-RTAGVRADSAISFH-----SGYS 391
QY 428 TIMSDGAGGNKMFVGRN---KAGOV---WTDITGNRAGVTI---NADGWNFSVN 475
Db 392 GLVATVSGSQTLVVALNSDLANPGQVAGSFSEAVNASNGQVRVWRSGSGDGGNDGGE 451
QY 476 GGSVSI 481
Db 452 GGLVNV 457

RESULT 10
AM3A_ORYSA
ID AM3A_ORYSA STANDARD; PRT; 440 AA.
AC P27932;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha-amy1ase isozyme 3A precursor (EC 3.2.1.1) (1,4-alpha-D-
DE glucan glucanohydrolase).
GN AMY1.2 OR AMY3A.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica M202; TISSUE=Etiolated leaf;
RX MEDLINE=91329692; PubMed=1714318;
RA Sutliff T.D., Huang N., Litts J.C., Rodriguez R.L.;
RT "Characterization of an alpha-amy1ase multigene cluster in rice.";
RL Plant Mol. Biol. 16:579-591(1991).
CC -|- FUNCTION: Important for breakdown of endosperm starch during
CC germination.
CC -|- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -|- COPACTOR: Binds 3 calcium ions per subunit (By similarity).
CC -|- SUBUNIT: Monomer.
CC -|- TISSUE SPECIFICITY: Most abundant in embryo-derived callus tissue.
CC -|- DEVELOPMENTAL STAGE: Expressed at a high level during germination
CC in the aleurones cells under the control of the plant hormone
CC gibberellic acid and in the developing grains at a low level.
CC -|- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC -----
CC EMBL; X56336; CAA39776.1; -.
DR PIR; S14958; S14958.
DR HSP; P04063; 1AFA.
DR Gramene; P27932; -.
DR InterPro; IPR006589; Alp_amy1_cat_sub.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR006046; Glyco_hydro_13.

```

DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; Multigene family.
FT SIGNAL 1 26
FT CHAIN 27 440
FT ACT SITE 207 207
FT ACT SITE 315 315
FT METAL 119 119
FT METAL 145 145
FT METAL 155 155
FT METAL 166 166
FT METAL 169 169
FT METAL 170 170
FT METAL 171 171
FT METAL 174 174
FT METAL 176 176
SQ SEQUENCE 440 AA; 48872 MW; 5E9B78C29AA91C2B CRC64;
Query Match 10.0%; Score 270; DB 1; Length 440;
Best Local Similarity 24.5%; Pred. No. 4.5e-11;
Matches 101; Conservative 58; Mismatches 155; Indels 98; Gaps 19;
QY 9 MMQYFEW-YLPNDGNHNRLSDASNLKDKGISAVWIPPAWKASQNDVGAYDLYDLG 67
DB 31 LFOGFNDWKKQGGWYNMLKQDQDIASGVTHVWLPPTPHSVSPQ--GYMPGRLYDLN 88
QY 68 EFNQGTIRTKYGRNQLQAVALKSGNIQVGVVNNHKGADATMVRVAVENPNNR 127
DB 89 -----ASKYGTAKELSLIAFAHAKIKCVADIVNHRCAD----- 125
QY 128 NQEVSGSYTTEATKFPFGRGNTHSNPKRWYHFDGVDMQDSR-KLNNRIYKPRGDKG 186
DB 126 -KDRGVYCI-----FKGGPRGC-----LDWGPSMICCDDTQY---SDGTG 163
QY 187 WDHEVDTEGNYDLYMADIDMDHPEVNNELRNKGVWYNTLGLDGRIDAVKHYSFT 246
DB 164 ---HRDT---GADFAAAPDIDHLPVQLQRELSDLRLRDRVDFGWRDLFAKYSAAVA 217
QY 247 RDWLNHVSATGKNMFAVAEPKNDLG-----AIENLVKNTNNHVSFD 290
DB 218 RTYVQNRPS-----FVVAELW-NSLSYDGDGKPAANQDQGRQELVNNWQVGGPATAFD 271
QY 291 VPLHNLNASKSGNYDMRQIFNGT--VQQRHPMHAVTFDNHDSPQEEALESFVBEWF 348
DB 272 FTTK-GILQSAVQGLWRRDKQKAPGMIGWYPEKAVTFVDNHDITGSTQRM-----WP 324
QY 349 KP-----LAVALTUTREGQPSVYGYDYGIPTHGVFAMKSKIDPILAEQK 395
DB 325 FPSDKVILGYAYILT-HPGVPCIFYDQVDFW-----NLQEIINALAATKR 369
RESULT 11
AMT4 PSEST
ID AMT4 PSEST
AC P13507; STANDARD; PRT; 548 AA.
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Glucan 1,4-alpha-maltotetrahydrolase precursor (EC 3.2.1.60) (G4-
DE amylase) (Maltotetraose-forming amylase) (Exo-maltotetrahydrolase)
DE (Maltotetraose-forming exo-amylase).
GN AMYP.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=MO-19;
RX MEDLINE=89155431; PubMed=2646279;
RA Fujita M., Torigoe K., Nakada T., Tausaki K., Kubota M., Sakai S.,
RA Tejisaaka Y.;
RT Cloning and nucleotide sequence of the gene (amyP) for
RT maltotetraose-forming amylase from Pseudomonas stutzeri MO-19.;
RL J. Bacteriol. 171:1333-1339(1989).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS), AND REVISIONS TO 286-302.
RC STRAIN=MO-19;
RX MEDLINE=97271999; PubMed=9126844;
RA Morishita Y., Hasegawa K., Matsuura Y., Katsube Y., Kubota M.,
RA Sakai S.;
RT "Crystal structure of a maltotetraose-forming exo-amylase from
RT Pseudomonas stutzeri.";
RL J. Mol. Biol. 267:661-672(1997).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF VARIANT GLN-240.
RC STRAIN=MO-19;
RX MEDLINE=97428332; PubMed=9281429;
RA Yoshioka Y., Hasegawa K., Matsuura Y., Katsube Y., Kubota M.;
RT "Crystal structures of a mutant maltotetraose-forming exo-amylase
RT co-crystallized with maltopentaose.";
RL J. Mol. Biol. 271:619-628(1997).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF VARIANTS.
RC STRAIN=MO-19;
RX MEDLINE=20027472; PubMed=10556241;
RA Hasegawa K., Kubota M., Matsuura Y.;
RT "Roles of catalytic residues in alpha-amylases as evidenced by the
RT structures of the product-complexed mutants of a maltotetraose-forming
RT amylase.";
RL Protein Eng. 12:819-824(1999).
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-alpha-D-glucosidic linkages
CC in amylaceous polysaccharides so as to remove successive
CC maltotetraose residues from the non-reducing chain ends.
CC -1- COFACTOR: Binds 2 calcium ions per subunit.
CC -1- PATHWAY: Starch degradation.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MISCELLANEOUS: THERE ARE SEVERAL ISOENZYME FORMS OF THIS PROTEIN.
CC -1- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M24516; AAA25707.1; -.
DR PIR; A32803; A32803.
DR PDB; 1GCV; 28-JAN-03.
DR PDB; 1JDA; 15-OCT-97.
DR PDB; 1JDC; 15-OCT-97.
DR PDB; 1JDD; 15-OCT-97.
DR PDB; 1Q13; 24-NOV-99.
DR PDB; 1Q15; 24-NOV-99.
DR PDB; 1Q15; 24-NOV-99.
DR PDB; 1QPK; 17-NOV-99.
DR PDB; 2AMG; 01-APR-97.
DR InterPro; IPR006047; Alpha_amy1_cat.
DR InterPro; IPR02044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF00686; CBM_20; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR ProDom; PD001568; CBD_4; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 548
FT GLUCAN 1,4-ALPHA-MALTOTETRAHYDROLASE.

SEQUENCE FROM N.A., AND SEQUENCE OF 34-45.
STRAIN=C599;
Diderichsen B., Christiansen L.;
"Cloning of a maltogenic alpha-amylase from Bacillus
stearothermophilus.";
FEMS Microbiol. Lett. 56:53-60(1988).
[2]
REVIEWS, AND X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
MEDLINE=99315215; PubMed=10397084;
Dauter Z., Dauter M., Brozowski A.M., Christensen S., Borchert T.V.,
Beier L., Wilson K.S., Davies G.J.;
"X-ray structure of Novamyl, the five-domain 'maltogenic' alpha-
amylase from Bacillus stearothermophilus: maltose and acarbose
complexes at 1.7-A resolution.";
Biochemistry 38:8395-8392(1999).
CC -|- FUNCTION: Converts starch into maltose.
CC -|- CATALYTIC ACTIVITY: Hydrolysis of (1->4)-alpha-D-glucosidic
linkages in polysaccharides so as to remove successive alpha-
maltose residues from the non-reducing ends of the chains.
CC -|- COFACTOR: Binds 3 calcium ions per subunit.
CC -|- SUBUNIT: Monomer.
CC -|- BIOTECHNOLOGY: Used in the food industry to prevent bread from
staling. Sold under the name Novamyl by Novozymes.
CC -|- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; M36539; AAA22233.1; -;
DR PIR; S28784; S28784.
DR PDB; 1QHO; 31-MAY-00.
DR PDB; 1QHP; 31-MAY-00.
DR InterPro; IPR006048; Alpha_amyl_C.
DR InterPro; IPR006047; Alpha_amyl_Cat.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR006046; Glyco_hydro_13.
DR InterPro; IPR002909; IPT_TIG.
DR Pfam; PF00128; alpha-amylase_1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR Pfam; PF01833; TIG; 1.
DR PRINTS; PD0110; ALPHAAMYLASE.
DR PRODOM; PD001568; CBD_4; 1.
DR SMART; SM00632; AmyC; 1.
KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
KW Signal; 3D-structure
FT SIGNAL 1 33
FT CHAIN 34 719 MALTOGENIC ALPHA-AMYLASE.
FT ACT_SITE 261 261
FT ACT_SITE 265 265
FT ACT_SITE 289 289
FT ACT_SITE 362 362
FT METAL 54 54
FT METAL 56 56 CALCIUM 1. (VIA CARBONYL OXYGEN).
FT METAL 59 59 CALCIUM 1.
FT METAL 60 60 CALCIUM 1.
FT METAL 81 81 CALCIUM 1 (VIA CARBONYL OXYGEN).
FT METAL 83 83 CALCIUM 1.
FT METAL 109 109 CALCIUM 2.
FT METAL 110 110 CALCIUM 2 (VIA CARBONYL OXYGEN).
FT METAL 112 112 CALCIUM 2.
FT METAL 134 134 CALCIUM 2.
FT METAL 135 135 CALCIUM 2.
FT METAL 164 164 CALCIUM 3.
FT METAL 217 217 CALCIUM 3 (VIA CARBONYL OXYGEN).
FT METAL 231 231 CALCIUM 3.
FT METAL 265 265 CALCIUM 3 (VIA CARBONYL OXYGEN).
FT CONFLICT 109 109 D -> N (IN REF. 1).

FT	CONFLICT	254	256	MISSING (IN REF. 1).
FT	CONFLICT	371	371	S -> SK (IN REF. 1).
FT	CONFLICT	379	391	ALAFILTSRGTPS -> RLISFSLRGVRPP (IN REF. 1).
SQ	SEQUENCE	719	AA; 78675	MW; B4OB61AD964F7D89 CRC64;

Query Match 9.6%; Score 259; DB 1; Length 719;
Best Local Similarity 22.3%; Pred. No. 4.4e-10;
Matches 122; Conservative 73; Mismatches 202; Indels 150; Gaps 25;

QY	5	TNGTWMQVFEWLPND	-----GNHNRRLSDASNLKDKGISAVWIPPAWKG-----ASQ	53
DB	58	TNNPAKSYGLYDPYKSKWQWVGDLGVRQKLPYLQKLGVTTWLSVLNLDLTACT	117	
QY	54	NDVGYGAYDLYDLGEBFNQKGTIRTKYGRNQALQAAVNALKSNGIOVYGVDVNMHKGADA	113	
DB	118	DMTGVHGYWRD---FKQ---IEEHFGNWTTFDTLVNDAHQNGIKIVIVDFVFNHSPFKA	171	
QY	114	TEMVRAVEVNNRNOQSVSGEYTIEMWTKFDPGPGNTHSNFKRWYHFDGVDWDSRKL	173	
DB	172	NDSTFA-EGGALYNNGTVMGN-----FDDATKGYFHHN-----	204	
QY	174	NNRIYKFRDGGKWD-----WEVDTEGNDYLMYADIMDHPVWVNLNMGVWYWTNT	227	
DB	205	-----GDISNWDDEYEAQWKNFTDPAGFS---LADLSQENGTAQYLTDAVQLV-A	252	
QY	228	LGLDGFRIIDAVKHIKYSFTRDWINHVRSATGKNMFAVAFWKNLDLGAENLKNKNW-NH	286	
DB	253	HGADGLRIDAVKHNSGFSKSLADKLYQK--KDFILGVEWYGDPT-ANHLEKVRVANN	309	
QY	287	S---VFDVPLHYNLYN--ASKSGGNYDMRQIPNGTVVQ-RHPMHAVTFVDNHDSDPEAL	340	
DB	310	SGVNVLDPLNTVIRNVFGTFTQWYDLNMVNTQGNKYKENLITFTDNDHMSRFLSV	369	
QY	341	ESFVEEWFKPLAYALTREOCQVPSVFG-----DYYGIPTHG-VPAMKSKIDPIL	390	
DB	370	NSNKANLHQALAFILT---SRGTPSIYYTEQYMAGGNDPY---NRGMPAFDTTTTAFK	423	
QY	391	EA-----RQKYAYGRQ--NDYLDHNNIIGWTRGNTAHPS	424	
DB	424	EVSTLAGLRNNAATQYGTTTORWINNDVYIYERKEFNDV---LVAINRNTQSSYSIS	479	
QY	425	GLATIMSDGA-----GKNMFPVGRNKAQGVWTDITGNRAGTVTINADGNGNFSVN	475	
DB	480	GLQTALPNGSYADYLSGLLGN-----GISVSNGSVASFTLA	516	
QY	476	GGSVSIVW	482	
DB	517	PGAVSVW	523	

Search completed: October 7, 2004, 00:13:25
Job time : 10.5063 secs

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OM protein - protein search, using sw model

Run on: October 6, 2004, 23:45:37 ; Search time 58.5516 Seconds
(without alignments)
2340.424 Million cell updates/sec

Title: US-09-925-576C-12
Perfect score: 2708
Sequence: 1 HHNGTGTMMQYFEWYLPND.....ADGNGFNVNGSVSIWVK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2708	100.0	485	3	AY97812 Bacillus
2	2708	100.0	485	4	AAB29260 Bacillus
3	2708	100.0	485	4	AAB29261 Bacillus
4	2708	100.0	485	5	ABB06938 Bacillus
5	2708	100.0	485	5	AAU12154 Bacillus
6	2708	100.0	485	5	AAB47855 Bacillus
7	2708	100.0	485	5	ABW76591 Termamyl-1
8	2675	98.8	480	4	ABM00046 AA560 SEQ
9	2613	96.5	485	2	AAW12956 Alpha-amy
10	2613	96.5	485	2	AY15420 Termamyl-1
11	2613	96.5	485	2	AY07386 Wild type
12	2613	96.5	485	3	AY99607 Bacillus
13	2613	96.5	485	5	ABB06939 Bacillus
14	2613	96.5	485	5	AAU12155 Bacillus
15	2613	96.5	485	5	AAB47856 Bacillus
16	2613	96.5	485	5	ABB76592 Bacillus
17	2596	95.9	516	5	ABB08773 Bacillus
18	2475.5	91.4	519	4	AAE09762 Bacillus
19	2475.5	91.4	519	4	AAE09763 Bacillus
20	2475.5	91.2	519	4	AAE09767 Bacillus
21	2469.5	91.2	519	4	AAE09764 Bacillus
22	2438	90.0	485	2	AAW12110 Alpha-amy
23	2437	90.0	485	2	AAW1836 Bacillus
24	2437	90.0	485	2	AAW31500 Bacillus
25	2437	90.0	485	2	AAW48261 Bacillus

ALIGNMENTS

RESULT 1
AY97812
ID AY97812 standard; protein; 485 AA.
XX
AC AY97812;
XX
DT 12-SEP-2003 (revised)
DT 21-AUG-2000 (first entry)
XX
DE Bacillus alkaline alpha-amyase AA560.
XX
KW Alkaline alpha-amyase; AA560; immunogenicity; allergenicity;
KW industrial product; pharmaceutical; hypoallergenic.
XX
OS Bacillus sp; 'DSM12649'.
XX
PN WC200022103-Al.
XX
PD 20-APR-2000.
XX
PF 12-OCT-1999; 99WO-DK000542.
XX
PR 13-OCT-1998; 98DK-00001301.
PR 04-OCT-1999; 99DK-00001418.
XX
(NOVO) NOVO-NORDISK AS.
PI Olsen AA, Von Der Osten C, Andersen KV, Ernst S, Roggen EL;
XX
DR WPI; 2000-329163/28.
DR N-PSDB; AAA30783.
XX
PT New modified polypeptides having an attached polymer for reducing immune
PT responses, useful in e.g. detergents, cleaning products, skin care
PT products, food or feed products, textile products or pharmaceuticals.
XX
PS Example 4; Page 102-105; 108pp; English.
XX
CC The invention relates to proteins with reduced immunogenicity, having one
CC or more modified amino acids, where the alpha-carbon atoms of the amino
CC acids are located less than 15 Angstroms from a ligand bound to the
CC protein. The modification may entail substitution of the endogenous
CC residue for a non-endogenous residue and/or attachment of polymeric
CC molecules such as carbohydrates or branched polyethylene glycols to the
CC amino acid residues. The residue to be modified is identified from the 3-
CC dimensional structure of the protein determined, for example, by X-ray
CC crystallography or NMR. A wide variety of enzymes may be modified
CC according to the invention, including proteases (especially subtilisins),

AY15422 Termamyl-1
AY15416 Bacillus
AY07382 Wild type
AY99609 Bacillus
AY99603 Bacillus
ABB06934 Bacillus
AAU12150 Bacillus
AAB47851 Bacillus
ABB76587 Termamyl-1
ABB9481 Amino aci
AAB30701 A Bacillu
AAW12144 Alpha-amy
AAW12109 Alpha-amy
ABB76643 Termamyl-1
AAW31499 Bacillus
AAW48260 Bacillus
AY15421 Termamyl-1
AY15415 Bacillus
AY25150 Bacillus
AY07391 Wild type

CC carbohydrates (such as amylase), isomerases, transferases and
CC oxidoreductases. The modified proteins of the invention may be used for
CC reducing the allergenicity of industrial products (i.e., those which are
CC not intended to enter the circulatory system. The proteins may be used in
CC cleaning agents (such as laundry products, dish-washing products or hard
CC surface cleaning products), skin-care products, textile treatment
CC products (e.g., bleaching agents) and food products. The modified
CC polypeptides can also be used for reducing the immunogenicity of
CC pharmaceuticals. The modified proteins have reduced immunogenicity or
CC allergenicity while maintaining a high percentage of activity. The
CC present sequence represents an alkaline alpha-amylase, AA560, from
CC Bacillus DSM 12649, which may be modified according to the invention.
CC (Updated on 12-SEP-2003 to standardise OS field)
XX
SQ

Query Match 100.0%; Score 2708; DB 3; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.7e-218;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDGISAVWIPPAWKGASQNDVGYGA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDGISAVWIPPAWKGASQNDVGYGA 60
QY 61 YDLYDLGEFNGKQGTIRTKYGTNRQLQAAVNALKSNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLYDLGEFNGKQGTIRTKYGTNRQLQAAVNALKSNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EYVNNRNQVSGEYTIETAWTKFDPGRGNTHSNFKRWYTHFGVDWDQSRKLNRIYKF 180
DB 121 EYVNNRNQVSGEYTIETAWTKFDPGRGNTHSNFKRWYTHFGVDWDQSRKLNRIYKF 180
QY 181 RGDGKGWDEVDTENGNYDLYMADIDMDHPEVVMNLRNWGVYNTLTGLDGFRIIDAVKH 240
DB 181 RGDGKGWDEVDTENGNYDLYMADIDMDHPEVVMNLRNWGVYNTLTGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSGTKNMFVAEFWKNLKGAIENLYLNKTNWHSVDFVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSGTKNMFVAEFWKNLKGAIENLYLNKTNWHSVDFVPLHYNLYNA 300
QY 301 SKSGGNYDMRQIFNGTVVQHPMHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTIRE 360
DB 301 SKSGGNYDMRQIFNGTVVQHPMHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTIRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPILQKQYAYGRQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPILQKQYAYGRQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGNKWMFVGRNKGQVWTDITGNRAGTVTINADGNGFNSVNGGSYS 480
DB 421 HPNSGLATIMSDGAGGNKWMFVGRNKGQVWTDITGNRAGTVTINADGNGFNSVNGGSYS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 2
AAB29260
ID AAB29260 standard; protein; 485 AA.
XX
AC AAB29260;
XX
DT 07-FEB-2001 (first entry)
XX
DE Bacillus sp. alpha-amylase #1.
XX
KW Alpha-amylase; laundry; detergent; textile desizing;
KW sweetener production; ethanol production; brewing; paper production.
XX
OS Bacillus sp.
XX
PN WO2000060060-A2.

XX 12-OCT-2000.
XX 28-MAR-2000; 2000WO-DK000149.
XX 31-MAR-1999; 99DK-00000439.
XX 13-APR-1999; 99DK-00000490.
XX 13-APR-1999; 99US-00290734.
XX (NOVO) NOVO NORDISK AS.
XX
XX Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;
PI Bisgard-Frantzen H, Svendsen A, Andersen C;
XX
XX WPI: 2001-006814/01.
XX N-PSDB; AAC63114.
XX
XX New polypeptides having alpha-amylase activity and nucleic acids encoding
PT the enzymes, useful as a detergent or a dishwash detergent composition,
PT for textile desizing, for liquefaction of starch, or for ethanol
PT production.
XX
PS Claim 3; Page 106-108; 116pp; English.
XX
CC The present invention relates to proteins having alpha-amylase activity
CC and their coding sequences. These proteins are useful in a number of
CC industrial applications, including detergents, hard surface cleaning
CC compositions, in compositions for desizing textiles, fabrics and
CC garments, in the production of pulp and paper, in beer-making and
CC brewing, and in starch conversion processes such as sweetener and ethanol
CC production
XX
SQ Sequence 485 AA;

Query Match 100.0%; Score 2708; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.7e-218;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDGISAVWIPPAWKGASQNDVGYGA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDGISAVWIPPAWKGASQNDVGYGA 60
QY 61 YDLYDLGEFNGKQGTIRTKYGTNRQLQAAVNALKSNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLYDLGEFNGKQGTIRTKYGTNRQLQAAVNALKSNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EYVNNRNQVSGEYTIETAWTKFDPGRGNTHSNFKRWYTHFGVDWDQSRKLNRIYKF 180
DB 121 EYVNNRNQVSGEYTIETAWTKFDPGRGNTHSNFKRWYTHFGVDWDQSRKLNRIYKF 180
QY 181 RGDGKGWDEVDTENGNYDLYMADIDMDHPEVVMNLRNWGVYNTLTGLDGFRIIDAVKH 240
DB 181 RGDGKGWDEVDTENGNYDLYMADIDMDHPEVVMNLRNWGVYNTLTGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSGTKNMFVAEFWKNLKGAIENLYLNKTNWHSVDFVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSGTKNMFVAEFWKNLKGAIENLYLNKTNWHSVDFVPLHYNLYNA 300
QY 301 SKSGGNYDMRQIFNGTVVQHPMHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTIRE 360
DB 301 SKSGGNYDMRQIFNGTVVQHPMHAVTFVDNHDSPQEEALESFVEEWFKPLAYALTIRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPILQKQYAYGRQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPILQKQYAYGRQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGNKWMFVGRNKGQVWTDITGNRAGTVTINADGNGFNSVNGGSYS 480
DB 421 HPNSGLATIMSDGAGGNKWMFVGRNKGQVWTDITGNRAGTVTINADGNGFNSVNGGSYS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

```
RESULT 3
AAB29261
ID AAB29261 standard; protein; 485 AA.
XX
AC AAB29261;
XX
DT 07-FEB-2001 (first entry)
XX
DE Bacillus sp. alpha-amylase #2.
XX
KW Alpha-amylase; laundry; detergent; textile desizing;
KW sweetener production; ethanol production; brewing; paper production.
XX
OS Bacillus sp.
XX
PN WO200060060-A2.
XX
PD 12-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-DK000149.
XX
PR 31-MAR-1999; 99DK-00000439.
XX
PR 13-APR-1999; 99DK-00000490.
XX
PR 13-APR-1999; 99US-00290734.
XX
PA (NOVO ) NOVO NORDISK AS.
XX
PI Outtrup H, Hoeck LH, Nielsen BR, Borchert TV, Nielsen VS;
PI Bisgaard-Frantzen H, Svendsen A, Andersen C;
XX
DR WPI; 2001-006814/01.
DR N-PSDB; AAC63115.
XX
PT New polypeptides having alpha-amylase activity and nucleic acids encoding
PT the enzymes, useful as a detergent or a dishwash detergent composition,
PT for textile desizing, for liquefaction of starch, or for ethanol
PT production.
XX
PS Claim 3; Page 111-112; 116pp; English.
XX
CC The present invention relates to proteins having alpha-amylase activity
CC and their coding sequences. These proteins are useful in a number of
CC industrial applications, including detergents, hard surface cleaning
CC compositions, in compositions for desizing textiles, fabrics and
CC garments, in the production of pulp and paper, in beer-making and
CC brewing, and in starch conversion processes such as sweetener and ethanol
CC production
XX
SQ Sequence 485 AA;
Query Match 100.0%; Score 2708; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.7e-218;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKGSQNDVGGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKGSQNDVGGA 60
Qy 61 YDLVDLGEFNQKGTIRTKYGTNRNLQAAVNALKSGIQYGVGVVNMHKGADATEMVRV 120
Db 61 YDLVDLGEFNQKGTIRTKYGTNRNLQAAVNALKSGIQYGVGVVNMHKGADATEMVRV 120
Qy 121 EVNPNRNRQESVGYTTIETAWTKFPFGCGNTHSNFKRWYHFDGVDWQSKLNRIYKF 180
Db 121 EVNPNRNRQESVGYTTIETAWTKFPFGCGNTHSNFKRWYHFDGVDWQSKLNRIYKF 180
Qy 181 RGDKGWDWEVDTEGNYDYLMYADIDMDHPEVNVNLRNMGVWYNTLTGLDGFPRIDAVKH 240
Db 181 RGDKGWDWEVDTEGNYDYLMYADIDMDHPEVNVNLRNMGVWYNTLTGLDGFPRIDAVKH 240
Qy 241 IKYSFTRDWINHRSATGKNMFAVEFWKNDLGAIENTNKNHNSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHRSATGKNMFAVEFWKNDLGAIENTNKNHNSVDFVPLHYNLYNA 300
Qy 301 SKSGENYDMROI FNGTIVVQHPMAVTFVDNHDSPPEALESFVEEWFKPLAYALTRE 360
Db 301 SKSGENYDMROI FNGTIVVQHPMAVTFVDNHDSPPEALESFVEEWFKPLAYALTRE 360
Qy 361 QGYPSEVFYGDYGIPTHTGVPAMKSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSEVFYGDYGIPTHTGVPAMKSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGNKMMFVGRNKAGQVWTDITGNRAGTIVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMMFVGRNKAGQVWTDITGNRAGTIVTINADGWNFSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485
RESULT 4
AAB06938
ID AAB06938 standard; protein; 485 AA.
XX
AC AAB06938;
XX
DT 19-JUN-2002 (first entry)
XX
DE Bacillus termamyl-like alpha-amylase protein SEQ ID NO:12.
XX
KW Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
KW washing; sweetener; ethanol; starch.
XX
OS Bacillus sp.
XX
PN WO200166712-A2.
XX
PD 13-SEP-2001.
XX
PF 07-MAR-2001; 2001WO-DK000144.
XX
PR 08-MAR-2000; 2000DK-00000376.
PR 15-MAR-2000; 2000US-0189857P.
PR 23-FEB-2001; 2001DK-00000303.
PR 26-FEB-2001; 2001US-0271382P.
XX
PA (NOVO ) NOVOZYMES AS.
XX
PI Andersen C, Borchert TV, Nielsen BR;
XX
DR WPI; 2002-239612/29.
XX N-PSDB; ABL50569.
XX
PT Novel variant of parent termamyl-like alpha-amylase useful as a component
PT in washing and dishwashing compositions, for textile desizing, for starch
PT liquefaction, and for producing sweeteners and ethanol from starch.
XX
PS Claim 1; Page 148-149; 153pp; English.
XX
CC The present invention describes a variant of a parent termamyl-like alpha
CC -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
CC positions of a group of 31 possible amino acid positions. The alteration
CC in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,
CC Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
CC Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
CC Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
CC washing and/or dishwashing, textile desizing, and starch liquefaction.
CC (I) is useful as a component in hard surface cleaning detergent
CC composition, and for producing sweeteners and ethanol from starch. (I)
CC has altered solubility, preferably increased solubility, in particular
CC under washing, dish washing or hard surface cleaning conditions. The
CC present sequence represents a Bacillus termamyl-like alpha-amylase which
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CC is used in the exemplification of the present invention
XX
SQ Sequence 485 AA;
Query Match 100.0%; Score 2708; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 3.7e-218;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAMKASQNDVGYGA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAMKASQNDVGYGA 60
QY 61 YLDYDLGEFNGKGTIRTKYGTNRQLQAAVNALKSNGIQVYGVVNMHKGADATENVRAV 120
DB 61 YLDYDLGEFNGKGTIRTKYGTNRQLQAAVNALKSNGIQVYGVVNMHKGADATENVRAV 120
QY 121 EVNPNRNQEVSGEYTIETAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 180
DB 121 EVNPNRNQEVSGEYTIETAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 180
QY 181 RGDGKGDWEVDTEGNGYDLYMADIDMDHPEVYNELRNWGVYNTLTGLDGRIDAVKH 240
DB 181 RGDGKGDWEVDTEGNGYDLYMADIDMDHPEVYNELRNWGVYNTLTGLDGRIDAVKH 240
QY 181 RGDGKGDWEVDTEGNGYDLYMADIDMDHPEVYNELRNWGVYNTLTGLDGRIDAVKH 240
DB 181 RGDGKGDWEVDTEGNGYDLYMADIDMDHPEVYNELRNWGVYNTLTGLDGRIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKMFVAVAFWKNLGAENYLNKTNWHSFVDPVLYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKMFVAVAFWKNLGAENYLNKTNWHSFVDPVLYNLYNA 300
QY 301 SKSGGNYDMRQIFNGTVVQRHPMHAFTVDNHDSPQEEALESFVEWFKPLAYALTIRE 360
DB 301 SKSGGNYDMRQIFNGTVVQRHPMHAFTVDNHDSPQEEALESFVEWFKPLAYALTIRE 360
QY 361 QGYPSVFGDYIGIPTHGVPAKSKIDPILFARQKYAYGRONDYLDHNNIIGWTRGNTA 420
DB 361 QGYPSVFGDYIGIPTHGVPAKSKIDPILFARQKYAYGRONDYLDHNNIIGWTRGNTA 420
QY 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480
QY 481 IWVNK 485
DB 481 IWVNK 485
RESULT 6
AAB47855
ID AAB47855 standard; protein; 485 AA.
XX
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AC AAB47855;
 XX 02-APR-2002 (first entry)
 XX Bacillus alpha amylase AA560.
 XX
 XX Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;
 KW starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
 KW bakery; cereal bar; ice cream; coffee whitener; salad dressing;
 KW cured meat; fermented meat; spice.
 XX
 XX Bacillus sp.
 XX
 XX WO200196537-A2.
 XX 20-DEC-2001.
 XX 13-JUN-2001; 2001WO-DK000404.
 XX 14-JUN-2000; 2000DK-00000917.
 XX 20-JUN-2000; 2000US-0212852P.
 XX (NOVO) NOVOZYMES AS.
 XX
 XX Nielsen BR, Weibye M;
 XX WPI; 2002-098064/13.
 XX N-PSDB; AAI72216.
 XX
 XX New modified alpha-amylase derived from the genus Bacillus and/or is a
 PT Termamyl-like alpha-amylase, which has been pre-oxidized for producing
 PT maltodextrin or glucose syrup.
 XX
 XX Claim 5; Page 43-44; 47pp; English.
 XX
 XX The sequences given in AAB47850-56 show modified alpha-amylases derived
 CC from the genus Bacillus. These alpha amylases are Termamyl-like alpha-
 CC amylase and they have been pre-oxidized. The alpha amylase is useful for
 CC producing a maltodextrin or glucose syrup, by treating starch with a pre-
 CC oxidized alpha-amylase until a product with a DE between 5-45 has been
 CC provided and/or until a product with a molecular weight of between 5-30
 CC kDa has been provided. The product comprises a maltodextrin with a DE of
 CC 18.5 and/or a maltodextrin with a molecular weight of 14-16 kDa. The
 CC alpha amylase is useful for producing a maltodextrin or glucose syrup,
 CC where the glucose syrup is useful as an ingredient in food, feed or
 CC pharmaceuticals. Glucose syrup is useful in confectionery such as
 CC candies, beverages such as isotonic drinks, bakery such as cereal bars,
 CC dairy and ice cream such as coffee whiteners, conventional foods such as
 CC salad dressings, and food ingredients and preparations such as cured
 CC meat, fermented meat, spices and seasoning encapsulated flavours
 XX
 XX Sequence 485 AA;
 SQ

Query Match 100.0%; Score 2708; DB 5; Length 485;
 Best Local Similarity 100.0%; Pred. No. 3.7e-218;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMTQYFEMWLPNDGNHNRLRSDASNLKDKGISAVWTTPPAKGSQNDVGYGA 60
 DB 1 HHNGTGTMTQYFEMWLPNDGNHNRLRSDASNLKDKGISAVWTTPPAKGSQNDVGYGA 60
 QY 61 YDLYDLGEFNQKGTIRTKYGRNLOQAVALNKGSIQVYGDVVMNHKGGADATEMVRV 120
 DB 61 YDLYDLGEFNQKGTIRTKYGRNLOQAVALNKGSIQVYGDVVMNHKGGADATEMVRV 120
 QY 121 EVNPNRNRQVSGEYTTIATWKFPDQGNTHSNFKWRWYHFDGVDWQSRKLNRIYKF 180
 DB 121 EVNPNRNRQVSGEYTTIATWKFPDQGNTHSNFKWRWYHFDGVDWQSRKLNRIYKF 180
 QY 181 RGDKGKDWEDVTENGNDYILMYADIDMDHPVNNELRNGVWTTNTLGLDGRIDAVKH 240
 DB 181 RGDKGKDWEDVTENGNDYILMYADIDMDHPVNNELRNGVWTTNTLGLDGRIDAVKH 240

QY 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWONDGAIENYLNKTNWHSVDFVPLHNLNA 300
 DB 241 IKYSFTRDWINHVRSAATGKNMFAVAEFWONDGAIENYLNKTNWHSVDFVPLHNLNA 300
 QY 301 SKSGNDYDMQIIFNGTIVQRHPMAVTFVDNHDQPEEALLESFVEEFKPLAYALTITRE 360
 DB 301 SKSGNDYDMQIIFNGTIVQRHPMAVTFVDNHDQPEEALLESFVEEFKPLAYALTITRE 360
 QY 361 QGYPSPVFGDYGIPTHGVPAMKSKIDPILAEAROKYAYGRONDYLDHNNIIGWTRGNNTA 420
 DB 361 QGYPSPVFGDYGIPTHGVPAMKSKIDPILAEAROKYAYGRONDYLDHNNIIGWTRGNNTA 420
 QY 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWGNFSVNGGSVS 480
 DB 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWGNFSVNGGSVS 480
 QY 481 IWVWK 485
 DB 481 IWVWK 485

RESULT 7
 ABB76591
 ID ABB76591 standard; protein; 485 AA.
 XX
 AC ABB76591;
 XX
 DT 19-AUG-2002 (first entry)
 XX
 DE Termamyl-like-alpha-amylase #6.
 XX
 XX Termamyl; alpha amylase; starch liquefaction; ethanol production;
 KW textile desizing; detergent; enzyme.
 XX
 OS Bacillus sp.
 XX
 XX WO200210355-A2.
 PD 07-FEB-2002.
 PF 12-JUL-2001; 2001WO-DK000488.
 XX
 PR 01-AUG-2000; 2000DK-00001160.
 PR 12-SEP-2000; 2000DK-00001354.
 PR 10-NOV-2000; 2000DK-00001687.
 PR 26-APR-2001; 2001DK-00000655.
 XX
 XX (NOVO) NOVOZYMES AS.
 PA
 XX Thisted T, Kjaerulff S, Andersen C, Fuglsang CC;
 PI
 XX WPI; 2002-280633/32.
 DR N-PSDB; ABL96212.
 XX
 XX Variant of parent Termamyl-like alpha amylase, useful in detergent
 PT compositions, for starch liquefaction, ethanol production, washing and/or
 PT dish washing, and textile desizing.
 XX
 PS Claim 8; Page 75-76; 90pp; English.
 XX
 CC This invention relates to variants of a parent Termamyl-like alpha-
 CC amylases. These are used for starch liquefaction, ethanol production,
 CC detergent, and textile desizing. The amylases have altered stability,
 CC particularly at high temperatures from 70-120plusoc and low pH in the
 CC range from pH 4.0-6.0. The present sequence is a termamyl-like-alpha-
 CC amylase
 XX
 SQ Sequence 485 AA;

Query Match 100.0%; Score 2708; DB 5; Length 485;
 Best Local Similarity 100.0%; Pred. No. 3.7e-218;
 Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX DE Bacillus Termamyl-like alpha-amylase.
 XX KW Bacillus; alpha-amylase; washing; textile desizing; starch liquefaction;
 XX KW saccharification; muten; enzyme stability; hybrid.
 XX OS Bacillus sp.
 XX PN WO200029560-A1.
 XX PD 25-MAY-2000.
 XX PF 16-NOV-1999; 99WO-DK000628.
 XX PR 16-NOV-1998; 98DK-00001495.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX PI Svendsen A, Kjaerulff S, Bisgard-Frantzen H, Andersen C;
 XX DR WPI; 2000-387777/33.
 XX PT Variant of parent termamyl-like alpha amylase useful for washing, textile
 PT desizing and starch liquefaction, comprising alterations in one or more
 PT solvent exposed amino acid residues.
 XX PS Claim 8; Page 61-62; 80pp; English.
 XX CC The present sequence is a parent alpha-amylase from which mutants with
 CC increased stability at acidic pH, low calcium concentration and high
 CC temperatures have been derived. The sequence encoding this protein was
 CC isolated from a Bacillus genomic DNA library. A variant may contain
 CC mutations in one or more solvent exposed amino acid residues to increase
 CC the overall hydrophobicity of the enzyme or the overall number of methyl
 CC groups in the side chains of exposed residues may be increased. The
 CC mutations can be incorporated by site-directed mutagenesis or by random
 CC mutagenesis. As a result of their increased stability, the variants are
 CC suitable for the industrial processing of starch, i.e. starch
 CC liquefaction and saccharification. They may also be useful for washing,
 CC dishwashing and textile desizing. Hybrid alpha-amylases comprising
 CC partial amino acid sequences derived from two or more alpha-amylases have
 CC also been created in order to increase enzyme stability
 XX SQ Sequence 485 AA;

Query Match 96.5%; Score 2613; DB 3; Length 485;
 Best Local Similarity 95.5%; Pred. No. 3.4e-210;
 Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 HHNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKIGISAVMTTPPAWKASQNDVGYGA 60
 DB 1 HHNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKIGISAVMTTPPAWKASQNDVGYGA 60
 QY 61 YDLYDLGEFNGKGTIRTKYGRNQAAVNAKLSNGIQVYGVVNMHKGADATEMVRVAV 120
 DB 61 YDLYDLGEFNGKGTIRTKYGRNQAAVNAKLSNGIQVYGVVNMHKGADATEMVRVAV 120
 QY 121 EVNPNRNRQVSEYITEAWTKFDFPGRGNTNHNFKRWYHFDGVDWQSRKLNRIYKF 180
 DB 121 EVNPNRNRQVSEYITEAWTKFDFPGRGNTNHNFKRWYHFDGVDWQSRKLNRIYKF 180
 QY 181 RDPGKGWDWEDTENGNYDLYMADIDMDHPEVNVNLRNGVWYNTLGLDGRFIDAVKH 240
 DB 181 RGHGKAWDWDVDTENGNYDLYMADIDMDHPEVNVNLRNGVWYNTLGLDGRFIDAVKH 240
 QY 241 IKTSFTEDWLNHVRSAATGKNMFAVAEPEWKNLDGAIENYLNKTNHNSVDFVPLHYNLYNA 300
 DB 241 IKTSFTEDWLNHVRSAATGKNMFAVAEPEWKNLDGAIENYLNKTNHNSVDFVPLHYNLYNA 300
 QY 301 SKSGGNYDMRQIFNGTVVQRPHMAVTFVDNHDSDQPEALESFVEWFKPLAYALTITRE 360
 DB 301 SKSGGNYDMRQIFNGTVVQRPHMAVTFVDNHDSDQPEALESFVEWFKPLAYALTITRE 360

QY 361 QGYPSVFYGDYGIPTHTGVPAMKSKIDPILFAROKYAYGRONDYLDHNNIIGWTREGNTA 420
 DB 361 QGYPSVFYGDYGIPTHTGVPAMRSDIDPILFAROKYAYGRONDYLDHNNIIGWTREGNTA 420
 QY 421 HPNSGLATIMSDGAGGKMWFGVGNKAGQVWTDITGNRAGTFTTNADGWGNSVNGGSVS 480
 DB 421 HPNSGLATIMSDGAGGKMWFGVGNKAGQVWTDITGNRAGTFTTNADGWGNSVNGGSVS 480
 QY 481 IWNK 485
 DB 481 IWNK 485
 RESULT 13
 ABB06939
 ID ABB06939 standard; protein; 485 AA.
 AC ABB06939;
 DT 19-JUN-2002 (first entry)
 DE Bacillus termamyl-like alpha-amylase protein SEQ ID NO:13.
 XX Bacillus; termamyl-like alpha-amylase; alpha-amylase; EC 3.2.1.1;
 KW variant; mutant; enzyme; protein co-ordinate data; cleaning; detergent;
 KW washing; sweetener; ethanol; starch.
 OS Bacillus sp.
 XX WO200166712-A2.
 PD 13-SEP-2001.
 PF 07-MAR-2001; 2001WO-DK000144.
 PR 08-MAR-2000; 2000DK-00000376.
 PR 15-MAR-2000; 2000US-0189857P.
 PR 23-FEB-2001; 2001DK-00000303.
 PR 26-FEB-2001; 2001US-0271382P.
 XX (NOVO) NOVOZYMES AS.
 XX Andersen C, Borchert TV, Nielsen BR;
 WPI; 2002-239612/29.

Novel variant of parent termamyl-like alpha-amylase useful as a component
 in washing and dishwashing compositions, for textile desizing, for starch
 liquefaction, and for producing sweeteners and ethanol from starch.
 Claim 8; Page 150-151; 153pp; English.
 The present invention describes a variant of a parent termamyl-like alpha
 -amylase (EC 3.2.1.1) (I) comprising an alteration at one or more
 positions of a group of 31 possible amino acid positions. The alteration
 in (I) may be at Arg28, Arg118, Asn174, Arg181, Gly182, Asp183, Gly184,
 Gly186, Trp189, Asn195, Met202, Tyr298, Asn299, Lys302, Ser303, Asn306,
 Arg310, Asn314, Arg320, His324, Glu345, Tyr396, Arg400, Trp439, Arg444,
 Asn445, Lys446, Glu449, Arg458, Asn471, or Asn484. (I) can be used for
 washing and/or dishwashing, textile desizing, and starch liquefaction.
 (I) is useful as a component in hard surface cleaning detergent
 composition, and for producing sweeteners and ethanol from starch. (I)
 has altered solubility, preferably increased solubility, in particular
 under washing, dish washing or hard surface cleaning conditions. The
 present sequence represents a Bacillus termamyl-like alpha-amylase which
 is used in the exemplification of the present invention
 Sequence 485 AA;

Query Match 96.5%; Score 2613; DB 5; Length 485;
 Best Local Similarity 95.5%; Pred. No. 3.4e-210;
 Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

```
QY 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVG YCA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVG YCA 60
QY 61 YDYLDFEFNQKGTIRTKYGTNRQLAAVNAKLSNGIQVYGVVNMHKGADATEMVR V 120
DB 61 YDYLDFEFNQKGTIRTKYGTNRQLAAVNAKLSNGIQVYGVVNMHKGADATEMVR V 120
QY 121 EVNPNRNQEVSGEYTIETAWTKFDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
DB 121 EVNPNRNQEVSGEYTIETAWTKFDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
QY 181 RGDGKAWDEVDTEGNYDYLMDYADIMDHPVNNELRWGVTNTLGLDGFRI DAVKH 240
DB 181 RGDGKAWDEVDTEGNYDYLMDYADIMDHPVNNELRWGVTNTLGLDGFRI DAVKH 240
QY 241 IKYSFTRDWINHVRSGTKNMFVAEFAFKNDLGAIENTYLNKTNWNHVSFVDPVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSGTKNMFVAEFAFKNDLGAIENTYLNKTNWNHVSFVDPVPLHYNLYNA 300
QY 301 SKSGGNYDMRQIFNGTIVQRPMPHVAFTFVDNHDSDQPEEALESFVEEWFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRQIFNGTIVQRPMPHVAFTFVDNHDSDQPEEALESFVEEWFKPLAYALTLTRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPILFARQKYAYGRNDYLDHNNIIGWTRGNTA 420
DB 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPILFARQKYAYGRNDYLDHNNIIGWTRGNTA 420
QY 421 HPNSGLATIMSDGAGGKWMFVGRNKGAGQVWTDITGNRAGTIVTINADGNGFNSVNGSGVS 480
DB 421 HPNSGLATIMSDGAGGKWMFVGRNKGAGQVWTDITGNRAGTIVTINADGNGFNSVNGSGVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 15
AAU12155
ID AAU12155 standard; protein; 485 AA.
AC AAU12155;
DT 09-APR-2002 (first entry)
DE Bacillus TERMAMYL-like alpha-amylase 707.
XX TERMAMYL; alpha-amylase; detergent; dishwashing; textile desizing;
KW starch liquefaction; ethanol production; hard surface cleaner; sweetener;
KW amylopectin; limit dextrin; NOVAMYL; 707.
XX Bacillus sp.
XX WO200188107-A2.
XX 22-NOV-2001.
XX 10-MAY-2001; 2001WO-DK000323.
XX 12-MAY-2000; 2000DK-00000779.
XX (NOVO ) NOVOZYMES AS.
XX Svendsen A, Jorgensen CT, Nielsen BR;
XX WPI; 2002-106123/14.
XX New variant of parent Termamyl-like alpha-amylase for use as a component
XX in washing and dishwashing compositions, for textile desizing, for starch
XX liquefaction, and for producing sweeteners and ethanol from starch.
XX Claim 5; Page 81-83; 84pp; English.
XX
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CC The invention relates to a variant of parent TERMAMYL-like alpha- amylase
CC comprising an alteration at regions 186-193, 261-276, 283-293 or 334-339,
CC or at position 234, where the variant has alpha-amylase activity and each
CC position corresponds to a position of a parent Termamyl-like alpha-
CC amylase sequence having a Bacillus licheniformis alpha-amylase sequence
CC of 483 amino acids, given in specification. The variant alpha- amylase, a
CC detergent additive comprising the variant or a detergent composition
CC comprising the variant, is useful for washing and/or dishwashing or
CC textile desizing. The alpha-amylase is useful for starch liquefaction or
CC ethanol production and as a component in a hard surface cleaning
CC detergent composition, and for producing sweeteners from starch. The
CC variant has altered alpha-1, 6-D-glucosidic branch linkage cleavage
CC activity on amylopectin, preferably increased alpha-1, 6-D-glucosidic
CC branch linkage cleavage activity of amylopectin or a limit dextrin
CC prepared by TERMAMYL (RTM) or NOVAMYL (RTM). The present sequence is a
CC natural variant of the TERMAMYL alpha-amylase, 707
XX
SQ Sequence 485 AA;
Query Match 96.5%; Score 2613; DB 5; Length 485;
Best Local Similarity 95.5%; Pred. No. 3.4e-210; Indels 0; Gaps 0;
Matches 463; Conservative 13; Mismatches 9;
QY 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVG YCA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVG YCA 60
QY 61 YDYLDFEFNQKGTIRTKYGTNRQLAAVNAKLSNGIQVYGVVNMHKGADATEMVR V 120
DB 61 YDYLDFEFNQKGTIRTKYGTNRQLAAVNAKLSNGIQVYGVVNMHKGADATEMVR V 120
QY 121 EVNPNRNQEVSGEYTIETAWTKFDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
DB 121 EVNPNRNQEVSGEYTIETAWTKFDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
QY 181 RGDGKAWDEVDTEGNYDYLMDYADIMDHPVNNELRWGVTNTLGLDGFRI DAVKH 240
DB 181 RGDGKAWDEVDTEGNYDYLMDYADIMDHPVNNELRWGVTNTLGLDGFRI DAVKH 240
QY 241 IKYSFTRDWINHVRSGTKNMFVAEFAFKNDLGAIENTYLNKTNWNHVSFVDPVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSGTKNMFVAEFAFKNDLGAIENTYLNKTNWNHVSFVDPVPLHYNLYNA 300
QY 301 SKSGGNYDMRQIFNGTIVQRPMPHVAFTFVDNHDSDQPEEALESFVEEWFKPLAYALTLTRE 360
DB 301 SKSGGNYDMRQIFNGTIVQRPMPHVAFTFVDNHDSDQPEEALESFVEEWFKPLAYALTLTRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPILFARQKYAYGRNDYLDHNNIIGWTRGNTA 420
DB 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPILFARQKYAYGRNDYLDHNNIIGWTRGNTA 420
QY 421 HPNSGLATIMSDGAGGKWMFVGRNKGAGQVWTDITGNRAGTIVTINADGNGFNSVNGSGVS 480
DB 421 HPNSGLATIMSDGAGGKWMFVGRNKGAGQVWTDITGNRAGTIVTINADGNGFNSVNGSGVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 15
AAU12155
ID AAB47856 standard; protein; 485 AA.
XX AAB47856;
XX AC AAB47856;
XX 02-APR-2002 (first entry)
XX Bacillus alpha amylase 707.
XX Alpha amylase; Bacillus; Termamyl-like; maltodextrin; glucose syrup;
XX starch; food; feed; pharmaceutical; confectionery; candy; isotonic drink;
XX bakery; cereal bar; ice cream; coffee whitener; salad dressing;
XX
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XX cured meat; fermented meat; spice.
XX Bacillus sp.
XX WO200196537-A2.
XX 20-DEC-2001.
XX 13-JUN-2001; 2001WO-DK000404.
XX 14-JUN-2000; 2000DK-00000917.
XX 20-JUN-2000; 2000US-0212852P.
XX (NOVO) NOVOZYMES AS.
XX
XX Nielsen BR, Weibye M;
XX WPI; 2002-098064/13.
XX
XX New modified alpha-amylase derived from the genus Bacillus and/or is a
XX Termamyl-like alpha-amylase, which has been pre-oxidized for producing
XX maltodextrin or glucose syrup.
XX
XX Claim 5; Page 44-46; 47pp; English.
XX
XX The sequences given in ABA47850-56 show modified alpha-amylases derived
XX from the genus Bacillus. These alpha amylases are Termamyl- like alpha-
XX amylase and they have been pre-oxidized. The alpha amylase is useful for
XX producing a maltodextrin or glucose syrup, by treating starch with a pre-
XX oxidized alpha-amylase until a product with a DE between 5-45 has been
XX provided and/or until a product with a molecular weight of between 5-30
XX kda has been provided. The product comprises a maltodextrin with a DE of
XX 18.5 and/or a maltodextrin with a molecular weight of 14-16 kda. The
XX alpha amylase is useful for producing a maltodextrin or glucose syrup,
XX where the glucose syrup is useful as an ingredient in food, feed or
XX pharmaceuticals. Glucose syrup is useful in confectionery such as
XX candies, beverages such as isotonic drinks, bakery such as cereal bars,
XX dairy and ice cream such as coffee whiteners, conventional foods such as
XX salad dressings, and food ingredients and preparations such as cured
XX meat, fermented meat, spices and seasoning encapsulated flavours
XX
XX Sequence 485 AA;

Query Match 96.5%; Score 2613; DB 5; Length 485;
Best Local Similarity 95.5%; Pred. No. 3.4e-210;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 1 HHNGTNGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
DB 1 HHNGTNGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYDLGEFNQKGTIRTKYGRLOQAQVVALKNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YDLYDLGEFNQKGTIRTKYGRLOQAQVVALKNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNRQEVSGEYTIETAEWTKDFPCGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
DB 121 EVNPNRNRQEVSGEYTIETAEWTKDFPCGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
QY 181 RGDGKGDWEDVTENGNDYLYMADIDMDHPEVNVNLRNMGVWYNTLTGLDGFRIADVKH 240
DB 181 RGHGKAWDWEVDTEGNDYLYMADIDMDHPEVNVNLRNMGVWYNTLTGLDGFRIADVKH 240
QY 241 IKYSFTEDWLNHVSATGKNFAVEFWKNDLGAENYLNKTNWNHVSFVDFPLHNLNLYNA 300
DB 241 IKYSFTEDWLNHVSATGKNFAVEFWKNDLGAENYLNKTNWNHVSFVDFPLHNLNLYNA 300
QY 301 SKSGGNDYDMROIENGTVVQRHPHMTFTVDNHDSDQPEEALSFVEEWFKPLAYALTLTRE 360
DB 301 SKSGGNDYDMROIENGTVVQRHPHMTFTVDNHDSDQPEEALSFVEEWFKPLAYALTLTRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMSKIDPILFARQKYAYGRQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGIPTHGVPAMSKIDPILFARQKYAYGRQNDYLDHNNIIGWTREGNTA 420

Search completed: October 7, 2004, 00:12:24
Job time : 60.5516 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:01:38 ; Search time 14.886 Seconds
(without alignments)
3134.012 Million cell updates/sec

Title: US-09-925-576C-12

Perfect score: 2708

Sequence: 1 HHNGTNGTMMQYFEWLPND.....ADGNGFVNGGVSIVWVK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2613	96.5	518	1 A27705	alpha-amylase (EC
2	1887	69.7	512	1 ALBSL	alpha-amylase (EC
3	1870.5	69.1	549	1 A54541	alpha-amylase (EC
4	1863.5	68.8	549	1 A24549	alpha-amylase (EC
5	1859.5	68.7	549	1 A24436	alpha-amylase (EC
6	1847	68.2	514	1 ALBSN	alpha-amylase (EC
7	1813	66.9	548	1 ALBSF	alpha-amylase (EC
8	1363	50.3	493	2 S15713	alpha-amylase (EC
9	1298	47.9	484	2 G95160	alpha-amylase (imp
10	1282	47.9	484	2 F98026	alpha-amylase (EC
11	1282	47.3	492	2 AH2079	alpha-amylase (imp
12	1148	42.4	491	2 C86781	alpha-amylase (imp
13	1114	41.1	506	2 G98247	cytoplasmic alpha-
14	1113	41.1	495	2 AD3038	alpha-amylase (EC
15	1107	40.9	494	1 B45738	alpha-amylase (EC
16	1098	40.5	494	2 AD0751	cytoplasmic alpha-
17	1085	40.1	495	2 B90962	cytoplasmic alpha-
18	1075	39.7	495	1 A45738	alpha-amylase (EC
19	1066	39.4	495	2 B85810	cytoplasmic alpha-
20	363.5	13.4	217	2 A19506	alpha-amylase (EC
21	320.5	11.8	482	2 S31478	alpha-amylase (EC
22	320	11.8	1196	2 A29130	beta-amylase (EC 3
23	283.5	10.5	421	2 S10514	alpha-amylase (EC
24	280	10.3	423	2 T09942	alpha-amylase (EC
25	280	10.3	504	2 A55861	alpha-amylase (EC
26	270.5	10.0	551	2 S05667	glucan 1,4-alpha-m
27	270	10.0	440	2 S14958	alpha-amylase (EC
28	263.5	9.7	435	2 S12625	alpha-amylase (EC
29	262.5	9.7	435	2 JC7137	alpha-amylase (EC

30	262	9.7	427	1	ALBHB	alpha-amylase (EC
31	261.5	9.7	547	2	A32803	glucan 1,4-alpha-m
32	261	9.6	826	2	E96720	probable alpha-amy
33	259	9.6	428	2	T05521	alpha-amylase (EC
34	256.5	9.5	428	2	S10013	alpha-amylase (EC
35	256.5	9.5	434	2	S12775	alpha-amylase (EC
36	256.5	9.5	438	1	ALBH	alpha-amylase (EC
37	254	9.4	429	1	JE0406	alpha-amylase (EC
38	253	9.3	437	2	S14956	alpha-amylase (EC
39	253	9.3	438	2	S14957	alpha-amylase (EC
40	252.5	9.3	710	2	S63598	cyclomaltodextrin
41	252.5	9.3	1449	2	T30552	glucosyltransferas
42	250.5	9.3	413	1	ALWT3	alpha-amylase (EC
43	248.5	9.2	437	2	S07040	alpha-amylase (EC
44	247.5	9.1	713	1	ALBSXR	cyclomaltodextrin
45	246.5	9.1	498	2	A48305	alpha-amylase (EC

ALIGNMENTS

RESULT 1

AZ7705
alpha-amylase (EC 3.2.1.1) precursor - Bacillus sp.
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase; G6-amylase
C;Species: Bacillus sp.
C;Date: 31-Mar-1989 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A27705
R;Tsukamoto, A.; Kimura, K.; Iehii, Y.; Takano, T.; Yamane, K.
Biochem. Biophys. Res. Commun. 151, 25-31, 1988
A;Title: Nucleotide sequence of the maltohexaose-producing amylase gene from an alkaloph
A;Reference number: A27705; MUID:88162814; PMID:3258152
A;Accession: A27705
A;Molecule type: DNA
A;Residues: 1-518 <TSU>
A;Cross-references: GB:M1862; NID:G142496; PIDN:AAA22231.1; PID:G142497
A;Experimental source: chromosomal DNA of strain 707
A;Note: amino end of mature protein also determined
C;Comment: This is the smallest of five starch-hydrolyzing enzymes from this organism.
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-518/Product: alpha-amylase #status experimental <MAT>
F;236-369/Domain: alpha-amylase core homology <AMY>
F;139,238,273/Binding site: calcium (Asn, Asp, His) #status predicted
F;269,299,366/Active site: Asp, Glu, Asp #status predicted

Query Match 96.5%; Score 2613; DB 1; Length 518;
Best Local Similarity 95.5%; Pred. No. 2.3e-174;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy	1	HHNGTNGTMMQYFEWLPNDGNHNRRLSDASNLKDGISAVWIPPAWKASQNDVGGA	60
Db	34	HHNGTNGTMMQYFEWLPNDGNHNRRLSDASNLKDGISAVWIPPAWKASQNDVGGA	93
Qy	61	YDLYLDFEFNQKQGITRTKYGTNRNLQAAVNAKLSNGIQVYGDVVMNHKGGADATEMVR	120
Db	94	YDLYLDFEFNQKQGITRTKYGTNRNLQAAVNAKLSNGIQVYGDVVMNHKGGADATEMVR	153
Qy	121	EVNPNRNRQVSGHYTTTEAWTKFDPGNGNTHSNFKRWTHFGDQVDQSKLNRIYKF	180
Db	154	EVNPNRNRQVSGHYTTTEAWTKFDPGNGNTHSNFKRWTHFGDQVDQSKLNRIYKF	213
Qy	181	RGDCGKGDWEVDTEGNGVDYLMVADIDMDHPEVVNELNMGVWYNTLTGLDGFRI	240
Db	214	RGHKAWDWEVDTEGNGVDYLMVADIDMDHPEVVNELNMGVWYNTLTGLDGFRI	273
Qy	241	IKYSFTRDWINHVRSAFGKMFVAEFAEKNDLGAIEYLNKTNWNSHVSFVDFPLHNL	300
Db	274	IKYSFTRDWINHVRSAFGKMFVAEFAEKNDLGAIEYLNKTNWNSHVSFVDFPLHNL	333

A:Reference number: I39772; MUID:91092499; PMID:2265757

A:Accession: I39772

A>Status: translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-32,'I' <JOK>

A:Cross-references: GB:M62637; NID:g142498; PIDN:AAA22232.1; PID:g142499

R:Kuhn, H.; Fietzek, P.P.; Lampen, J.O.

J. Bacteriol. 149, 372-373, 1982

A>Title: N-terminal amino acid sequence of Bacillus licheniformis alpha-amylase: comparison with other sequences

A:Reference number: A26151; MUID:82098050; PMID:6172418

A:Accession: A26151

A:Molecule type: protein

A:Residues: 30-37,'E',39-41,'X',43-47 <KUH>

R:Machius, M.; Wiegand, G.; Huber, R.

J. Mol. Biol. 246, 545-559, 1995

A>Title: Crystal structure of calcium-depleted Bacillus licheniformis alpha-amylase at 2.2 angstrom resolution

A:Reference number: S53788; MUID:95182462; PMID:7877175

A:Accession: S53788

A:Molecule type: protein

A:Residues: 'D',220-227 <MAC>

A>Note: sequence represents amino end of an internal fragment created by a single enzymatic cleavage

R:Machius, M.; Wiegand, G.; Huber, R.

submitted to the Brookhaven Protein Data Bank, July 1995

A:Reference number: A65206; PDB:1BPL

A:Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 32-210;222-511

A>Note: structural studies suggest 163 is Leu rather than Arg

R:Sung, H.K.; Hwang, K.Y.; Chang, C.; Suh, S.W.

submitted to the Brookhaven Protein Data Bank, October 1996

A:Reference number: A66860; PDB:1VUS

A:Contents: annotation; X-ray crystallography, 1.7 angstroms, residues 32-210;222-511

C:Genetics:

A:Gene: amyL

C:Function:

A>Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A:Pathway: glycogen/starch degradation

C:Superfamily: alpha-amylase, amylolytic enzymes

C:Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide hydrolase

F:1-29/Domain: signal sequence #status predicted <Sig>

F:30-512/Product: alpha-amylase #status experimental <MAT>

F:227-360/Domain: alpha-amylase core homology <AMW>

F:133,229,264/Binding site: calcium (Asn, Asp, His) #status experimental

F:260,290,357/Active site: Asp, Glu, Asn #status experimental

Query Match 69.7%; Score 1887; DB 1; Length 512;
Best Local Similarity 68.0%; Pred. No. 8.1e-124;
Matches 330; Conservative 69; Mismatches 76; Indels 10; Gaps 4;

QY 6 NGTMMQYFEWYLPNDGNHNRLSDASNLKDGISAVWIPIPAWKAGSQNDVGAYDLVD 65
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
DB 33 NGTLMOYFEWYMPNDGQHKLQNSDAYLAEBHGITAVMIIPPAKYGTSDADVGYAYDLVD 92
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
QY 66 LGFENQGTIRTKYTGRNOLCAA VNALKSNGIQVYGDVVNMHKGGADATFEMVRVAVNP 125
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
DB 93 LGFHQGTQVTKTKYTGKELQSATKLSHRSDINVYGDVVNMHKGGADATEDVAVEVDPA 152
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
QY 126 NRNEVSGETYIEAWTKPDPFGRGNTSHNFKRWYTHFDGVWDQSRKLNRIYKFRGDGK 185
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
DB 153 DRNRVISGEHLIKAWTHFFPGRGSTYSDFKWHWYHFDGTDWDSRKL-NRIYKFQ--GK 209
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
QY 186 GWDEWVTENGNYDLYMAYDTMDHPVEVNELRKNGWYWTNTGLDGFPRIDAVKHICYSF 245
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
DB 210 AWDWEVSNENGYDLYMAYDIYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKFSF 269
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
QY 246 TRDWINHVRSATGKMFAVAFBNKDLCAL ENYLKTNWNHSHVEDVPLHYNLNASKSGG 305
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
DB 270 LRDNVNVHREXTKGEMFTVAEYQNQDGALENLYLNKTFNNHSVFDPVPLHYQHAATQGG 329
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
QY 306 NYDMRQIFNGTWQRPHMAVTVFDNHDSQPREALSEFVEEFKPLAYALTLTREGQPS 365
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
DB 330 GYDMRKLLNSTVSKHPLKAVTFVDNHDTPQGQSLESTVQTWFCKPLAYAFLTRSGYPQ 389
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
QY 366 VFYGDYGIPTFHG-----VPAMSKSIDPLEARQKYAGRQNDYLDHHNIIGHTREGNTA 420
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :

Db 390 VFYGMVG--TKGDSQREIPALKHKIBPILKARKQYAYGAQHDYDFDHDHDIIVGWTREGDSS 447
Qy 421 HPNSGLATIMSDGAGGNKMFVGRNKGAGQVWTDITGNRAGTVTITNADGWNFSVNGSVS 480
Db 448 VANSGLAALITDGPCKAKRMVYGRQNAGETWHDITGNRSEPVWVNSEGWFHVGGSVS 507
Qy 481 IWNK 485
Db 508 IYQR 512

RESULT 3
A54541
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain DN1792)
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 28-Oct-1994 #sequence_revision 18-Aug-1995 #text_change 13-Jun-1997
C;Accession: A54541
R;Jorgensen, P.L.; Poulsen, G.B.; Diderichsen, B.
FEMS Microbiol. Lett. 77, 271-276, 1991
A;Title: Cloning of a chromosomal alpha-amylase gene from Bacillus stearothermophilus.
A;Reference number: A54541
A;Accession: A54541
A;Molecule type: DNA
A;Residues: 1-549 <JQR>
A;Cross-references: GB:X59476
A;Experimental source: chromosomal DNA of strain DN1792
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-549/Product: alpha-amylase #status predicted <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 69.1%; Score 1870.5; DB 1; Length 549;
Best Local Similarity 66.9%; Pred. No. 1.3e-122;
Matches 320; Conservative 74; Mismatches 83; Indels 1; Gaps 1;
Qy 6 NGTMMQYFEWVLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKAGSONDVGYGAYDLYD 65
Db 39 NGTMMQYFEWVLPDDGTLTWKVAEANNLSLGLTALWLPAYKGRSDVGYGYDLYD 98
Qy 66 LGFENQKGTIRTKYGTNRNLQQAQAAVNAKLSNGIQYGVDMVNMHKGADATEMVRVAVENPN 125
Db 99 LGFENQKGTVRTKYGTAKYQLQAIQAAHAGMQYADVDFHKGADTEWDAVEVNP 158
Qy 126 NRQEVSGEYTIETAWTKFDPFGNGTHSNFKRWYHFDGVDWDSRKLNNRIYKFRGDGK 185
Db 159 DRNQEISGTQIQIAWTKFDPFGNGTHSNFKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
Qy 186 GMDWEVDTEGNDYLMYADIDMDHPVNLNMGVYNTTGLDGRIDAVKHKYSF 245
Db 218 AWDWEVDTEGNDYLMYADIDMDHPVNLNMGVYNTTGLDGRIDAVKHKYSF 277
Qy 246 TRDWINHVRSGATGNMFAVAEFWKNLDCATENYLNKTNWNSHVPDVLPHYLNASKSGG 305
Db 278 FPDWLSVRSQTGKPLFTVGEYWSYDINKLHNYITKIDGTWMSLTDAPLHNFYTSKSGG 337
Qy 306 NYDMRQIFNGTVQVRHMPHIAVTFVDNHDSPQEEALESFVEWFKFLAYALTLTREQGYPS 365
Db 338 AFDMRTLWNTLMKDQPLAVTFVDNHDTEPGALQSWDPWFKFLAYALTLTREQGYPC 397
Qy 366 VFYGDYGIPTGHVPAWMSKIDPILKARKQYAYGRQNDYLDHNNIIGWTRGNTAHNPSG 425
Db 398 VFYGDYGIPTGHVPAWMSKIDPILKARKQYAYGRQNDYLDHNNIIGWTRGNTAHNPSG 457

Qy 426 LATIMSDGAGGNKMFVGRNKGAGQVWTDITGNRAGTVTITNADGWNFSVNGSVSIWV 483
Db 458 LAALITDGPCKAKRMVYGRQNAGETWHDITGNRSDTITNADGWNFSVNGSVSIWV 515

RESULT 4
A24549
alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus (strain NZ-3)
N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase
C;Species: Bacillus stearothermophilus
C;Date: 30-Jun-1988 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C;Accession: A24549; I39501; I39770
R;Gray, G.L.; Mainzer, S.E.; Rey, M.W.; Lamea, M.H.; Kindle, K.L.; Carmona, C.; Requadt,
J. Bacteriol. 166, 635-643, 1986
A;Title: Structural genes encoding the thermophilic alpha-amylases of Bacillus stearother
A;Reference number: A91817; MUID:86195857; PMID:3009417
A;Accession: A24549
A;Molecule type: DNA
A;Residues: 1-549 <GRA>
A;Cross-references: GB:M13255; NID:g142512; PIDN:AAA22241.1; PID:g142513
A;Experimental source: genomic DNA of strain NZ-3
R;Satoh, H.; Nishida, H.; Isono, K.
J. Bacteriol. 170, 1034-1040, 1988
A;Title: Evidence for movement of the alpha-amylase gene into two phylogenetically dista
A;Reference number: I39501; MUID:88139156; PMID:3257753
A;Accession: I39501
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 536-549 <RES>
A;Cross-references: GB:M29577; NID:g142476; PIDN:AAA22225.1; PID:g142478
A;Experimental source: strain DY-5
A;Accession: I39770
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 536-549 <RE2>
A;Cross-references: GB:M29578; NID:g142484; PIDN:AAA22228.1; PID:g142486
A;Experimental source: strain 799
C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the
C;Genetics:
A;Start codon: GTG
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysac
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-549/Product: alpha-amylase #status predicted <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 68.8%; Score 1863.5; DB 1; Length 549;
Best Local Similarity 66.9%; Pred. No. 3.8e-122;
Matches 320; Conservative 73; Mismatches 84; Indels 1; Gaps 1;
Qy 6 NGTMMQYFEWVLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKAGSONDVGYGAYDLYD 65
Db 39 NGTMMQYFEWVLPDDGTLTWKVAEANNLSLGLTALWLPAYKGRSDVGYGYDLYD 98
Qy 66 LGFENQKGTIRTKYGTNRNLQQAQAAVNAKLSNGIQYGVDMVNMHKGADATEMVRVAVENPN 125
Db 99 LGFENQKGTVRTKYGTAKYQLQAIQAAHAGMQYADVDFHKGADTEWDAVEVNP 158
Qy 126 NRQEVSGEYTIETAWTKFDPFGNGTHSNFKRWYHFDGVDWDSRKLNNRIYKFRGDGK 185
Db 159 DRNQEISGTQIQIAWTKFDPFGNGTHSNFKRWYHFDGVDWDSRKL-SRIYKFRGIGK 217
Qy 186 GMDWEVDTEGNDYLMYADIDMDHPVNLNMGVYNTTGLDGRIDAVKHKYSF 245
Db 218 AWDWEVDTEGNDYLMYADIDMDHPVNLNMGVYNTTGLDGRIDAVKHKYSF 277
Qy 246 TRDWINHVRSGATGNMFAVAEFWKNLDCATENYLNKTNWNSHVPDVLPHYLNASKSGG 305

Db 278 FPDWLSVRSQTGKPLFTVGEYMSYDINKLHNYITKTNGTMSLFDAPLHNKFTYASKSGG 337

QY 306 NYDMROIENGTVQVRHMAHTVFDVNDHDSQPEALESFVEEWPKPPLAYALTITRBOGYPS 365

Db 338 AFDMSTMMNTLMKQDPTLATVFDVNDHDEPQALQSWDPWPKPLAYAFILTRBOGYPC 397

QY 366 VFYGDYIGTPTGVHPAMKSKIDPILBARQKYAGRQNDYLDHNNIIGTWREGNTAHPNSG 425

Db 398 VFYGDYIGPQYNIPLSKSKIDPLLIARRDYAGTQHDYLDHSDIIGTWREGVTEKPGSG 457

QY 426 LATIMSDGAGGNKMFVGRNKAQVWTDITGNRAGTVTTINADGWNFSVNGSVSIWV 483

Db 458 LAALITDGGGSKMYVKGHAGKVFDLTGNRSDTVTINSDDGGEFKVNGGVSVMV 515

RESULT 5

A24436

alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid pAT5

N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C;Species: Bacillus stearothermophilus

C;Date: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999

C;Accession: A24436; I39777

R;Nakajima, R.; Imanaka, T.; Aiba, S.

J. Bacteriol. 163, 401-406, 1985

A;Reference number: A24436; MUID:85234394; PMID:3924897

A;Accession: A24436

A;Molecule type: DNA

A;Residues: 1-549 <NA>

A;Cross-references: GB:M1450

A;Experimental source: plasmid pAT5

A;Note: amino end of the mature protein also determined

R;Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen, B.

Gene 96, 37-41, 1990

A;Title: In vivo genetic engineering: homologous recombination as a tool for plasmid construction

A;Reference number: I39772; MUID:91092499; PMID:2465757

A;Accession: I39777

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-45 <RES>

A;Cross-references: GB:M62638; NID:gl42514; PIDN:AAA22242.1; PID:gl42515

C;Comment: Alpha-amylase genes have been found on plasmids and in multiple copies on the chromosome

C;Genetics:

A;Gene: amyS

A;Genome: plasmid

A;Start codon: GTG

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide degradation

F;1-34/Domain: signal sequence #status predicted <SIG>

F;35-549/Product: alpha-amylase #status experimental <MAT>

F;235-368/Domain: alpha-amylase core homology <AMY>

F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted

F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 68.7%; Score 1859.5; DB 1; Length 549;

Best Local Similarity 66.7%; Pred. No. 7.3e-122;

Matches 319; Conservative 73; Mismatches 85; Indels 1; Gaps 1;

QY 6 NGTMMQYFEWYLPNDGNHNNRLSDASNLKDGISAVWIPPAWKASQNDVGVGYDLYD 65

Db 39 NGTMMQYFEWYLPDDGTLTWTKVANEANLSSGLTALWLPAYKGTSRSDVGVGYDLYD 98

QY 66 LGFBNQKGTTRTKYGTNQLQAAVNAKNSGIVYGDVWVNHKGADATEMVPAVEVNP 125

Db 99 LGFBNQKGAVRTKYGTGKAOYLQIAHAAGMQVYADVDFHKGAGDGTWVDVAVEVNS 158

QY 126 NRNQVSGEYTIKAWTKFDPFGNGTHSNPKRWYHFDGVDYDQSKLNRIYKFRGDGK 185

Db 159 DRNQEISGTYIQIANTKFPFGKNGTYSSFKRWYHFDGVDNDSRKL-SRIYKFRGIGK 217

QY 186 GWDWEVDTENGNDYLYMAYDIDMDHPVNVNLRNWGVWYNTLTGLDGFRIADVHKIKYSP 245

RESULT 6

ALBN

alpha-amylase (EC 3.2.1.1) precursor - Bacillus amylioliquefaciens

N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C;Species: Bacillus amylioliquefaciens

C;Date: 30-Nov-1980 #sequence_revision 30-Jun-1987 #text_change 18-Jun-1999

C;Accession: A92389; A90307; I39756; I39763; A00843

R;Takkinen, K.; Pettersson, R.F.; Kalkkinen, N.; Palva, I.; Soderlund, H.; Kaariainen, L.

J. Biol. Chem. 258, 1007-1013, 1983

A;Title: Amino acid sequence of alpha-amylase from Bacillus amylioliquefaciens deduced from cDNA

A;Reference number: A92389; MUID:83108808; PMID:6185474

A;Contents: pUB110

A;Accession: A92389

A;Molecule type: DNA

A;Residues: 1-514 <NA>

A;Cross-references: GB:J01542; GB:J01543; GB:M12033; GB:M12034; NID:gl42428; PIDN:AAA22151

R;Chung, H.S.; Friedberg, F.

Biochem. J. 185, 387-395, 1980

A;Title: Sequence of the N-terminal half of Bacillus amylioliquefaciens alpha-amylase.

A;Reference number: A90307; MUID:80241725; PMID:6156671

A;Accession: A90307

A;Molecule type: protein

A;Residues: 32-53, 'I', 55-63, 'L', 65-78, 'D', 80-83, 'S', 85-222 <CHU>

R;Palva, I.; Pettersson, R.F.; Kalkkinen, N.; Lehtovaara, P.; Sarvas, M.; Soderlund, H.;

Gene 15, 43-51, 1981

A;Title: Nucleotide sequence of the promoter and NH2-terminal signal peptide region of the alpha-amylase gene

A;Reference number: I39756; MUID:82051296; PMID:6170539

A;Accession: I39756

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-96 <RES>

A;Cross-references: EMBL:V00092; NID:g39297; PIDN:CAA23430.1; PID:g39298

R;Ruohonen, L.; Hackman, P.; Lehtovaara, P.; Knowles, J.K.C.; Karaenen, S.

Gene 59, 161-170, 1987

A;Title: Efficient secretion of Bacillus amylioliquefaciens alpha-amylase cells by its own signal peptide

A;Reference number: I39763; MUID:88137952; PMID:2830166

A;Accession: I39763

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-39 <RES>

A;Cross-references: GB:M18424; NID:gl42430; PIDN:AAA22192.1; PID:gl42431

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: alpha-amylase, amylioliquefaciens type; alpha-amylase core homology

C;Keywords: extracellular protein; glycosidase; hydrolase; polysaccharide degradation

F;1-31/Domain: signal sequence #status predicted <SIG>

F;32-514/Product: alpha-amylase #status predicted <MPT>

F;229-362/Domain: alpha-amylase core homology <AMY>

F;133,231,266/Binding site: calcium (Asn, Asp, His) #status predicted

F;262,292,359/Active site: Asp, Glu, Asp #status predicted

Query Match 68.2%; Score 1847; DB 1; Length 514;

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquifaciens type; alpha-amylase core homology
C;Keywords: extracellular protein; glycosidase; heat-stable protein; hydrolase; polysaccharide
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-548/Product: alpha-amylase #status experimental <MAT>
F;235-368/Domain: alpha-amylase core homology <AMY>
F;139,237,272/Binding site: calcium (Asp, Asp, His) #status predicted
F;268,298,365/Active site: Asp, Glu, Asp #status predicted

Query Match 66.9%; Score 1813; DB 1; Length 548;
Best Local Similarity 65.9%; Pred. No. 1.3e-118;
Matches 315; Conservative 70; Mismatches 91; Indels 2; Gaps 2;

Qy 6 NGTMQYFEWYLPNDGNHNRRLRSKDNLKDGISAVWIPPAAWKAGSQNDVGYGYDLYD 65
Db NGTMQYFEWYLPDDGTWTKVANEANNLSSLGITALSPPAYKGTSRSDVGVGYDLYD 98
Qy 66 LGSEFNOKGIRTKYGTGRNQLQAAVNAKNGQYQVGVVNNHKKGGADATETMRAVEVNP 125
Db LGSEFNOKGIRTKYGTGRNQLQAAVNAKNGQYQVGVVNNHKKGGADATETMRAVEVNP 158
Qy 126 NRNOEVSGETTIEAWTKFPPGGRGNTHSKFKRWYHFDGVDNDSRKLNNRIYKPRGDGK 185
Db NRNOEVSGETTIEAWTKFPPGGRGNTHSKFKRWYHFDGVDNDSRKLNNRIYKPRGDGK 217
Qy 186 GNDWEVDTEGNYDYLMYADIDMDHPEVNNELRNWGVYTTNTLGLDGFRIADVKHKIYSF 245
Db GNDWEVDTEGNYDYLMYADIDMDHPEVNNELRNWGVYTTNTLGLDGFRIADVKHKIYSF 277
Qy 246 TRDWINHVSATSGKNMFAVAEPWKNDLGAIENYLNKTNWHSVDFVPLHYNLYNASKSGG 305
Db TRDWINHVSATSGKNMFAVAEPWKNDLGAIENYLNKTNWHSVDFVPLHYNLYNASKSGG 337
Qy 306 NYDMRQIFNGTVVQRPHMAVTFVDNHDQPEEALSSFVEEMPKLAYALTLTREOGYPS 365
Db NYDMRQIFNGTVVQRPHMAVTFVDNHDQPEEALSSFVEEMPKLAYALTLTREOGYPS 396
Qy 366 VFYGDYVGIPTGHVPAWKSKIDPILBAROKYAYGRONDYLDHNNIIGWTREGNTHAPNSG 425
Db VFYGDYVGIPTGHVPAWKSKIDPILBAROKYAYGRONDYLDHNNIIGWTREGNTHAPNSG 456
Qy 426 LATIMSDGAGGNKWMFVGRNKAQGVWTDITGNRAGTFTVINADGWNFSVNGSGSVTW 483
Db LATIMSDGAGGNKWMFVGRNKAQGVWTDITGNRAGTFTVINADGWNFSVNGSGSVTW 514

RESULT 8
S15713
alpha-amylase (EC 3.2.1.1) - Bacillus circulans
C;Species: Bacillus circulans
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C;Accession: S15713
R;Marcel, T.
submitted to the EMBL Data Library, May 1991
A;Reference number: S15713
A;Accession: S15713
A;Molecule type: DNA
A;Residues: 1-493 <WAR>
A;Cross-references: EMBL:X60779; NID:g39411; PIDN:CAA43194.1; PID:g39412
C;Genetics:
A;Gene: amyE
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: alpha-amylase, amyloliquifaciens type; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;200-333/Domain: alpha-amylase core homology <AMY>

Query Match 50.3%; Score 1363; DB 2; Length 493;
Best Local Similarity 51.1%; Pred. No. 2.4e-87;
Matches 246; Conservative 78; Mismatches 149; Indels 8; Gaps 3;

```
QY 6 NGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVGAYDLYD 65
Db 4 NHTMMQF FEWHLAADGDHWRKLAEMAPELKAGKIDTVWVPVTKAVSAEDTGYGYDLYD 63
QY 66 LGFEFNQKGTIRTKYGRNLOQAANVNAKLSNGIQVYGDVVMNKHGGADATMVRAVEVNP 125
Db 64 LGFEFDQKGTIRTKYGRNLOQAANVNAKLSNGIQVYGDVVMNKHGGADATMVRAVEVNP 123
QY 126 NRNQVSGEYTTIETAWTKFDPGGRGNTHSNFKRWYHFDGVDQSKLNRIYKFRGDGK 185
Db 124 DRTKELSEPEFEIGWTKFTFPGRGDQYSSFKWNSHFNGTDFD-AKEERTGYRIAGENK 182
QY 186 GMDWEVDTEGNGYDLYMAYADIDMDHPEVNVNLRNMGVWVNTLTGLDGFRIADVGHKY 245
Db 183 KWNENVDDEGNGYDLYMAYADIDMDHPEVNVNLRNMGVWVNTLTGLDGFRIADVGHKY 242
QY 246 TRDWINHVRSATGKMFVAEFAEWMKNDLGAENYLNKTNWNHVSFVDPVPLHYNLYNASKS 305
Db 243 IKFEFAAEMIRKRGQDFYIVGFEFVNSNLDACREFLDTVDYQIDLFDVSLHYKLHEASLGR 302
QY 306 NYDMROI FNGTVVQRHPMEAVTPVDNHDQPEBALESFVEEWFKPLAYALTLTREOGY 365
Db 303 DFLSKIFDPTLVQTHETHAVTFVDNHDQPEBALESFVEEWFKPLAYALTLTREOGY 362
QY 366 VFYGDYGI-----PTHGVPAMSKIDPILAEARKQYAYGRQNDYLDHNNIIGWTREGNTAH 421
Db 363 VFYGDYGI GGPFPVVG---KKEILDILLSARCKAYGQEDYFDHANTIGWVRGVEI 419
QY 422 PNSGLATIMSDGAGGNKMFVGRNKGAVQVWTDITGNRAGTVTINADGWNFSVNGSGSVI 481
Db 420 EGSACVAVISNGDGEKRMFIGHSHRAGEVWVLDITKSCDDQITTEEDGWATFHVCGGGSV 479
QY 482 W 482
Db 480 W 480

RESULT 9
G95160
alpha-amylase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: G95160
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: G95160
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-484 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK75480.1; PID:g14972868; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
C:Gene: SPI382
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 47.9%; Score 1298; DB 2; Length 484;
Best Local Similarity 50.6%; Pred. No. 7.8e-83;
Matches 243; Conservative 69; Mismatches 162; Indels 6; Gaps 4;

QY 6 NGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVGAYDLYD 65
Db 3 NOTLMMQYFEWYLPNDGQHWTRLAENAPHLAHLGISHVWMPAPAFKATNEKDVGVGYDLYD 62
QY 66 LGFEFNQKGTIRTKYGRNLOQAANVNAKLSNGIQVYGDVVMNKHGGADATMVRAVEVNP 125
Db 63 LGFEFNQKGTIRTKYGRNLOQAANVNAKLSNGIQVYGDVVMNKHGGADATMVRAVEVNP 122
QY 126 NRNQVSGEYTTIETAWTKFDPGGRGNTHSNFKRWYHFDGVDQSKLNRIYKFRGDGK 185
Db 124 DRTKELSEPEFEIGWTKFTFPGRGDQYSSFKWNSHFNGTDFD-AKEERTGYRIAGENK 182
QY 186 GMDWEVDTEGNGYDLYMAYADIDMDHPEVNVNLRNMGVWVNTLTGLDGFRIADVGHKY 243
Db 183 KWNENVDDEGNGYDLYMAYADIDMDHPEVNVNLRNMGVWVNTLTGLDGFRIADVGHKY 242
QY 246 TRDWINHVRSATGKMFVAEFAEWMKNDLGAENYLNKTNWNHVSFVDPVPLHYNLYNASKS 303
Db 243 IKFEFAAEMIRKRGQDFYIVGFEFVNSNLDACREFLDTVDYQIDLFDVSLHYKLHEASLGR 302
QY 306 NYDMROI FNGTVVQRHPMEAVTPVDNHDQPEBALESFVEEWFKPLAYALTLTREOGY 365
Db 303 DFLSKIFDPTLVQTHETHAVTFVDNHDQPEBALESFVEEWFKPLAYALTLTREOGY 362
QY 482 W 482
Db 480 W 480
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Db 123 DRTVBLGEPFTINGWTSFTFDGRQDTYNGFHHWYHFTGTDYDAKRS-KSGIYLIQGDNK 181
QY 186 GMDWE--VDTENGNYDLYMAYADIDMDHPEVNVNLRNMGVWVNTLTGLDGFRIADVGHKY 243
Db 182 GWANEELVDNENGNYDLYMAYADIDMDHPEVNVNLRNMGVWVNTLTGLDGFRIADVGHKY 241
QY 244 SFTRDWINHVRSATGKMFVAEFAEWMKNDLGAENYLNKTNWNHVSFVDPVPLHYNLYNASKS 303
Db 242 FMRNFIRDMKKEYGDDFYVGFGEFVNSNLDACREFLDTVDYQIDLFDVSLHYKLHEASLGR 301
QY 304 GNYDMROI FNGTVVQRHPMEAVTPVDNHDQPEBALESFVEEWFKPLAYALTLTREOGY 363
Db 302 GANYDLRGIFTDSLVELKPDKAFTVFDNHDQPEBALESFVEEWFKPLAYALTLTREOGY 361
QY 364 PSVFYGDYGI P--THGVPAMSKIDPILAEARKQYAYGRQNDYLDHNNIIGWTREGNTAH 422
Db 362 PCVFYGDYGI SGYQAQEDFKEILDRLJLAIRKDLAYGQNDYFDHANCIGWVRSG--AEN 419
QY 423 NSGLATIMSDGAGGNKMFVGRNKGAVQVWTDITGNRAGTVTINADGWNFSVNGSGSVI 482
Db 420 QSPIAVLISNDQENSKSMFVGQEWNTQTFVLLGNHQGVTDIDERGQGFVPSARSVSW 479

RESULT 10
F98026
alpha-amylase (BC 3.2.1.1) precursor [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C:Accession: F98026
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: F98026
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-484 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAI00043.1; PID:g15458876; GSPDB:GN00174
C:Genetics:
C:Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase

Query Match 47.9%; Score 1296; DB 2; Length 484;
Best Local Similarity 50.4%; Pred. No. 1.1e-82;
Matches 242; Conservative 71; Mismatches 161; Indels 6; Gaps 4;

QY 6 NGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVGAYDLYD 65
Db 3 NOTLMMQYFEWYLPNDGQHWTRLAENAPHLAHLGISHVWMPAPAFKATNEKDVGVGYDLYD 62
QY 66 LGFEFNQKGTIRTKYGRNLOQAANVNAKLSNGIQVYGDVVMNKHGGADATMVRAVEVNP 125
Db 63 LGFEFNQKGTIRTKYGRNLOQAANVNAKLSNGIQVYGDVVMNKHGGADATMVRAVEVNP 122
QY 126 NRNQVSGEYTTIETAWTKFDPGGRGNTHSNFKRWYHFDGVDQSKLNRIYKFRGDGK 185
Db 123 DRTVBLGEPFTINGWTSFTFDGRQDTYNGFHHWYHFTGTDYDAKRS-KSGIYLIQGDNK 181
QY 186 GMDWE--VDTENGNYDLYMAYADIDMDHPEVNVNLRNMGVWVNTLTGLDGFRIADVGHKY 243
Db 182 GWANEELVDNENGNYDLYMAYADIDMDHPEVNVNLRNMGVWVNTLTGLDGFRIADVGHKY 241
QY 244 SFTRDWINHVRSATGKMFVAEFAEWMKNDLGAENYLNKTNWNHVSFVDPVPLHYNLYNASKS 303
Db 242 FMRNFIRDMKKEYGDDFYVGFGEFVNSNLDACREFLDTVDYQIDLFDVSLHYKLHEASLGR 301
QY 304 GNYDMROI FNGTVVQRHPMEAVTPVDNHDQPEBALESFVEEWFKPLAYALTLTREOGY 363
```

Db 302 GANYDLRGITDLSVLEIKPKAVTFVNDHDTQRCQALESTVEWFKPAAYALILLRQDGL 361
Qy 364 PSVFGYDYGIP-THGVPAKMSKIDPILAEARQKAYGRQNDYLDHNNIIGTWREGNTAHP 422
Db 362 PCVFGYDYGISGQYAOQDPKEILLRLAIRKOLAYGEONDYDFHANCIGWVRSG--AEN 419
Qy 423 NSGLATIMSDGAGNKWFMVGRNKAGQWTDITGNRAGTVTINADGNFNSVNGSGSVIW 482
Db 420 QSPIAVLISNDQENSKSMFVGQEWNTQTFVDLLSGHQGVTDIBEGYQGFVPSARSVSW 479
RESULT 11
AH2079
alpha-amylase [imported] - Nostoc sp. (strain PCC 7120)
C/Species: Nostoc sp. PCC 7120
A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C/Accession: AH2079
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AH2079
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-492 <KUR>
A/Cross-references: GB:BA000019; PIDN:BA073889.1; PID:g17131281; GSPDB:GN00179
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: alr2190
C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
Query Match 47.3%; Score 1282; DB 2; Length 492;
Best Local Similarity 49.8%; Pred. No. 1e-81;
Matches 244; Conservative 78; Mismatches 152; Indels 16; Gaps 5;
Qy 6 NGTMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKG-ASQNDVGVGYDLY 64
Db 5 NGTMQYFHWYIPNDGNLWSKVASAPELADAGFTAMWLPAYKGFAGSFDVGIVGYDLF 64
Qy 65 DLGFNQKGTIRTKYGRNQLQAVALNKSNGIQVGVVNMHKGADATEMVRAVEVNP 124
Db 65 DLGFNQKGTIRTKYGRNQLQAVALNKSNGIQVGVVNMHKGADATEMVRAVEVNP 124
Qy 125 NNRNOEVSGETTAEATKFPDPRGNTHSNFKRWYHFDVGDVMDQSRKLNRIYKPRGDG 184
Db 125 DRLNPKGGLQDIKTYTHYFPGQKYSNFEWHWHFDDAVDYNEYS-GDRSTVYLLG 183
Qy 185 KGWDWEYDTEGNYDLYMAYADIMDHPVNVNLRNNGVWYNTLGLDGFRIADAVKHYS 244
Db 184 KNFDYVALEKGNFAYLWGCDDLPQNEWVRGEVTVYWGKCLDTTKVDGFRIDAIKHISTW 243
Qy 245 FTDRWNHVSATGKMFVAEFAWNDLGAENLYLNTNNHNSVDFVPLHYNLNAKSG 304
Db 244 FPEWIDALERHAKGLFMVGEYVNDINTLLWTVDAVRGKMSVDFVPLHYNFHAQKSG 303
Qy 305 GNYDMRQIFNGTVVQRHPHMAVTFVDNHDSDPEALESFVEEWFKPLAYALTITREOGYP 364
Db 304 GNYDMRQIFNGTVVQRHPHMAVTFVDNHDSDPEALESFVEEWFKPLAYALTITREOGYP 363
Qy 365 SVFYDYGIPTHG-----VPAMSKIDPILAEARQKAYGRQNDYLDHNNIIGW 413
Db 364 CVFHADYGAIEYEDWGDGNGRNYIFMPSHRWIDKLLYARKHAYGQYNYLDHNNIIGW 423
Qy 414 TRENTAHPNSGLATIMSDGAGNKWFMVGRNKAGQWTDITGNRAGTVTINADGNFNS 473
Db 424 TRLDGADHP-QGMVAVIMSDGSEGIKMWEGV--KPTNKFIDLTEHKEAVYTNEWGMGEFR 480
Qy 474 VNGSGSVIHW 483
Db 481 CLGGSVSVWV 490

RESULT 12

C86781

alpha-amylase [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C/Species: Lactococcus lactis subsp. lactis

C/Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C/Accession: C86781

R:Bohlin, A.; Winkler, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A/Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp

A/Reference number: A86625; MUID:21235186; PMID:11337471

A/Accession: C86781

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-491 <STO>

A/Cross-references: GB:AE005176; PID:g12724224; PIDN:AAK05349.1; GSPDB:GN00146

A/Experimental source: strain IL1403

C/Genetics:

A/Gene: amyL

C/Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 42.4%; Score 1148; DB 2; Length 491;

Best Local Similarity 43.2%; Pred. No. 2.2e-72;

Matches 207; Conservative 96; Mismatches 172; Indels 4; Gaps 3;

Qy 8 TMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKAS-QNDVGVGYDLYDL 66

Db 3 TILQAFEWYLPSPDSQHNNIKENIPDLGLGFGSLWLPASKAASGVEDVGYGYDLYDL 62

Qy 67 GEFNQKGTIRTKYGRNQLQAVALNKSNGIQVGVVNMHKGADATEMVRAVEVNP 126

Db 63 GEFNQKGTIRTKYGRNQLQAVALNKSNGIQVGVVNMHKGADATETETIADKAED 122

Qy 127 RNOEVSGETTAEATKFPDPRGNTHSNFKRWYHFDVGDVMDQSRKLNRIYKPRGDG 186

Db 123 HLNNIENKTYEVTWTKFTFPGQKQYDNIYTWNNFTGIDYDE-RKQEEILEF--SGHE 179

Qy 187 WDWEYDTEGNYDLYMAYADIMDHPVNVNLRNNGVWYNTLGLDGFRIADAVKHYSFT 246

Db 180 WDENVDSNNFDYLMGADLDFSVSETVEQLEKWHFSEMTKIDGFRDAIKHIDPKYF 239

Qy 247 RDWINHVSATGKMFVAEFAWNDLGAENLYLNTNNHNSVDFVPLHYNLNAKSGGN 306

Db 240 DKWLEQRAKDLRKLFVGEYVNDLGLKLEYLLEQSSDRIQLFDVPLHFNKKEASSTNGE 299

Qy 307 YDMRQIFNGTVVQRHPHMAVTFVDNHDSDPEALESFVEEWFKPLAYALTITREOGYPSV 366

Db 300 FDMRTULFDHTLTASQPELSVTFVDNHDHTQEQALQSWIPAWFKEHAYSLLILRRKKTPTV 359

Qy 367 FYGDYGIPTGHPAMKSKIDPILAEARQKAYGRQNDYLDHNNIIGTWREGNTAHPNSGL 426

Db 360 FWGLDYGIPSHNVNPGDNLRTMLARKDSEFIRENDYDFHPIIGWNTILKIDNKEYGL 419

Qy 427 ATTMDSGAGNKWFMVGRNKAGQWTDITGNRAGTVTINADGNFNSVNGSGSVIWNK 485

Db 420 SCILTNKNGSKYMIIDKAVAGKYIDLFRHPIPTLDQNGGAEFVNDGSGSVVWYDK 478

RESULT 13

C98247

cytoplasmic alpha-amylase (1,4-alpha-d-glucan glucanohydrolase) [imported] - Agrobacteri

C/Species: Agrobacterium tumefaciens

C/Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002

C/Accession: G98247

R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qureshi, B.; Goldman, B.;

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A/Reference number: A97359; MUID:21608551; PMID:11743194

A/Accession: G98247

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-506 <KUR>

A;Cross-references: GB:AE007870; PIDN:AAK89505.1; PID:g15159379; GSPDB:GN00170
 C;Genetics:
 A;Gene: AGR_L_1863

A;Map position: linear chromosome
 C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Query Match 41.1%; Score 1114; DB 2; Length 506;
 Best Local Similarity 44.9%; Pred. No. 5.4e-70;
 Matches 222; Conservative 79; Mismatches 177; Indels 16; Gaps 6;

QY 3 NGTGMQYFEWYLPNDGNHNRSLSDASNLKDGISAVWIPPAWKASQN-DVGYGAY 61
 DB 11 NMAGRLLQFFHYYPDGGKLMSEVAEAKESLAKMGITDVLPPAYKGAAGYSVGYDTY 70

QY 62 DLYDLGEFNQKGTIRTKYGRNOLQAVALNKSNGIQVYGVVNMHKGADATMVRV 121
 DB 71 DLFDELGEFQKGVATKYGDRAALEHAGKTLKONGIRVTHDVVNLHMGADAKEKVRVR 130

QY 122 VNPNNRQEVSGEYTTIEAWTKFDPGRGNTHSNFKRWYHFDGVDWDSQSKLNN--RIYK 179
 DB 131 VNPDDRTDIDDEFPALAYTRFTFPGRNKGKSKFIWDLKCFSGVDHIEBPTEDGIFRLVN 190

QY 180 FRDGGKGMWEDVTENGVDYLMYADIDMDHPVNVNELRWGVMYVNTLGLDGFRLDAVK 239
 DB 191 EYGDGE-WNEEVQDENGDFYLMGADVEFRNRAVYBELKYWGRLSEQVQVDFGLDAK 249

QY 240 HIKYSTRWINHVRSAATGKMFVAFWKNLDGALENYLNKTNWHSVDFVPLHYNLYN 299
 DB 250 HIPAWFRDVGHRMRETVDPLFVVAEYWHPDLEALKSLYELVDKQLMDFVALHHSFID 309

QY 300 ASKSGGNYDMRQIFNGTVQORHPMHAFTFVDNHSQPEEALESFVBEWFKPLAYALTTLTR 359
 DB 310 ASKQGDGDMRSIFDGLSLVSAVDPHATVLDNHDTPQLQSLAPVFPFKPLAYAIIILLR 369

QY 360 EQYPSVFGYDYG--IPTHGVPAKSKID-----PILEARQKAYGRQNDYLDHNI 409
 DB 370 EGVPCVFPDLFGTSYTDGNDGNEYKIDIPAECLPKLIEARSFANGPQTDIFDDAS 429

QY 410 IIGWTRGNTAHNSGLATIMSGAGNKMVFGRNKGAGVQVTDITGNRAGTWTINADGW 469
 DB 430 CIAFIRHGTADAP--GCVVMSNGEPEGEKQADLGPERRAGSVWRDFLGHREHITLDESCK 487

QY 470 GNFSVNGSGSVIWW 483
 DB 488 GTPTNGSGSVVWV 501

RESULT 14
 AD3038
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens (strain C58, Dupont)
 C;Species: Agrobacterium tumefaciens
 C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AD3038

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-495 <KUR>

A;Cross-references: GB:AE008689; PIDN:AAK44722.1; PID:g17742354; GSPDB:GN00187

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: amya

A;Map position: linear chromosome

C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

Best Local Similarity 45.2%; Pred. No. 6.2e-70;
 Matches 221; Conservative 79; Mismatches 173; Indels 16; Gaps 6;

QY 8 TMOYFEWYLPNDGNHNRSLSDASNLKDGISAVWIPPAWKASQN-DVGYGAYDLYDL 66
 DB 5 TLLQFFHYYPDGGKLMSEVAEAKESLAKMGITDVLPPAYKGAAGYSVGYDTYDLYDL 64

QY 67 GEFNQKGTIRTKYGRNOLQAVALNKSNGIQVYGVVNMHKGADATMVRVAVVNPNN 126
 DB 65 GEFQKGTIVATKYGDRAALEHAGKTLKONGIRVTHDVVNLHMGADAKEKVRVRVNPDD 124

QY 127 RNOEVSGEYTTIEAWTKFDPGRGNTHSNFKRWYHFDGVDWDSQSKLNN--RIYKFRGDG 184
 DB 125 RTDIDDEFPALAYTRFTFPGRNKGKSKFIWDLKCFSGVDHIEBPTEDGIFRLVNEYGDG 184

QY 185 KGWMEVDTENGVDYLMYADIDMDHPVNVNELRWGVMYVNTLGLDGFRLDAVKHIKYS 244
 DB 185 E-WNEEVQDENGDFYLMGADVEFRNRAVYBELKYWGRLSEQVQVDFGLDAKHPAW 243

QY 245 FTRDWINHVRSAATGKMFVAFWKNLDGALENYLNKTNWHSVDFVPLHYNLYNASKSG 304
 DB 244 FRDVGHRMRETVDPLFVVAEYWHPDLEALKSLYELVDKQLMDFVALHHSFHDASKQG 303

QY 305 GNYDMRQIFNGTVQORHPMHAFTFVDNHSQPEEALESFVBEWFKPLAYALTTLTREOGVP 364
 DB 304 GDFMRSIFDGLSLVSAVDPHATVLDNHDTPQLQSLAPVFPFKPLAYAIIILLREGV 363

QY 365 SVFYGYDYG--IPTHGVPAKSKID-----PILEARQKAYGRQNDYLDHNIIGWT 414
 DB 364 CVFYDPLFGTSYTDGNDGNEYKIDIPAECLPKLIEARSFANGPQTDIFDDASCIAP 423

QY 415 REGNTAHNSGLATIMSGAGNKMVFGRNKGAGVQVTDITGNRAGTWTINADGNGNSV 474
 DB 424 RHGTADAP--GCVVMSNGEPEGEKQADLGPERRAGSVWRDFLGHREHITLDESCKGTPT 481

QY 475 NGSGSVIWW 483
 DB 482 NGSGSVVWV 490

RESULT 15
 B45738
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium typhimurium

N;Alternate names: 1,4-alpha-D-glucan glucanohydrolase

C;Species: Salmonella typhimurium

C;Date: 07-Apr-1994 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999

R;Raha, M.; Kawagishi, I.; Mueller, V.; Kihara, M.; Macnab, R.M.

J. Bacteriol. 174, 6644-6652, 1992

A;Title: Escherichia coli produces a cytoplasmic alpha-amylase, amyaA.

A;Reference number: A45738; MUID:9301517; PMID:1400215

A;Accession: B45738

A;Molecule type: DNA

A;Residues: 1-494 <RAH>

A;Cross-references: GB:L01643; NID:g154043; PIDN:AAA27110.1; PID:g154045

C;Genetics:

A;Gene: amya

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology

C;Keywords: cytosol; glycosidase; hydrolase; polysaccharide degradation

F;202-335/Domain: alpha-amylase core homology <AMI>

F;239,265,332/Active site: His, Glu, Asp #status predicted

Query Match 40.9%; Score 1107; DB 1; Length 494;
 Best Local Similarity 44.1%; Pred. No. 1.6e-69;
 Matches 217; Conservative 78; Mismatches 179; Indels 18; Gaps 6;

QY 6 NGTMOYFEWYLPNDGNHNRSLSDASNLKDGISAVWIPPAWKASQN-DVGYGAYDLY 64
 DB 3 NPTLLQYFHWYYPDGGKLMSEVAEAKESLAKMGITDVLPPAYKGAAGYSVGYDTYDLF 62

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 6, 2004, 23:59:28 ; Search time 46.501 Seconds
(without alignments)
3290.816 Million cell updates/sec

Title: US-09-925-576C-12
Perfect score: 2708
Sequence: 1 HHNGTNGTMQYFEWYLPND.....ADGWNFSVGGSVSIWNK 485

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2409	89.0	516	2	O82839
2	1942	71.7	533	2	Q9AQ54
3	1934	71.4	513	16	O81YJ4
4	1926	71.1	513	16	O81AS4
5	1889.5	69.8	613	2	O59222
6	1874	69.2	519	2	O9RQ78
7	1872.5	69.1	549	2	O31193
8	1867.5	69.0	521	2	P71034
9	1867.5	69.0	549	2	O9KW76
10	1813.5	67.0	501	2	O93148
11	1576.5	58.2	507	16	O87HG6
12	1363	50.3	493	2	O03657
13	1336	49.3	481	16	O89YD1
14	1307.5	48.3	486	16	O8D708
15	1307.5	48.3	488	16	O8E0M2
16	1300.5	48.0	488	16	O8E696

17	1298	47.9	484	16	Q97Q49
18	1296	47.9	484	16	O8DPC8
19	1282	47.3	492	16	O8YUZ1
20	1279.5	47.2	486	2	O68875
21	1262.5	46.5	484	2	O50583
22	1260.5	46.5	485	2	O53786
23	1148	42.4	491	16	O9C859
24	1114	41.1	506	16	O8U916
25	1098	40.5	494	16	O8Z5S5
26	1085	40.1	495	16	O8XBB6
27	1080	39.9	495	16	O8FGL8
28	1073	39.5	495	16	O7UAB0
29	1071	39.5	495	16	O83R40
30	1048.5	38.7	529	3	O877B1
31	494.5	18.3	461	1	O33476
32	494.5	18.3	461	1	O8NKR4
33	475.5	17.6	461	1	O8NKR5
34	467	17.2	469	1	O50200
35	462.5	17.1	460	1	O9P9L0
36	462.5	17.1	460	1	O08452
37	462.5	17.1	473	17	O8U3I9
38	459	16.9	432	14	O8JZK3
39	444	16.4	457	1	O93647
40	320.5	11.8	482	2	O60051
41	284.5	10.5	421	10	O7X9T1
42	280	10.3	423	10	O42678
43	280	10.3	504	1	O60224
44	279	10.3	416	10	O8LJ06
45	278	10.3	424	10	O8LP27

ALIGNMENTS

RESULT 1

ID	O82839	PRELIMINARY;	PRT;	516 AA.
AC	O82839;			
DT	01-NOV-1998 (TrEMBLrel. 08, Created)			
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)			
DE	Amylase.			
OS	Bacillus sp.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI TaxID=1409;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=KSM-1378;			
RX	MEDLINE=98342096; PubMed=9675143;			
RA	Igarashi K., Hatada Y., Ikawa K., Araki H., Ozawa T., Kobayashi T., Ozaki K., Ito S.;			
RA	"Improved thermostability of a Bacillus alpha-amylase by deletion of an arginine-glycine residue is caused by enhanced calcium binding.";			
RL	Biochem. Biophys. Res. Commun. 248:372-377(1998).			
DR	EMBL; AB008763; BAA32431.1; -			
DR	HGSP; P06278; 1VJS.			
DR	GO; GO:0004556; F:alpha-amylase activity; IEA.			
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.			
DR	InterPro; IPR006047; Alpha_amyl_cat.			
DR	InterPro; IPR006589; Alp_amyl_cat_sub.			
DR	InterPro; IPR006046; Glyco_hydro_13.			
DR	Pfam; PF00128; alpha-amylase; 1.			
DR	PRINTS; PR00110; ALPHAMYLASE.			
DR	SMART; SM00642; Amy; 1.			
DR	SEQUENCE 516 AA; 58841 MW; D90A8C90ECC182F8 CRC64;			

Query Match 89.0%; Score 2409; DB 2; Length 516;

Best Local Similarity 86.0%; Pred. No. 5.9e-143;

Matches 417; Conservative 37; Mismatches 31; Indels 0; Gaps 0;

Qy	1	HHNGTNGTMQYFEWYLPNDGNHNRRLRSASNLDKXGISAIVTTPPAWKGSQNDVGYGA	60
Db	32	HHNGTNGTMQYFEWHLPLNDGNHNRRLRDDAANLKSXGITAIVTTPPAWKGTSQNDVGYGA	91

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QY 61 YLDYDLGEFNQKGTIRTKYTRNLOQAANVNAKLSNGIQVYGDVVMNHKGGADATEMVRV 120
Db 92 YDYDLGEFNQKGTIRTKYTRNLOQAANVNAKLSNGIQVYGDVVMNHKGGADATEMVRV 151
QY 121 EVNPNRNQSVSGEYTIETAWTKDFPGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
Db 152 EVNPNRNQSVSGEYTIETAWTKDFPGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 211
QY 181 RGCGKWDWEVDTEGNYDYLYADIDMDHPVNVNLRNKGWYTYTTLGLDGRIDAVKH 240
Db 212 RGCGKWDWEVDTEGNYDYLYADIDMDHPVNVNLRNKGWYTYTTLGLDGRIDAVKH 271
QY 241 IKYSFTRDWLNHVSATGKMPFAVAFWKNLDGAIENYLNKTNWHSFVDPVPLHYNLXNA 300
Db 272 IKYSFTRDWLNHVSATGKMPFAVAFWKNLDGAIENYLNKTNWHSFVDPVPLHYNLXNA 331
QY 301 SKSGGNYDMRQIFNGTVVQHPHMAVTFVDNHDSPQEALESFVEWFKPLAYALTITRE 360
Db 332 SKSGGNYDMRQIFNGTVVQHPHMAVTFVDNHDSPQEALESFVEWFKPLAYALTITRE 391
QY 361 QGYPSPFYGYDYGIPHGVPAKMSKIDPILBAROKYAYGRQNDYLDHNNIIGWTRGNTA 420
Db 392 QGYPSPFYGYDYGIPHGVPAKMSKIDPILBAROKYAYGRQNDYLDHNNIIGWTRGNTA 451
QY 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTTINADGWNFGVNGSVS 480
Db 452 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTTINADGWNFGVNGSVS 511
QY 481 IWYNK 485
Db 512 VWVKQ 516
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RESULT 2

Q9AQ54 PRELIMINARY; PRT; 533 AA.

AC Q9AQ54; (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Alpha-amylose.

OS Bacillus megaterium.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1404;

RN [1]

RA Kim Y.B., Lee B.N., Son H.J., Lee J.W., Kim B.J., Kim Y.-W., Park K.-H.;

RT "Cloning of maltopentaose-producing amylose from Bacillus megaterium KSM B-404."

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF220440; AAK00598.1; -.

DR HSSP; P06278; 1VSJ.

DR GO; GO:0004556; F:alpha-amylose activity; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006047; Alpha amyl cat.

DR InterPro; IPR006589; Alp_aml_cat_sub.

DR Pfam; PF00128; alpha-amylose; 1.

DR SMART; SM00642; Amy; 1.

SQ SEQUENCE 533 AA; 60557 MW; 789CECD6A19C7DDE CRC64;

Query Match 71.7%; Score 1942; DB 2; Length 533;
Best Local Similarity 69.6%; Pred. No. 1.1e-113;
Matches 336; Conservative 57; Mismatches 86; Indels 4; Gaps 2;

QY 6 NGTWMQYFEWYLPNDGNHNNLRSDASNLKDKGISAVWIPPAWKASQNDVGYGAYDLYD 65
Db 52 NGTLMQYFEWYLPNDGNHNNLRSDAENLAQKGLTSWVIPPAYKGTQNDVGYGAYDLYD 111

QY 66 LGBFNQKGTIRTKYTRNLOQAANVNAKLSNGIQVYGDVVMNHKGGADATEMVRVFN 125
Db 112 LGBFNQKGTIRTKYTRNLOQAANVNAKLSNGIQVYGDVVMNHKGGADATEMVRVFN 171

QY 126 NRNOEVSGETTIEAWTKDFPGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 185
Db 172 NRNOEVSGETTIEAWTKDFPGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 230
QY 186 GMDWEVDTEGNYDYLYADIDMDHPVNVNLRNKGWYTYTTLGLDGRIDAVKH 245
Db 231 GMDWEVDTEGNYDYLYADIDMDHPVNVNLRNKGWYTYTTLGLDGRIDAVKH 290
QY 246 TRDWNHVSATGKMPFAVAFWKNLDGAIENYLNKTNWHSFVDPVPLHYNLNASKSG 305
Db 291 TRDWNHVSATGKMPFAVAFWKNLDGAIENYLNKTNWHSFVDPVPLHYNLNASKSG 350
QY 306 NYDMRQIFNGTVVQHPHMAVTFVDNHDSPQEALESFVEWFKPLAYALTITRE 365
Db 351 NYDMRQIFNGTVVQHPHMAVTFVDNHDSPQEALESFVEWFKPLAYALTITRE 410
QY 366 VFYGYDYGIPHGVPAKMSKIDPILBAROKYAYGRQNDYLDHNNIIGWTRGNTA 422
Db 411 VFYGYDYGIPHGVPAKMSKIDPILBAROKYAYGRQNDYLDHNNIIGWTRGNTA 470
QY 423 NSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTTINADGWNFGVNGSVS 482
Db 471 NSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTTINADGWNFGVNGSVS 530
QY 483 VNK 485
Db 531 VQR 533

RESULT 3

Q81YJ4 PRELIMINARY; PRT; 513 AA.

AC Q81YJ4; (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Alpha-amylose.

GN AMYS OR BA3551.

OS Bacillus anthracis (strain Ames).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=198094;

RN [1]

RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T., Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R., Holtzapple E.K., Okstad O.A., Helgason E., Ristone J., Wu M., Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M., DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H., Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D., Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F., Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C., Hazen A., Cline R., Redmond C., Thwaitte J.E., White O., Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolisko A.-B., Fraser C.M.;

RT "The genome sequence of Bacillus anthracis Ames and comparison to RT closely related bacteria."

RL Nature 423:81-86(2003).

DR EMBL; AB017035; AAP27311.1; -.

DR TIGR; BA3551; -.

DR GO; GO:0004556; F:alpha-amylose activity; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR006047; Alpha amyl cat.

DR InterPro; IPR006589; Alp_aml_cat_sub.

DR Pfam; PF00128; alpha-amylose; 1.

DR SMART; SM00642; Amy; 1.

KW Complete proteome.

SQ SEQUENCE 513 AA; 58445 MW; 558D6EF282FD159B CRC64;

Query Match 71.4%; Score 1934; DB 16; Length 513;
Best Local Similarity 69.4%; Pred. No. 3.4e-113;
Matches 335; Conservative 59; Mismatches 85; Indels 4; Gaps 2;

SQ	SEQUENCE	613 AA; 69537 MW; 14684A30FC2895E8 CRC64;	
	Query Match	69.8%; Score 1889.5; DB 2; Length 613;	
	Best Local Similarity	68.1%; Pred. No. 2.6e-110;	
	Matches	327; Conservative 64; Mismatches 88; Indels 1; Gaps 1;	
QY	6	NGTMMQYFEWYLPNDGNHNRRLRSASNLKDKGISAVWIPPAWKASQNDVGYGAYDLYD 65	
DB	36	NETMMQYFEWDLNDGTGLTKVKNNEANLSSGITALWLPAYKGTSGSDVGYGVYDLYD 95	
QY	66	LGFEFNQGTIRTKYGTNRNQLQAANVALKNGIQYGVGVVNMHKGADATWVRVAVENPN 125	
DB	96	LGFEFNQGTIRTKYGTNRNQLQAANVALKNGIQYGVGVVNMHKGADATWVRVAVENPN 155	
QY	126	NRNQEVSGEYTIKAWTKFDPGRGNTHSNFKRWYHFDGVDQSRKLNRIYKFRGDK 185	
DB	156	NRNQEVSGEYTIKAWTKFDPGRGNTHSNFKRWYHFDGVDQSRKLNRIYKFRGDK 214	
QY	186	GWDEVDTEGNDYDLYMADIDMDHPEVNMELNMGVYVNTLGLDGFRIIDAVKHIKYSF 245	
DB	215	GWDEVDTEGNDYDLYMADIDMDHPEVNMELNMGVYVNTLGLDGFRIIDAVKHIKYSF 274	
QY	246	TRDWINHVSATCKMFAVAFWKNDLGAENLYLNKTNHNSVDFVPLHYNLYNASKSG 305	
DB	275	FPDMLTVRNQTKNLFAVGEFNSYDVNKLHNYITKTNGSMSLFDAPLHNNFYTASKSG 334	
QY	306	NYDMRQIFNGTVVQRHPMHAVTVDNHDSDPEEALSFVEEWFKPLAYALTLTREOGYPS 365	
DB	335	YFDMRYLLNLTMKDQPSLAVTLVDNHDTPQGSQSWEPFVKPLAYAFILTRQGYPC 394	
QY	366	VYFGDYGIPTGHPVPMKSKIDPILARQKYAYGRQNDYLDHNNIIGWTRGNHTAHNSG 425	
DB	395	VYFGDYGIPTGHPVPMKSKIDPILARQKYAYGRQNDYLDHNNIIGWTRGNHTAHNSG 454	
QY	426	LATIMSDGAGNKMVFGRNKAQVWTDITGNRAGTVTTINADGWNFSVNGSGSVIWNK 485	
DB	455	LAALITDGPCKGKMYVGGKHAGKVFYDLTGNRSDTITINADGWNFSVNGSGSVIWNK 514	
RESULT 6			
ID	Q9ROT8	PRELIMINARY; PRT; 519 AA.	
AC	Q9ROT8		
DT	01-MAY-2000	(TrEMBLrel. 13, Created)	
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)	
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)	
DE	Raw starch digesting amylase precursor.		
OS	Cytophaga sp.		
OC	Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;		
OC	Flexibacteraceae; Cytophaga.		
OX	NCBI_TaxID=29535;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Jiang C.L., Chen L.S., Chen M.Y.;		
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF067653; AAF00567.1; --		
DR	HSP; P06278; 1VJS.		
DR	GO; GO:0004556; P:alpha-amylase activity; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	InterPro; IPR006047; Alpha_ami_cat.		
DR	InterPro; IPR006589; Alp_ami_cat_sub.		
DR	Pfam; PF00128; alpha-amylase; 1.		
DR	PRINTS; PR00110; ALPHAMYLASE.		
DR	SMART; SM00642; Amy; 1.		
KW	Signal.		
FT	SIGNAL		
FT	CHAIN		
SQ	SEQUENCE	519 AA; 58337 MW; 3B6B88A4DF98B163 CRC64;	
	Query Match	69.2%; Score 1874; DB 2; Length 519;	
	Best Local Similarity	67.1%; Pred. No. 2e-109;	
	Matches	325; Conservative 68; Mismatches 87; Indels 4; Gaps 2;	

QY	5	TNGTMMQYFEWYLPNDGNHNRRLRSASNLKDKGISAVWIPPAWKASQNDVGYGAYDLY 64	
DB	37	TNGTMMQYFEWYLPNDGNHNRRLRSASNLKDKGISAVWIPPAWKASQNDVGYGAYDLY 96	
QY	65	DLGEFNQGTIRTKYGTNRNQLQAANVALKNGIQYGVGVVNMHKGADATWVRVAVENPN 124	
DB	97	DLGEFNQGTIRTKYGTNRNQLQAANVALKNGIQYGVGVVNMHKGADATWVRVAVENPN 156	
QY	125	NRNQEVSGEYTIKAWTKFDPGRGNTHSNFKRWYHFDGVDQSRKLNRIYKFRGDK 184	
DB	157	NRNQEVSGEYTIKAWTKFDPGRGNTHSNFKRWYHFDGVDQSRKLNRIYKFRGDK 215	
QY	185	KGWDEVDTEGNDYDLYMADIDMDHPEVNMELNMGVYVNTLGLDGFRIIDAVKHIKYS 244	
DB	216	KGWDEVDTEGNDYDLYMADIDMDHPEVNMELNMGVYVNTLGLDGFRIIDAVKHIKYS 275	
QY	245	FPDWINHVSATCKMFAVAFWKNDLGAENLYLNKTNHNSVDFVPLHYNLYNASKSG 304	
DB	276	FLKDWVDNARATGKEMFTVGEYQNDLGAENLYLNKTNHNSVDFVPLHYNLYNASKSG 335	
QY	305	GNYDMRQIFNGTVVQRHPMHAVTVDNHDSDPEEALSFVEEWFKPLAYALTLTREOGY 364	
DB	336	GYDMRNLNLTNLVSNPTKAVTLVENHDTQPGSLESTVQPFKPLAYAFILTRSGGY 395	
QY	365	SVFYGDY---GIPTHGVPMKSKIDPILARQKYAYGRQNDYLDHNNIIGWTRGNHTAH 421	
DB	396	SVFYGDYGTGTTTRETIPALKSKIEPLKARKDAYGTQDYIDNPVIGWTRGDSYTK 455	
QY	422	PNSGLATIMSDGAGNKMVFGRNKAQVWTDITGNRAGTVTTINADGWNFSVNGSGSVI 481	
DB	456	AKSGLATVITDGPCKGKMYVGGKHAGKVFYDLTGNRSDTITINADGWNFSVNGSGSV 515	
QY	482	WYWK 485	
DB	516	WYWK 519	
RESULT 7			
ID	O31193	PRELIMINARY; PRT; 549 AA.	
AC	O31193		
DT	01-JAN-1998	(TrEMBLrel. 05, Created)	
DT	01-JAN-1998	(TrEMBLrel. 05, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Alpha amylase.		
GN	AMI.		
OS	Bacillus stearothermophilus.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.		
OX	NCBI_TaxID=1422;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ATCC 31195;		
RA	da Silva A.C.R., Fernandes B., Pueyo M.T.;		
RL	Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF032864; AAB8961.1; --		
DR	PIR; A54541; A54541.		
DR	HSP; P06278; 1VJS.		
DR	GO; GO:0004556; P:alpha-amylase activity; IEA.		
DR	GO; GO:0005975; P:carbohydrate metabolism; IEA.		
DR	InterPro; IPR006047; Alpha_ami_cat.		
DR	InterPro; IPR006589; Alp_ami_cat_sub.		
DR	Pfam; PF00128; alpha-amylase; 1.		
DR	PRINTS; PR00110; ALPHAMYLASE.		
DR	SMART; SM00642; Amy; 1.		
SQ	SEQUENCE	549 AA; 62651 MW; 2CA689EDACC4D262 CRC64;	
	Query Match	69.1%; Score 1872.5; DB 2; Length 549;	
	Best Local Similarity	67.2%; Pred. No. 2.6e-109;	
	Matches	321; Conservative 73; Mismatches 83; Indels 1; Gaps 1;	

QY	6	NGTMMQYFEWYLPNDGNHNRRLRSASNLKDKGISAVWIPPAWKASQNDVGYGAYDLYD 65	
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Db 39 NGTMMQYFEWYLPDDGTLWTWKVANEANLLSLGITALWLPAYKGTSDVGYGYDLYD 98
Qy 66 LGFENQKGTIRTKYGTNRNQLQAQAAVNAKLSNGIQVYGDVVMNHKGADATMVRVAVENPN 125
Db 99 LGFENQKGTIRTKYGTNRNQLQAQAAVNAKLSNGIQVYGDVVMNHKGADATMVRVAVENPN 158
Qy 126 NRNEQVSGEYTIETAWTKFDPFGRGNTHSNFKRWYHFDGVDWDSRKL-SRIYKPRGIGK 185
Db 159 DRNQEISGTQIQAWTKFDPFGRGNTHSNFKRWYHFDGVDWDSRKL-SRIYKPRGIGK 217
Qy 186 GWDNEVDTEGNYDYLMDHPEVNVNRLNKGWYVNTLGLDGRIDAVKHKYSF 245
Db 218 AWDNEVDTEGNYDYLMDHPEVNVNRLNKGWYVNTLGLDGRIDAVKHKYSF 277
Qy 246 TRDWINHVSATGKMFVAFWFKNDLGAENYLNKTNWNSVDFDPLHYNLYNASKSGG 305
Db 278 FPDWLSVRSQTGKPLFTVGYWSDINKLHNYITKINGTMSLFDAPLHNFYTASKSGG 337
Qy 306 NYDMRQIFNGTVVORHPHIAVTFVDNHSOPEALESFVEWFKPLAYALTTLTREQGYPS 365
Db 338 AFDMRTLTMTNLMKDQPTLAVTFVDNHDTEPGALQSWDPWFKPLAYALTTLTREQGYPC 397
Qy 366 VFYGDYGIPTGHPVPMKSKIDPILAEARQYAYGRNDYLDHNIIGWTRGNTAHNPSG 425
Db 398 VFYGDYGIPTGHPVPMKSKIDPILAEARQYAYGRNDYLDHNIIGWTRGNTAHNPSG 457
Qy 426 LATIMSDGAGNKMVFGRNKGAGVWTDITGNRAGTVTINADGNFVNGSGSVIWW 483
Db 458 LAALITDGPCKGKMYVKGQKAGKVFYDLTGNRSDTVTINSDGNGEKFVNGSGSVVW 515

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RESULT 8
P71034
ID P71034 PRELIMINARY; PRT; 521 AA.
AC P71034;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DE Alpha-amylase (EC 3.2.1.1).
OS Bacillus sp. MK 716.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=54116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MK 716;
RA Sidhu G.S., Chakrabarti T.;
RT "Molecular cloning and expression of the gene encoding for
thermostable alpha-amylase of a thermophilic bacterial isolate.";
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75445; AAB18785.1; -.
DR HSP; P06278; 1VJS.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase_1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW SIGNAL.
FT CHAIN 35 521 ALPHA-AMYLASE.
SQ SEQUENCE 521 AA; 59311 MW; 5612A885960922E1 CRC64;

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Query Match 69.0%; Score 1867.5; DB 2; Length 521;
Best Local Similarity 66.9%; Pred. No. 5.1e-109;
Matches 320; Conservative 73; Mismatches 84; Indels 1; Gaps 1;

Qy 6 NGTMMQYFEWYLPDDGTLWTWKVANEANLLSLGITALWLPAYKGTSDVGYGYDLYD 65
Db 39 NGTMMQYFEWYLPDDGTLWTWKVANEANLLSLGITALWLPAYKGTSDVGYGYDLYD 98

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Qy 66 LGFENQKGTIRTKYGTNRNQLQAQAAVNAKLSNGIQVYGDVVMNHKGADATMVRVAVENPN 125
Db 99 LGFENQKGTIRTKYGTNRNQLQAQAAVNAKLSNGIQVYGDVVMNHKGADATMVRVAVENPN 158
Qy 126 NRNEQVSGEYTIETAWTKFDPFGRGNTHSNFKRWYHFDGVDWDSRKL-SRIYKPRGIGK 185
Db 159 DRNQEISGTQIQAWTKFDPFGRGNTHSNFKRWYHFDGVDWDSRKL-SRIYKPRGIGK 217
Qy 186 GWDNEVDTEGNYDYLMDHPEVNVNRLNKGWYVNTLGLDGRIDAVKHKYSF 245
Db 218 AWDNEVDTEGNYDYLMDHPEVNVNRLNKGWYVNTLGLDGRIDAVKHKYSF 277
Qy 246 TRDWINHVSATGKMFVAFWFKNDLGAENYLNKTNWNSVDFDPLHYNLYNASKSGG 305
Db 278 FPDWLSVRSQTGKPLFTVGYWSDINKLHNYITKINGTMSLFDAPLHNFYTASKSGG 337
Qy 306 NYDMRQIFNGTVVORHPHIAVTFVDNHSOPEALESFVEWFKPLAYALTTLTREQGYPS 365
Db 338 AFDMRTLTMTNLMKDQPTLAVTFVDNHDTEPGALQSWDPWFKPLAYALTTLTREQGYPC 397
Qy 366 VFYGDYGIPTGHPVPMKSKIDPILAEARQYAYGRNDYLDHNIIGWTRGNTAHNPSG 425
Db 398 VFYGDYGIPTGHPVPMKSKIDPILAEARQYAYGRNDYLDHNIIGWTRGNTAHNPSG 457
Qy 426 LATIMSDGAGNKMVFGRNKGAGVWTDITGNRAGTVTINADGNFVNGSGSVIWW 483
Db 458 LAALITDGPCKGKMYVKGQKAGKVFYDLTGNRSDTVTINSDGNGEKFVNGSGSVVW 515

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RESULT 9
Q9KMY6
ID Q9KMY6 PRELIMINARY; PRT; 549 AA.
AC Q9KMY6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Alpha-amylase (EC 3.2.1.1).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US100;
RA Beijar S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y17557; CAB93517.1; -.
DR PIR; A54541; A54541.
DR HSP; P06278; 1VJS.
DR GO; GO:0004556; P:alpha-amylase activity; IEA.
DR GO; GO:0016798; P:hydrolyase activity, acting on glycosyl bonds; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase_1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR SMART; SM00642; Amy; 1.
KW Glycoelidase; Hydrolase.
SQ SEQUENCE 549 AA; 62582 MW; 8DA3E66DF9120BCE CRC64;

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Query Match 69.0%; Score 1867.5; DB 2; Length 549;
Best Local Similarity 66.9%; Pred. No. 5.4e-109;
Matches 320; Conservative 73; Mismatches 84; Indels 1; Gaps 1;

Qy 6 NGTMMQYFEWYLPDDGTLWTWKVANEANLLSLGITALWLPAYKGTSDVGYGYDLYD 65
Db 39 NGTMMQYFEWYLPDDGTLWTWKVANEANLLSLGITALWLPAYKGTSDVGYGYDLYD 98
Qy 66 LGFENQKGTIRTKYGTNRNQLQAQAAVNAKLSNGIQVYGDVVMNHKGADATMVRVAVENPN 125
Db 99 LGFENQKGTIRTKYGTNRNQLQAQAAVNAKLSNGIQVYGDVVMNHKGADATMVRVAVENPN 158
Qy 126 NRNEQVSGEYTIETAWTKFDPFGRGNTHSNFKRWYHFDGVDWDSRKL-SRIYKPRGIGK 185

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Db 322 SGGYDMRQIWMGILMKDNPVKAATLVNHDTPQLQALESTVDMWFKFLAVAFILLREEG 381
Qy 363 YPSVYFYGGYGG-----IPTHGVPAKMSKIDPILFARQKAYAGRQNDYLDHNNIIGW 413
Db 382 YPSVYADYCAQYSDKGYNNMAKVP-----YIEBLVTLRKEYAGKQNSYLDHWDVLGW 437
Qy 414 TREGNTAHPNSGLATIMSAGAGNKMFMVGRNKAQGVWTDITGNRAGTVTINADGWNFSV 473
Db 438 TREGDAEHPNS--MAVINSDGPGTKWMTYG--KPSRYVDKLGIIRTEBVTWDANGWAEPF 494
Qy 474 VNGGSVSIWV 483
Db 495 VNGGSVSVWV 504

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RESULT 12
Q03657 PRELIMINARY; PRT; 493 AA.
AC Q03657;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Amylase.
GN AMYE.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1397;
RN [1]
RP SEQUENCE FROM N.A.
RA Marcel T.;
RL Nucleic Acids Res. 0:0-0(0).
DR EMBL; X60779; CAA43194.1; -.
DR PIR; S15713; S15713.
DR HSSP; P06278; 1VJS.
DR DR GO:0004556; P:alpha-amylase activity; IEA.
DR GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; Glyco hydro_I3.
DR PRINTS; PR00110; ALPHAMYLASE.
DR SMART; SM00642; Amy; 1.
SQ SEQUENCE 493 AA; 56537 MW; FECCD2F805BB4694 CRC64;

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Query Match 50.3%; Score 1363; DB 2; Length 493;
Best Local Similarity 51.1%; Pred. No. 1.9e-77;
Matches 246; Conservative 78; Mismatches 149; Indels 8; Gaps 3;
Qy 6 NGTMMQYFEWYLPNDGNHNRSLSDASNLKDKGISAVMIPPAMKSGASQNDVGYGAYDLYD 65
Db 4 NHTMMQYFEWHLAADGDHKKRLAEMAPELKAKGIDTVWVPVTKAVSAEDTGYGYDLYD 63
Qy 66 LGFENQKGTTRTKYGTNRNQLQAAVNAKLSNGIOYQVGDVVMNHKGGADATEMVRVAVNPN 125
Db 64 LGFEDQKGTTRTKYGTNRNQLQAAVNAKLSNGIOYQVGDVVMNHKGGADATEMVRVAVNPN 123
Qy 126 NRNOEVSGETYIEAWTKFDPFGNGNTHSNFKRWYHFDGVDWDSRKLNNRIYKFRGDGK 185
Db 124 DRYKEISEPEIEGWTFTFPGRGDQYSSFAKNSEHNGTDFD-AREERTGVFRIAGENK 182
Qy 186 GWDVEVDTENGNDYLMYADIDMDHPEVNVNELRWGVYNTNTLGLDGRIDAVKHKYSF 245
Db 183 KWNENVDDFNGVDYLMFANIDYNHPDVRREMDGKWLIDTLCQCGFRDLAKIHNEF 242
Qy 246 TRDWINHVRATGKNMFAVAFKNDLGAENYLNKTNWHSVDFVPLHYNLNASKSGG 305
Db 243 IKEFAEMIRKRGQDFYIVGEFNNSLDACREFLDITVDYQIDLVDVSLHYKLHEASLKR 302
Qy 306 NYDMRQIFNGTVQRHPMHAVTFVDNHDSDPEALESFVEWFKPLAYALTLTREOCYPS 365
Db 303 DFDLSKIFDDTLVQTHETHAVTFVDNHDSDPEALESWIGWFKPSAYALTLLRROGYPV 362

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Qy 366 VFYGDYGYI-----PTHGVPAKMSKIDPILFARQKAYAGRQNDYLDHNNIIGWREGNTAH 421
Db 363 VFYGDYGYIGGPEPVDG---KKEILDILLSARCNAKAYGEQEDYDPDHANTIGWVRGVBEI 419
Qy 422 PNSGLATIMSAGAGNKMFMVGRNKAQGVWTDITGNRAGTVTINADGWNFSVNGSGSVSI 481
Db 420 EGSQCAVVISNGDDGEXRMFIEGRHAGEVWVDLTKSCDDQITIEEDGWATFHVCGGGSV 479
Qy 482 W 482
Db 480 W 480

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RESULT 13

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Q89YP1 PRELIMINARY; PRT; 481 AA.
AC Q89YP1;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Alpha-amylase precursor.
GN BT4690.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016946; AA079795.1; -.
DR GO:0004556; P:alpha-amylase activity; IEA.
DR GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR006047; Alpha amyl cat.
DR InterPro; IPR006589; Alp amyl cat sub.
DR Pfam; PF00128; alpha-amylase; 1.
DR SMART; SM00642; Amy; 1.
KW Complete proteome.
SQ SEQUENCE 481 AA; 55343 MW; B6BF237011F5EE1A CRC64;

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Query Match 49.3%; Score 1336; DB 16; Length 481;
Best Local Similarity 49.6%; Pred. No. 9e-76;
Matches 238; Conservative 90; Mismatches 150; Indels 2; Gaps 2;

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Qy 6 NGTMMQYFEWYLPNDGNHNRSLSDASNLKDKGISAVMIPPAMKSGASQNDVGYGAYDLYD 65
Db 3 NGVMMQYFEWHLNDGKWKQIKEDALHLHDIGVTAWIIPYAKADEQDEGATYDLYD 62
Qy 66 LGFENQKGTTRTKYGTNRNQLQAAVNAKLSNGIOYQVGDVVMNHKGGADATEMVRVAVNPN 125
Db 63 LGFEDQKGTTRTKYGTNRNQLQAAVNAKLSNGIOYQVGDVVMNHKGGADATEMVRVAVNPN 122
Qy 126 NRNOEVSGETYIEAWTKFDPFGNGNTHSNFKRWYHFDGVDWDSRKLNNRIYKFRGDGK 185
Db 123 ERTKALGEPEIEGWTFTFPGRGDQYSSFAKNSEHNGTDFD-ARSGVFOIQEGEK 181
Qy 186 GWDVEVDTENGNDYLMYADIDMDHPEVNVNELRWGVYNTNTLGLDGRIDAVKHKYSF 245
Db 182 AWSEGVDSSENGYDFLLCNDILDHPEVVSSELNRWGWVSNELNLDGMRDLAKHMKDQF 241
Qy 246 TRDWINHVRATGKNMFAVAFKNDLGAENYLNKTNWHSVDFVPLHYNLNASKSGG 305
Db 242 VAQFLDAVRSEGRNDFYAVGEYWNGLDLEADVIEAVGHKVNLFDPVPLHYNMFQASQEGK 301
Qy 306 NYDMRQIFNGTVQRHPMHAVTFVDNHDSDPEALESFVEWFKPLAYALTLTREOCYPS 365
Db 302 DYDLRLDKLTLVHEHHPDLAVTIVDNHDTQSGSLESNVEDWFKPLAYALTLLMKEGYPC 361
Qy 366 VFYGDYGYIPTHGVPAKMSKIDPILFARQKAYAGRQNDYLDHNNIIGWREGNTAHPNSG 425

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362 LFYDGYGKIGKSPHTRI-IDILLDARKKAYGDIQIEYFDPHSPSTGTGRTGDDEHNGSG 420
426 LATIMSDGAGGNKWMFVGRNKAQGVWTDITGNRAGTVTINADGWNFSVNGSGSVISWVWK 485
421 LVFLMSNDEAGSKIMSLGKHKHGEVWHEITGTSISEBITLDEEGNGEFSVESRNLAWVVK 480

RESULT 14
Q8DT08 PRELIMINARY; PRT; 486 AA.
AC Q8DT08;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Intracellular alpha-amylase (EC 3.2.1.1).
GN AMYA OR SMU.1590.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=UA159 / ATCC 700610 / Serotype C;
RX MEDLINE=22295063; PubMed=12397186;
RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,
RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;
RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RT pathogen."
RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439 (2002).
DR EMBL: AE014990; AAC59233.1; -.
DR GO: GO:0004556; P:alpha-amylase activity; IEA.
DR GO: GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_amyl_cat.
DR Pfam: PF00128; alpha-amylase; 1.
DR SMART: SM00642; Amy; 1.
DR Glycosidase; Hydrolase;
KW Complete proteome.
SQ SEQUENCE 486 AA; 56457 MW; EF482B92FB37C4D8 CRC64;

Query Match 48.3%; Score 1307.5; DB 16; Length 486;
Best Local Similarity 50.0%; Pred. No. 5.6e-74;
Matches 242; Conservative 72; Mismatches 165; Indels 5; Gaps 4;

QY 5 TNGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVGYGYDLY 64
DB 2 TNETMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVGYGYDLY 61

QY 65 DLGEFNQKGTIRTKYGTNRNQLQAQVNAKSNQIQVYGVDMVNHKGGADATEMVRVAVNP 124
DB 62 DLGEFNQKGTIRTKYGTNRNQLQAQVNAKSNQIQVYGVDMVNHKGGADATEMVRVAVNP 121

QY 125 NNRRQVSGBYTTAEWTKFDPGCRGNTHSNFKRWYHFDGVDWQDSQRKLNRR--IYKFRG 184
DB 122 SNRQEKISEPYELEGWTFQFNPGQDNYSDFKWHYHFTGVDYDALHN-ENGIVMILGDN 180

QY 185 KGW--DWEVDTEGNGYDLYMADIMDPHPEVNEIRNWGWYVNTGLDGFRIADVKH 242
DB 181 KGWASQENIDQENGNYDLYMADIMDPHPEVNEIRNWGWYVNTGLDGFRIADVKH 240

QY 243 YSFTRDWINHVSATGKNMFAVAFKNDLGAENYLNKTNWHSVDPVPLHYNLYNASK 302
DB 241 KTFMAQPIRYIREHLKADLYVFGYWKDSHFDITDYLHVSVDLQDPLDVLMLHSLFPAQ 300

QY 303 SGGNYDMRQIFNGTVQRHPHMAVTFVDNHDSPPEEALESFVSEWFKPLAYALTLTREQ 362
DB 301 KGSDFDLSTLDDLSMKSHDPFAVTFVDNHDSPPEEALESFVSEWFKPLAYALTLTREQ 360

QY 363 YPSVFGYDYGIP-THGVPAWKSIDPILFARQKAYGRQNDYLDHNNIGWTEGNTAH 421
DB 361 IPCVFGYDYGIGFEFAQESQTVLDKLLYIRQVHYVGSQEDYFDYANCIGWTCIGDEEH 420

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QY 422 PMSGLATIMSDGAGGNKWMFVGRNKAQGVWTDITGNRAGTVTINADGWNFSVNGSGSVI 481
DB 421 PD-GVAVIISNGEANGKRMNGEFGNRNKFVDYLNCTEVEILDQDQGWGDFPVQASLSA 479

QY 482 WYWK 485
DB 480 WYWK 483

RESULT 15
Q8EOM2 PRELIMINARY; PRT; 488 AA.
AC Q8EOM2;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Alpha amylase family protein.
GN SAG0708.
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=22222988; PubMed=12200547;
RA Tettelin H., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margalit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Pinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae."
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
DR EMBL: AE014223; AAM99595.1; -.
DR TIGR: SAG0708; -.
DR GO: GO:0004556; P:alpha-amylase activity; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro: IPR006047; Alpha_amyl_cat.
DR InterPro: IPR006589; Alp_amyl_cat_sub.
DR InterPro: IPR006046; Glyco_hydro_13.
DR Pfam: PF00128; alpha-amylase; 1.
DR PRINTS: PR00110; ALPHAAMYLASE.
DR SMART: SM00642; Amy; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 488 AA; 56555 MW; 57249E354B2F053E CRC64;

Query Match 48.3%; Score 1307.5; DB 16; Length 488;
Best Local Similarity 49.6%; Pred. No. 5.6e-74;
Matches 241; Conservative 81; Mismatches 155; Indels 9; Gaps 5;

QY 5 TNGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVGYGYDLY 64
DB 2 TNELMQAFWYLPNDGNHNRRLSDASNLKDKGISAVWIPPAWKASQNDVGYGYDLY 61

QY 65 DLGEFNQKGTIRTKYGTNRNQLQAQVNAKSNQIQVYGVDMVNHKGGADATEMVRVAVNP 124
DB 62 DLGEFNQKGTIRTKYGTNRNQLQAQVNAKSNQIQVYGVDMVNHKGGADATEMVRVAVNP 121

QY 125 NNRRQVSGBYTTAEWTKFDPGCRGNTHSNFKRWYHFDGVDWQDSQRKLNRR--IYKFRG 182
DB 122 ENRQEAISEPYELEGWTFQFNPGQDNYSDFKWHYHFTGVDYDALHN-ENGIVMILG 178

QY 183 DKGW--DWEVDTEGNGYDLYMADIMDPHPEVNEIRNWGWYVNTGLDGFRIADVKH 240
DB 179 DNKGWADDDLLDDENGNFYDMYNDIDFKHPEVNEIRNWGWYVNTGLDGFRIADVKH 238

QY 241 IKYSFTEDWINHVSATGKNMFAVAFKNDLGAENYLNKTNWHSVDPVPLHYNLYNASK 300

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Db	299	SHQ	RDF	DMRT	IFDD	SLV	IDN	PEY	AVT	FVEN	HTQ	SGQ	AL	ESR	VED	WFK	PLAY	GILL	LRQ	358		
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Qy	420	AHP	NS	GLAT	IMSD	GAG	GKN	MFV	GRN	KAG	QVMT	DTI	TGN	RAG	TVT	IN	ADG	WGN	ESV	NGGSV	479	
Db	419	EH	-NS	CLAV	LITNG	QGW	KHME	VEGE	IYAG	KTFV	DYLG	NC	QEV	VIGD	DDG	WGD	FLV	ES	ASI	477		
Qy	480	SI	WVK	485																		
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Search completed: October 7, 2004, 00:19:02
 Job time : 48.501 secs

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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:12:34 ; Search time 15.0278 Seconds
(without alignments)
1666.155 Million cell updates/sec

Title: US-09-925-576C-12

Perfect score: 2708

Sequence: 1 HHNGTGTMMQYFEWLPND.....ADGNGFVNGSGSVIWNK 485

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2708	100.0	485	4	US-09-290-734-24 Sequence 24, Appl
2	2708	100.0	485	4	US-09-290-734-26 Sequence 26, Appl
3	2708	100.0	485	4	US-09-417-359A-5 Sequence 5, Appl
4	2708	100.0	485	4	US-09-545-586-24 Sequence 24, Appl
5	2708	100.0	485	4	US-09-545-586-26 Sequence 26, Appl
6	2613	96.5	485	3	US-08-600-656-7 Sequence 7, Appl
7	2613	96.5	485	3	US-09-170-670-6 Sequence 6, Appl
8	2613	96.5	485	3	US-09-193-068-6 Sequence 6, Appl
9	2613	96.5	485	3	US-09-183-412-6 Sequence 6, Appl
10	2613	96.5	485	3	US-09-354-191A-7 Sequence 7, Appl
11	2613	96.5	485	4	US-09-291-023A-13 Sequence 13, Appl
12	2613	96.5	485	4	US-09-290-734-6 Sequence 6, Appl
13	2613	96.5	485	4	US-09-381-687-5 Sequence 5, Appl
14	2613	96.5	485	4	US-09-545-586-6 Sequence 6, Appl
15	2613	96.5	485	4	US-09-540-715A-13 Sequence 13, Appl
16	2613	96.5	485	4	US-09-769-864-6 Sequence 6, Appl
17	2437	90.0	485	2	US-08-446-803-2 Sequence 2, Appl
18	2437	90.0	485	2	US-08-861-837-2 Sequence 2, Appl
19	2437	90.0	485	3	US-08-600-656-2 Sequence 2, Appl
20	2437	90.0	485	3	US-09-170-670-2 Sequence 2, Appl
21	2437	90.0	485	3	US-09-170-670-8 Sequence 8, Appl
22	2437	90.0	485	3	US-09-193-068-2 Sequence 2, Appl
23	2437	90.0	485	3	US-09-193-068-8 Sequence 8, Appl
24	2437	90.0	485	3	US-09-183-412-2 Sequence 2, Appl
25	2437	90.0	485	3	US-09-183-412-8 Sequence 8, Appl
26	2437	90.0	485	3	US-09-284-097-5 Sequence 5, Appl
27	2437	90.0	485	3	US-09-354-191A-2 Sequence 2, Appl

28	2437	90.0	485	4	US-09-290-734-2	Sequence 2, Appl
29	2437	90.0	485	4	US-09-290-734-8	Sequence 8, Appl
30	2437	90.0	485	4	US-09-381-687-3	Sequence 3, Appl
31	2437	90.0	485	4	US-09-545-586-2	Sequence 2, Appl
32	2437	90.0	485	4	US-09-545-586-8	Sequence 8, Appl
33	2437	90.0	485	4	US-09-769-864-2	Sequence 2, Appl
34	2437	90.0	485	4	US-09-769-864-8	Sequence 8, Appl
35	2429	89.7	485	2	US-08-446-803-1	Sequence 1, Appl
36	2429	89.7	485	2	US-08-861-837-1	Sequence 1, Appl
37	2429	89.7	485	2	US-08-600-308A-12	Sequence 12, Appl
38	2429	89.7	485	3	US-08-683-838A-12	Sequence 12, Appl
39	2429	89.7	485	3	US-08-600-656-1	Sequence 1, Appl
40	2429	89.7	485	3	US-09-170-670-1	Sequence 1, Appl
41	2429	89.7	485	3	US-09-170-670-1	Sequence 1, Appl
42	2429	89.7	485	3	US-09-193-068-1	Sequence 1, Appl
43	2429	89.7	485	3	US-09-193-068-7	Sequence 7, Appl
44	2429	89.7	485	3	US-09-183-412-1	Sequence 1, Appl
45	2429	89.7	485	3	US-09-183-412-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-290-734-24
; Sequence 24, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgaard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoesck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-290-734-24

Query Match		100.0%;	Score 2708;	DB 4;	Length 485;
Best Local Similarity		100.0%;	Pred. No. 6.4e-225;		
Matches 485;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	HHNGTGTMMQYFEWLPNDGNEHNRILRS	ASNLKDKGISAVMIPPAAWKASQNDVGGA	60	
Db	1	HHNGTGTMMQYFEWLPNDGNEHNRILRS	ASNLKDKGISAVMIPPAAWKASQNDVGGA	60	
Qy	61	YDLYDLGEFNGKQGTIRTKYCTRNLQQA	AVNALKSNGIQVYGVVMMHKGADATEMVR	120	
Db	61	YDLYDLGEFNGKQGTIRTKYCTRNLQQA	AVNALKSNGIQVYGVVMMHKGADATEMVR	120	
Qy	121	EVNPNNEQSVSGEYTEAWTKFDFGCRGN	THSNFKRWYHFDGVDWDSRKLNNRIYKF	180	
Db	121	EVNPNNEQSVSGEYTEAWTKFDFGCRGN	THSNFKRWYHFDGVDWDSRKLNNRIYKF	180	
Qy	181	RGDGKGDWEDVTENGNYDYLMTADIMDH	PEVNNELRWGVWYTNLTGLDGFDAVKH	240	
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Qy	241	IKYSFTRDWINHVRSAFGKMFVAEAFKND	LGAIEYLNKTNWHSVDFVPLHYNLYNA	300	
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Db 301 SKSGGNYDMROIENGTVVQRHPMHA VTFVDNHD SQPEEALSFVEBFWKPLAYALTLTRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPIL EARKQYAYGRNDYLDHNNIIGTWREGNTA 420
Db 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPIL EARKQYAYGRNDYLDHNNIIGTWREGNTA 420
QY 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480
QY 481 IWYNK 485
Db 481 IWYNK 485

RESULT 2
US-09-290-734-26
; Sequence 26, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgaard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989el - Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; CURRENT FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-290-734-26

Query Match 100.0%; Score 2708; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 6.4e-225;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWYLPNDGNHNNLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Db 1 HNGTGTMMQYFEWYLPNDGNHNNLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
QY 61 YDLIDLGEFNQKGTIRTKYGTNRQLQAAVNALKSNGIQYVGVVMMHKGADATEMVRV 120
Db 61 YDLIDLGEFNQKGTIRTKYGTNRQLQAAVNALKSNGIQYVGVVMMHKGADATEMVRV 120
QY 121 EVNPNRNQEVSGEYTI EAWTKFDFPGRGNTHSNFKRWYHFDGVWDQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTI EAWTKFDFPGRGNTHSNFKRWYHFDGVWDQSRKLNRIYKF 180
QY 181 RGDGKWDHEVDTENGNDYLYMADIDMDHPVNNELRNWGVWYNTLTGLDGRIDAVKH 240
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QY 241 IKYSFTRDWINHVRSATGKNMFAVAFKNDLCAIENYLNKTNWNHVSFVDPVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSATGKNMFAVAFKNDLCAIENYLNKTNWNHVSFVDPVPLHYNLYNA 300
QY 301 SKSGGNYDMROIENGTVVQRHPMHA VTFVDNHD SQPEEALSFVEBFWKPLAYALTLTRE 360
Db 301 SKSGGNYDMROIENGTVVQRHPMHA VTFVDNHD SQPEEALSFVEBFWKPLAYALTLTRE 360
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QY 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480

Db 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480
QY 481 IWYNK 485
Db 481 IWYNK 485

RESULT 3
US-09-417-359A-5
; Sequence 5, Application US/09417359A
; Patent No. 6461849
; GENERAL INFORMATION:
; APPLICANT: Olsen, Arne Agerlin
; APPLICANT: Osten, Claus von der
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Ernst, Steffen
; APPLICANT: Roggen, Erwin Ludo
; TITLE OF INVENTION: A Modified Polypeptide
; FILE REFERENCE: 5666.200-US
; CURRENT APPLICATION NUMBER: US/09/417,359A
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: PA 1998 01301
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PA 1999 01418
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/105,624
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/157,426
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-417-359A-5

Query Match 100.0%; Score 2708; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 6.4e-225;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNGTGTMMQYFEWYLPNDGNHNNLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Db 1 HNGTGTMMQYFEWYLPNDGNHNNLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
QY 61 YDLIDLGEFNQKGTIRTKYGTNRQLQAAVNALKSNGIQYVGVVMMHKGADATEMVRV 120
Db 61 YDLIDLGEFNQKGTIRTKYGTNRQLQAAVNALKSNGIQYVGVVMMHKGADATEMVRV 120
QY 121 EVNPNRNQEVSGEYTI EAWTKFDFPGRGNTHSNFKRWYHFDGVWDQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTI EAWTKFDFPGRGNTHSNFKRWYHFDGVWDQSRKLNRIYKF 180
QY 181 RGDGKWDHEVDTENGNDYLYMADIDMDHPVNNELRNWGVWYNTLTGLDGRIDAVKH 240
Db 181 RGDGKWDHEVDTENGNDYLYMADIDMDHPVNNELRNWGVWYNTLTGLDGRIDAVKH 240
QY 241 IKYSFTRDWINHVRSATGKNMFAVAFKNDLCAIENYLNKTNWNHVSFVDPVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSATGKNMFAVAFKNDLCAIENYLNKTNWNHVSFVDPVPLHYNLYNA 300
QY 301 SKSGGNYDMROIENGTVVQRHPMHA VTFVDNHD SQPEEALSFVEBFWKPLAYALTLTRE 360
Db 301 SKSGGNYDMROIENGTVVQRHPMHA VTFVDNHD SQPEEALSFVEBFWKPLAYALTLTRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPIL EARKQYAYGRNDYLDHNNIIGTWREGNTA 420
Db 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPIL EARKQYAYGRNDYLDHNNIIGTWREGNTA 420
QY 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGGSVS 480

Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 4

US-09-545-586-24
; Sequence 24, Application US/09545586
; Patent No. 6528298
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6528298e1 -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/545.586
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US/09/290.734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-545-586-24

Query Match 100.0%; Score 2708; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 6.4e-225;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMOYFEWYLPNDGNHNRLRSDASNLKDGISAVWIPPAWKASQNDVGGA 60
Db 1 HHNGTGTMOYFEWYLPNDGNHNRLRSDASNLKDGISAVWIPPAWKASQNDVGGA 60
Qy 61 YDLGLGEFNQKGTIRTKYGRNQLQAAVNALKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLGLGEFNQKGTIRTKYGRNQLQAAVNALKNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQEVSGEYTTIEAWTKDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTTIEAWTKDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Qy 181 RGDGKGWDEVDTEGNGYDYLMYADIDMDHPVNVNLRNMGVWYTNLTGLDGFPRIDAVKH 240
Db 181 RGDGKGWDEVDTEGNGYDYLMYADIDMDHPVNVNLRNMGVWYTNLTGLDGFPRIDAVKH 240
Qy 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLNKTNWNSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLNKTNWNSVDFVPLHYNLYNA 300
Qy 301 SKSGNDYMRQIFNGTVVQRHPHVAFTVDNHDQPEALESFVEEFKPLAYALTITRE 360
Db 301 SKSGNDYMRQIFNGTVVQRHPHVAFTVDNHDQPEALESFVEEFKPLAYALTITRE 360
Qy 361 QGYPSVFYDYGIPTHGVPAWMSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFYDYGIPTHGVPAWMSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGNKMFVGNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 5

US-09-545-586-26
; Sequence 26, Application US/09545586
; Patent No. 6528298
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6528298e1 -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/545.586
; CURRENT FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US/09/290.734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-545-586-26

Query Match 100.0%; Score 2708; DB 4; Length 485;
Best Local Similarity 100.0%; Pred. No. 6.4e-225;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HHNGTGTMOYFEWYLPNDGNHNRLRSDASNLKDGISAVWIPPAWKASQNDVGGA 60
Db 1 HHNGTGTMOYFEWYLPNDGNHNRLRSDASNLKDGISAVWIPPAWKASQNDVGGA 60
Qy 61 YDLGLGEFNQKGTIRTKYGRNQLQAAVNALKNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLGLGEFNQKGTIRTKYGRNQLQAAVNALKNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQEVSGEYTTIEAWTKDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTTIEAWTKDFPGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Qy 181 RGDGKGWDEVDTEGNGYDYLMYADIDMDHPVNVNLRNMGVWYTNLTGLDGFPRIDAVKH 240
Db 181 RGDGKGWDEVDTEGNGYDYLMYADIDMDHPVNVNLRNMGVWYTNLTGLDGFPRIDAVKH 240
Qy 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLNKTNWNSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLNKTNWNSVDFVPLHYNLYNA 300
Qy 301 SKSGNDYMRQIFNGTVVQRHPHVAFTVDNHDQPEALESFVEEFKPLAYALTITRE 360
Db 301 SKSGNDYMRQIFNGTVVQRHPHVAFTVDNHDQPEALESFVEEFKPLAYALTITRE 360
Qy 361 QGYPSVFYDYGIPTHGVPAWMSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFYDYGIPTHGVPAWMSKIDPILFARQKAYGRQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGNKMFVGNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGNKAGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 6

US-08-600-656-7
; Sequence 7, Application US/08600656
; Patent No. 6093562
; GENERAL INFORMATION:
; APPLICANT: Bisgard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan

APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6093562o No. 6093562disk of No. 6093562th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA: 1172/97
APPLICATION NUMBER: US/08/600,656
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4318.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-600-656-7

Query Match 96.5%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDGISAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDGISAVWIPPAWKASQNDVGYGA 60
QY 61 YLDYLGFEFNQKGTIRTKYGTNRQLOAAVNAALKSNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YLDYLGFEFNQKGTIRTKYGTNRQLOAAVNAALKSNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNQVSGEYTIETAWTKPDPGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
DB 121 EVNPNRNQVSGEYTIETAWTKPDPGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
QY 181 RGDGKWDWEVDTENGNYDLYMADIDMDHPEVNNELRNWGVYNTLTGLDGFRIIDAVKH 240
DB 181 RGHKAWDWEVDTENGNYDLYMADIDMDHPEVNNELRNWGVYNTLTGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAFWKNDLGAIENYLNKTNWNHVSFVDPVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAFWKNDLGAIENYLNKTNWNHVSFVDPVPLHYNLYNA 300
QY 301 SKSGGNYDMRQIFNGTVVQRHPHVAFTVDNHDSDQPEEALSFVEEWFKPLAYALTIRE 360
DB 301 SKSGGNYDMRQIFNGTVVQRHPHVAFTVDNHDSDQPEEALSFVEEWFKPLAYALTIRE 360
QY 361 QGYPVSFYGDYIGIPTHGVPAWKSKIDPILAEARQKAYGRONDYLDHNNIIGTREGNTA 420
DB 361 QGYPVSFYGDYIGIPTHGVPAWKSKIDPILAEARQKAYGRONDYLDHNNIIGTREGNTA 420
QY 421 HPNSGLATIMSDGAGGKWMFVGRNKAGQVWTDITGNRAGTGTINADGWNFSVNGSGVS 480
DB 421 HPNSGLATIMSDGAGGKWMFVGRNKAGQVWTDITGNRAGTGTINADGWNFSVNGSGVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 8
US-09-193-068-6
; Sequence 6, Application US/09193068
; Patent No. 6197565
; GENERAL INFORMATION:

Db 481 IWVWK 485
RESULT 7
US-09-170-670-6
; Sequence 6, Application US/09170670
; Patent No. 6187576
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben
; APPLICANT: Blegard-Frantzen Henrik
; TITLE OF INVENTION: Alpha-Amylase Mutants
; FILE REFERENCE: 5276.200-US
; CURRENT APPLICATION NUMBER: US/09/170,670
; CURRENT FILING DATE: 1998-10-13
; EARLIER APPLICATION NUMBER: 1172/97
; EARLIER FILING DATE: 1997-10-13
; EARLIER APPLICATION NUMBER: 60/063,306
; EARLIER FILING DATE: 1997-10-28
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-170-670-6

Query Match 96.5%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
QY 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDGISAVWIPPAWKASQNDVGYGA 60
DB 1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDGISAVWIPPAWKASQNDVGYGA 60
QY 61 YLDYLGFEFNQKGTIRTKYGTNRQLOAAVNAALKSNGIQVYGDVVMNHKGGADATEMVRV 120
DB 61 YLDYLGFEFNQKGTIRTKYGTNRQLOAAVNAALKSNGIQVYGDVVMNHKGGADATEMVRV 120
QY 121 EVNPNRNQVSGEYTIETAWTKPDPGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
DB 121 EVNPNRNQVSGEYTIETAWTKPDPGRGNTHSNFKRWYHFDGVDWDQSRKLNRIYKF 180
QY 181 RGDGKWDWEVDTENGNYDLYMADIDMDHPEVNNELRNWGVYNTLTGLDGFRIIDAVKH 240
DB 181 RGHKAWDWEVDTENGNYDLYMADIDMDHPEVNNELRNWGVYNTLTGLDGFRIIDAVKH 240
QY 241 IKYSFTRDWINHVRSAATGKNMFAVAFWKNDLGAIENYLNKTNWNHVSFVDPVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVRSAATGKNMFAVAFWKNDLGAIENYLNKTNWNHVSFVDPVPLHYNLYNA 300
QY 301 SKSGGNYDMRQIFNGTVVQRHPHVAFTVDNHDSDQPEEALSFVEEWFKPLAYALTIRE 360
DB 301 SKSGGNYDMRQIFNGTVVQRHPHVAFTVDNHDSDQPEEALSFVEEWFKPLAYALTIRE 360
QY 361 QGYPVSFYGDYIGIPTHGVPAWKSKIDPILAEARQKAYGRONDYLDHNNIIGTREGNTA 420
DB 361 QGYPVSFYGDYIGIPTHGVPAWKSKIDPILAEARQKAYGRONDYLDHNNIIGTREGNTA 420
QY 421 HPNSGLATIMSDGAGGKWMFVGRNKAGQVWTDITGNRAGTGTINADGWNFSVNGSGVS 480
DB 421 HPNSGLATIMSDGAGGKWMFVGRNKAGQVWTDITGNRAGTGTINADGWNFSVNGSGVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

; APPLICANT: Svendsen, Allan
; APPLICANT: Kjruliff, S ren
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Andersen, Carsten
; TITLE OF INVENTION: -Amylase Variants
; FILE REFERENCE: 5709.000-US
; CURRENT APPLICATION NUMBER: US/09/193,068
; CURRENT FILING DATE: 1998-11-16
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-193-068-6

Query Match 96.5%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217; Indels 0; Gaps 0;
Matches 463; Conservative 13; Mismatches 9;
Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISA VWPAPKAGASQNDVG YGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISA VWPAPKAGASQNDVG YGA 60
Qy 61 YDYLGEFNQKGTIRTKYGTNRNLOQA AVNALKSGIQVYGDVVMNHKGGADATEMVR AV 120
Db 61 YDYLGEFNQKGTIRTKYGTNRNLOQA AVNALKSGIQVYGDVVMNHKGGADATEMVR AV 120
Qy 121 EVNPNRNQSVSGEYTTIEAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 180
Db 121 EVNPNRNQSVSGEYTTIEAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 180
Qy 181 RGDKGWDWEVDYENGNDYLMYADIDMDHPEVVNLRNNGVWYTNLTGLDGFPRIDAVKH 240
Db 181 RGDKGWDWEVDYENGNDYLMYADIDMDHPEVVNLRNNGVWYTNLTGLDGFPRIDAVKH 240
Qy 241 IKYSFTRDWINHVRATGKNMFAVAEFWKNDLGAENLYLNKTNHNSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRATGKNMFAVAEFWKNDLGAENLYLNKTNHNSVDFVPLHYNLYNA 300
Qy 301 SKSGGNDMEQIENGTVVQRHPHVAFTFVDNHSQPEALESFVEEFKPLAYALTITRE 360
Db 301 SKSGGNDMEQIENGTVVQRHPHVAFTFVDNHSQPEALESFVEEFKPLAYALTITRE 360
Qy 361 QGYPSVFYGYDYGIPTHGVPAKSKIDPILAEARKYAYGRQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFYGYDYGIPTHGVPAKSKIDPILAEARKYAYGRQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGKNMFMVGRNKAGQVWTDITGNRAGTGTINADGWGNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGKNMFMVGRNKAGQVWTDITGNRAGTGTINADGWGNFSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 9

US-09-183-412-6
; Sequence 6, Application US/09183412
; Patent No. 6204232
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaeruliff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/183,412
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: 60/064,662

; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 60/093,234
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 1240/97
; EARLIER FILING DATE: 1997-10-30
; EARLIER APPLICATION NUMBER: PA 1998 00936
; EARLIER FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-183-412-6

Query Match 96.5%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217; Indels 0; Gaps 0;
Matches 463; Conservative 13; Mismatches 9;
Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISA VWPAPKAGASQNDVG YGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISA VWPAPKAGASQNDVG YGA 60
Qy 61 YDYLGEFNQKGTIRTKYGTNRNLOQA AVNALKSGIQVYGDVVMNHKGGADATEMVR AV 120
Db 61 YDYLGEFNQKGTIRTKYGTNRNLOQA AVNALKSGIQVYGDVVMNHKGGADATEMVR AV 120
Qy 121 EVNPNRNQSVSGEYTTIEAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 180
Db 121 EVNPNRNQSVSGEYTTIEAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 180
Qy 181 RGDKGWDWEVDYENGNDYLMYADIDMDHPEVVNLRNNGVWYTNLTGLDGFPRIDAVKH 240
Db 181 RGDKGWDWEVDYENGNDYLMYADIDMDHPEVVNLRNNGVWYTNLTGLDGFPRIDAVKH 240
Qy 241 IKYSFTRDWINHVRATGKNMFAVAEFWKNDLGAENLYLNKTNHNSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRATGKNMFAVAEFWKNDLGAENLYLNKTNHNSVDFVPLHYNLYNA 300
Qy 301 SKSGGNDMEQIENGTVVQRHPHVAFTFVDNHSQPEALESFVEEFKPLAYALTITRE 360
Db 301 SKSGGNDMEQIENGTVVQRHPHVAFTFVDNHSQPEALESFVEEFKPLAYALTITRE 360
Qy 361 QGYPSVFYGYDYGIPTHGVPAKSKIDPILAEARKYAYGRQNDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSVFYGYDYGIPTHGVPAKSKIDPILAEARKYAYGRQNDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGKNMFMVGRNKAGQVWTDITGNRAGTGTINADGWGNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGKNMFMVGRNKAGQVWTDITGNRAGTGTINADGWGNFSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 10

US-09-354-191A-7
; Sequence 7, Application US/09354191A
; Patent No. 6297038
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6297038o No. 6297038disk of No. 6297038th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401

```
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,191A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/600,656
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4319.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 485 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-354-191A-7

Query Match          96.5%; Score 2613; DB 3; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY      1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISA VMI PPAWKGASQNDVGYGA 60
DB      1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISA VMI PPAWKGASQNDVGYGA 60

QY      61 YDLYDLGEFNGKGTIRTKYGTNRNQLQAANVAKLSNGIQYGVGVMMHKGADATENVRAV 120
DB      61 YDLYDLGEFNGKGTIRTKYGTNRNQLQAANVAKLSNGIQYGVGVMMHKGADATENVRAV 120

QY      121 EVNPNRNQEVSGEYTIETAWTKFPDPPGRGNTHSNFKRWYHFDGVVDWQSRKLNRIYKF 180
DB      121 EVNPNRNQEVSGEYTIETAWTKFPDPPGRGNTHSNFKRWYHFDGVVDWQSRKLNRIYKF 180

QY      181 RGDGKGDWEVDTEGNGYDLYMADIDMDHPVNVNELRNWGVYNTLTGLDGFRI DAVKH 240
DB      181 RGHGKAWDEVDTEGNGYDLYMADIDMDHPVNVNELRNWGVYNTLTGLDGFRI DAVKH 240

QY      241 IKYSFTRDWINHVSATGKNMFAVAFWKNDLGAENYLNKTNWHSVFDVPLHYNLYNA 300
DB      241 IKYSFTRDWINHVSATGKNMFAVAFWKNDLGAENYLNKTNWHSVFDVPLHYNLYNA 300

QY      301 SKSGGNYDMRQIFNGTVVQHPMHA VTFVDNHDSDQPEEALSFVEEWFKPLAYALTIRE 360
DB      301 SKSGGNYDMRNI FNGTVVQHPHSHAVTFVDNHDSDQPEEALSFVEEWFKPLAYALTIRE 360

QY      361 QGYPSVFYGDYGIPTHGVPAMSKIDPIL EARKQYAGKQNDYLDHNNIIGWTREGNTA 420
DB      361 QGYPSVFYGDYGIPTHGVPAMSKIDPIL EARKQYAGKQNDYLDHNNIIGWTREGNTA 420

QY      421 HPNSGLATIMSDGAGGKWMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGSGVS 480
DB      421 HPNSGLATIMSDGAGGKWMFVGRNKAGQVWTDITGNRTGTGTINADGWNFSVNGSGVS 480

QY      481 IWVWK 485
DB      481 IWVWK 485

RESULT 11
US-09-291-023A-13
; Sequence 13, Application US/09291023A
; Patent No. 6309871
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; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic Acid
; TITLE OF INVENTION: Encoding Same
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/291,023A
; CURRENT FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: DK 1999 00438
; PRIOR FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 13
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
; US-09-291-023A-13

Query Match          96.5%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY      1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISA VMI PPAWKGASQNDVGYGA 60
DB      1 HNGTGTMMQYFEWYLPNDGNHNRRLSDASNLKDKGISA VMI PPAWKGASQNDVGYGA 60

QY      61 YDLYDLGEFNGKGTIRTKYGTNRNQLQAANVAKLSNGIQYGVGVMMHKGADATENVRAV 120
DB      61 YDLYDLGEFNGKGTIRTKYGTNRNQLQAANVAKLSNGIQYGVGVMMHKGADATENVRAV 120

QY      121 EVNPNRNQEVSGEYTIETAWTKFPDPPGRGNTHSNFKRWYHFDGVVDWQSRKLNRIYKF 180
DB      121 EVNPNRNQEVSGEYTIETAWTKFPDPPGRGNTHSNFKRWYHFDGVVDWQSRKLNRIYKF 180

QY      181 RGDGKGDWEVDTEGNGYDLYMADIDMDHPVNVNELRNWGVYNTLTGLDGFRI DAVKH 240
DB      181 RGHGKAWDEVDTEGNGYDLYMADIDMDHPVNVNELRNWGVYNTLTGLDGFRI DAVKH 240

QY      241 IKYSFTRDWINHVSATGKNMFAVAFWKNDLGAENYLNKTNWHSVFDVPLHYNLYNA 300
DB      241 IKYSFTRDWINHVSATGKNMFAVAFWKNDLGAENYLNKTNWHSVFDVPLHYNLYNA 300

QY      301 SKSGGNYDMRQIFNGTVVQHPMHA VTFVDNHDSDQPEEALSFVEEWFKPLAYALTIRE 360
DB      301 SKSGGNYDMRNI FNGTVVQHPHSHAVTFVDNHDSDQPEEALSFVEEWFKPLAYALTIRE 360

QY      361 QGYPSVFYGDYGIPTHGVPAMSKIDPIL EARKQYAGKQNDYLDHNNIIGWTREGNTA 420
DB      361 QGYPSVFYGDYGIPTHGVPAMSKIDPIL EARKQYAGKQNDYLDHNNIIGWTREGNTA 420

QY      421 HPNSGLATIMSDGAGGKWMFVGRNKAGQVWTDITGNRAGTVTINADGWNFSVNGSGVS 480
DB      421 HPNSGLATIMSDGAGGKWMFVGRNKAGQVWTDITGNRTGTGTINADGWNFSVNGSGVS 480

QY      481 IWVWK 485
DB      481 IWVWK 485

RESULT 12
US-09-290-734-6
; Sequence 6, Application US/09290734
; Patent No. 6361989
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Biegaard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
```

; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6361989e1 -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/290,734
; PRIORITY FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-290-734-6

Query Match 96.5%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLSDASNLKDGISAVWIPPAWKASQNDVGGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLSDASNLKDGISAVWIPPAWKASQNDVGGA 60
Qy 61 YDLYLGEFNGKQIRTKYGTNRNQLAAVNAKNSGQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYLGEFNGKQIRTKYGTNRNQLAAVNAKNSGQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQEVSGEYTTIEAWTKFDPGCGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTTIEAWTKFDPGCGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Qy 181 RGDCGKGDWEVDTEGNGYDYLMYADIDMDHPEVNVNLRNMGVWYTNLTGLDGFRIIDAVKH 240
Db 181 RGDCGKGDWEVDTEGNGYDYLMYADIDMDHPEVNVNLRNMGVWYTNLTGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAENYLNKTNHNSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAENYLNKTNHNSVDFVPLHYNLYNA 300
Qy 301 SKSGNGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTITNADGNGFNSVNGGSVS 360
Db 301 SKSGNGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTITNADGNGFNSVNGGSVS 360
Qy 361 QGYPSPVGYDYGIPTHGVPAKSKIDPILAEARQKAYGRONDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSPVGYDYGIPTHGVPAKSKIDPILAEARQKAYGRONDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTITNADGNGFNSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTITNADGNGFNSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 13

US-09-381-687-5
; Sequence 5, Application US/09381687
; Patent No. 6486113
; GENERAL INFORMATION:
; APPLICANT: HATADA, Yuji
; APPLICANT: IKAWA, Kaori
; APPLICANT: ITO, Susumu
; APPLICANT: IGARASHI, Kazuaki
; APPLICANT: HAGIHARA, Hiroshi
; APPLICANT: HAYASHI, Yasuhiro
; APPLICANT: ARAKI, Hiroyuki
; APPLICANT: OKAZAKI, Katsuya
; TITLE OF INVENTION: MUTANT ALPHA-AMYLASES
; FILE REFERENCE: 2173-0115P
; CURRENT APPLICATION NUMBER: US/09/381,687
; PRIORITY FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp. #707
US-09-381-687-5
Query Match 96.5%; Score 2613; DB 4; Length 485;
Best Local Similarity 95.5%; Pred. No. 9.7e-217;
Matches 463; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLSDASNLKDGISAVWIPPAWKASQNDVGGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLSDASNLKDGISAVWIPPAWKASQNDVGGA 60
Qy 61 YDLYLGEFNGKQIRTKYGTNRNQLAAVNAKNSGQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYLGEFNGKQIRTKYGTNRNQLAAVNAKNSGQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQEVSGEYTTIEAWTKFDPGCGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Db 121 EVNPNRNQEVSGEYTTIEAWTKFDPGCGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
Qy 181 RGDCGKGDWEVDTEGNGYDYLMYADIDMDHPEVNVNLRNMGVWYTNLTGLDGFRIIDAVKH 240
Db 181 RGDCGKGDWEVDTEGNGYDYLMYADIDMDHPEVNVNLRNMGVWYTNLTGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAENYLNKTNHNSVDFVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKNMFAVAEFKNDLGAENYLNKTNHNSVDFVPLHYNLYNA 300
Qy 301 SKSGNGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTITNADGNGFNSVNGGSVS 360
Db 301 SKSGNGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTITNADGNGFNSVNGGSVS 360
Qy 361 QGYPSPVGYDYGIPTHGVPAKSKIDPILAEARQKAYGRONDYLDHNNIIGWTREGNTA 420
Db 361 QGYPSPVGYDYGIPTHGVPAKSKIDPILAEARQKAYGRONDYLDHNNIIGWTREGNTA 420
Qy 421 HPNSGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTITNADGNGFNSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTITNADGNGFNSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 14

US-09-545-586-6
; Sequence 6, Application US/09545586
; Patent No. 6528298
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgaard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hoeck, Lisbeth Hedegaard
; TITLE OF INVENTION: No. 6528298e1 -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/09/545,586
; PRIORITY FILING DATE: 2000-04-07
; PRIORITY FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-545-586-6

Query Match	96.5%;	Score 2613;	DB 4;	Length 485;
Best Local Similarity	95.5%;	Pred. No. 9.7e-217;		
Matches 463;	Conservative 13;	Mismatches 9;	Indels 0;	Gaps 0;
QY	1	HHNGTNGTMMQYFEWYLPNDGNHNRRLRSDASNLKDGISAVWIPPAAWKASQNDVGYGA	60	
Db	1	HHNGTNGTMMQYFEWYLPNDGNHNRRLNSDASNLKSGITAVWIPPAAWKASQNDVGYGA	60	
QY	61	YDLYDLGFEFNQKGTIRTKYGTNRNQLQAAVNALKSGIQVYGDVVMNHKGGADATEMVRV	120	
Db	61	YDLYDLGFEFNQKGTIRTKYGTNRSLQAAVTSLKNGIQVYGDVVMNHKGGADATEMVRV	120	
QY	121	EVNPNNRNQSVGEYTTIEAWTKFDPGCRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF	180	
Db	121	EVNPNNRNQSVGEYTTIEAWTRFDPGCRGNTHSSFKRWYHFDGVDWDSRRLNNRIYKF	180	
QY	181	RGDGKWDWEVDTEGNGYDILMYADIDMDHPEVVNELRNWGVWYNTLGLDGFRIIDAVKH	240	
Db	181	RGHGKAWDWEVDTEGNGYDILMYADIDMDHPEVVNELRNWGVWYNTLGLDGFRIIDAVKH	240	
QY	241	IKYSFTRDWINHVRSATGKNMFAVAEFWKNDLGAIENTYLNKTNWNHVSFVDPVPLHYNLYNA	300	
Db	241	IKYSFTRDWINHVRSATGKNMFAVAEFWKNDLGAIENTYLNKTNWNHVSFVDPVPLHYNLYNA	300	
QY	301	SKSGGNYDMROI FNGTVVQRHPMHAFTFVDNHDSPQEEALESFVEEWFKPLAYALTLTRE	360	
Db	301	SKSGGNYDMRNI FNGTVVQRHPSHAFTFVDNHDSPQEEALESFVEEWFKPLAYALTLTRE	360	
QY	361	QGYPSVFYGDYGIPTHGVPAMKSKIDPILKQYAYGRQNDYLDHNNIIGWTREGNTA	420	
Db	361	QGYPSVFYGDYGIPTHGVPAMRSKIDPILKQYAYGRQNDYLDHNNIIGWTREGNTA	420	
QY	421	HPNSGLATIMSDGAGGKMMFVGRNKAGQVWTDITGNRAGTGTITINADGWNFSVNGGSVS	480	
Db	421	HPNSGLATIMSDGAGGKMMFVGRNKAGQVWSDITGNRTGTITINADGWNFSVNGGSVS	480	
QY	481	IWNK 485		
Db	481	IWNK 485		

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Job time : 16.0278 secs

Search completed: October 7, 2004, 00:47:13
Job time : 16.0278 secs

RESULT 15
US-09-540-715A-13
; Sequence 13, Application US/09540715A
; Patent No. 6623948
; GENERAL INFORMATION:
; APPLICANT: Outtrup, Helle
; APPLICANT: Borchert, Torben
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nielsen, Vibeke
; APPLICANT: Hoeck, Lisbeth
; TITLE OF INVENTION: Polypeptides Having Alkaline Alpha-amylase Activity And Nucleic
; FILE REFERENCE: 5821.010-US
; CURRENT APPLICATION NUMBER: US/09/540, 715A
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/291,023
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus
US-09-540-715A-13

Query Match		96.5%;	Score 2613;	DB 4;	Length 485;
Best Local Similarity		95.5%;	Pred. No. 9.7e-217;		
Matches 463;		Conservative 13;	Mismatches 9;	Indels 0;	Gaps 0;
QY	1	HHNGTNGTMMQYFEWYLPNDGNHNRRLRSDASNLKDGISAVWIPPAAWKASQNDVGYGA	60		
Db	1	HHNGTNGTMMQYFEWYLPNDGNHNRRLNSDASNLKSGITAVWIPPAAWKASQNDVGYGA	60		

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2004, 00:19:14 ; Search time 53.4478 Seconds
(without alignments)
2920.093 Million cell updates/sec

Title: US-09-925-576C-12

Perfect score: 2708

Sequence: 1 HHNGTGTMMQYFEWYLPND.....ADGWNFSVNGSGSVIWNK 485

Scoring table: BLOSUM62

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Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- Published Applications AA:*
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 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	2708	100.0	485	10	US-09-925-576C-12
4	2708	100.0	485	12	US-10-327-837-24
5	2708	100.0	485	12	US-10-327-837-26
6	2708	100.0	485	14	US-10-209-812-5
7	2708	100.0	485	16	US-10-477-725-12
8	2613	96.5	485	9	US-09-854-346-12
9	2613	96.5	485	9	US-09-918-543-12
10	2613	96.5	485	10	US-09-925-576C-12
11	2613	96.5	485	12	US-10-327-837-24
12	2613	96.5	485	12	US-10-327-837-26
13	2613	96.5	485	14	US-10-209-812-5
14	2613	96.5	485	16	US-10-477-725-12
15	2613	96.5	485	16	US-10-477-725-13

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18	2437	90.0	485	9	US-09-769-864-8	Sequence 8, Appli
19	2437	90.0	485	9	US-09-854-346-4	Sequence 4, Appli
20	2437	90.0	485	9	US-09-902-188A-2	Sequence 2, Appli
21	2437	90.0	485	9	US-09-918-543-4	Sequence 4, Appli
22	2437	90.0	485	9	US-09-795-211-2	Sequence 2, Appli
23	2437	90.0	485	10	US-09-925-576C-4	Sequence 4, Appli
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27	2437	90.0	485	12	US-10-327-837-2	Sequence 2, Appli
28	2437	90.0	485	12	US-10-327-837-8	Sequence 8, Appli
29	2437	90.0	485	16	US-10-477-725-4	Sequence 4, Appli
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32	2429	89.7	485	9	US-09-854-346-2	Sequence 2, Appli
33	2429	89.7	485	9	US-09-902-188A-1	Sequence 1, Appli
34	2429	89.7	485	9	US-09-918-543-2	Sequence 2, Appli
35	2429	89.7	485	9	US-09-795-211-1	Sequence 1, Appli
36	2429	89.7	485	10	US-09-925-576C-2	Sequence 2, Appli
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40	2429	89.7	485	12	US-10-327-837-1	Sequence 1, Appli
41	2429	89.7	485	12	US-10-327-837-7	Sequence 7, Appli
42	2429	89.7	485	14	US-10-184-771-12	Sequence 12, Appli
43	2429	89.7	485	16	US-10-477-725-2	Sequence 2, Appli
44	2409	89.0	516	9	US-09-986-676A-2	Sequence 2, Appli
45	2409	89.0	516	9	US-09-971-611-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-854-346-12
; Sequence 12, Application US/09854346
; Patent No. US20020068352A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020068352Alozymes A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Jorgensen, Christel Thea
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Alpha-amylase variants with altered 1,6 activity
; FILE REFERENCE: 6140.200-US
; CURRENT APPLICATION NUMBER: US/09/854,346
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-854-346-12

Query Match		100.0%;	Score 2708;	DB 9;	Length 485;
Best Local Similarity		100.0%;	Pred. No. 1e-242;		
Matches 485;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	HHNGTGTMMQYFEWYLPNDGHNHNRILSDASNLKDKGISAVWIPPAWKGASNDVGYGA	60		
Db	1	HHNGTGTMMQYFEWYLPNDGHNHNRILSDASNLKDKGISAVWIPPAWKGASNDVGYGA	60		
Qy	61	YDLYDLGEFQKQKTIKTYGTRNQLQAAVNAKLSNGIQVYGVVNMHKGADATEMVRV	120		
Db	61	YDLYDLGEFQKQKTIKTYGTRNQLQAAVNAKLSNGIQVYGVVNMHKGADATEMVRV	120		
Qy	121	EVNPNRNRQVSGEYTIETAWTKDFPGRGNTNHNFKRWTHFGVDWQSKLNRIYKF	180		
Db	121	EVNPNRNRQVSGEYTIETAWTKDFPGRGNTNHNFKRWTHFGVDWQSKLNRIYKF	180		
Qy	181	RGDGKGHWEDVTENGNDYLMYADIDMDHPEVNVNELRNWGVWYNTLTGLDGFRIKAVKH	240		

Db 181 RGDGKGDWEVDYDENGNDYDLYADIDMDHDPVNVNELRWGQVWYNTLTGLDGFIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKMFVAEFWKNLDLGAIEYLNKTNWNHVSFVDPVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKMFVAEFWKNLDLGAIEYLNKTNWNHVSFVDPVPLHYNLYNA 300
Qy 301 SKSGGNDYMDROIENGTVVQRHPHMAVTFVDNHDSDPEEALSFVEEFKPLAYALTLTRE 360
Db 301 SKSGGNDYMDROIENGTVVQRHPHMAVTFVDNHDSDPEEALSFVEEFKPLAYALTLTRE 360
Qy 361 QGYPSPFYGDYGIPTHGVPAMKSKIDPILFARQKAYAGQNDYLDHNNIIGWTRGNTA 420
Db 361 QGYPSPFYGDYGIPTHGVPAMKSKIDPILFARQKAYAGQNDYLDHNNIIGWTRGNTA 420
Qy 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTINADGNGNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTINADGNGNFSVNGGSVS 480
Qy 481 IWYWK 485
Db 481 IWYWK 485

RESULT 2

US-09-918-543-12
; Sequence 12, Application US/09918543
; Patent No. US20020155574A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020155574A1, A/S
; APPLICANT: Thisted, Thomas
; APPLICANT: Kjaerulff, Soren
; APPLICANT: Andersen, Carsten
; APPLICANT: Fugleang, Claus Crone
; TITLE OF INVENTION: Alpha-amylase mutants with altered properties
; FILE REFERENCE: 10062 200-US
; CURRENT APPLICATION NUMBER: US/09/918,543
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-918-543-12

Query Match 100.0%; Score 2708; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Qy 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAAVNALKSGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAAVNALKSGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQVSGEYITIAWTKFDPPGRGNTHSNFKRWYHFDGVDWDQSRKLNNRIYKF 180
Db 121 EVNPNRNQVSGEYITIAWTKFDPPGRGNTHSNFKRWYHFDGVDWDQSRKLNNRIYKF 180
Qy 181 RGDGKGDWEVDYDENGNDYDLYADIDMDHDPVNVNELRWGQVWYNTLTGLDGFIDAVKH 240
Db 181 RGDGKGDWEVDYDENGNDYDLYADIDMDHDPVNVNELRWGQVWYNTLTGLDGFIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKMFVAEFWKNLDLGAIEYLNKTNWNHVSFVDPVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKMFVAEFWKNLDLGAIEYLNKTNWNHVSFVDPVPLHYNLYNA 300
Qy 301 SKSGGNDYMDROIENGTVVQRHPHMAVTFVDNHDSDPEEALSFVEEFKPLAYALTLTRE 360
Db 301 SKSGGNDYMDROIENGTVVQRHPHMAVTFVDNHDSDPEEALSFVEEFKPLAYALTLTRE 360
Qy 361 QGYPSPFYGDYGIPTHGVPAMKSKIDPILFARQKAYAGQNDYLDHNNIIGWTRGNTA 420
Db 361 RGDGKGDWEVDYDENGNDYDLYADIDMDHDPVNVNELRWGQVWYNTLTGLDGFIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKMFVAEFWKNLDLGAIEYLNKTNWNHVSFVDPVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKMFVAEFWKNLDLGAIEYLNKTNWNHVSFVDPVPLHYNLYNA 300
Qy 301 SKSGGNDYMDROIENGTVVQRHPHMAVTFVDNHDSDPEEALSFVEEFKPLAYALTLTRE 360
Db 301 SKSGGNDYMDROIENGTVVQRHPHMAVTFVDNHDSDPEEALSFVEEFKPLAYALTLTRE 360

Qy 361 QGYPSPFYGDYGIPTHGVPAMKSKIDPILFARQKAYAGQNDYLDHNNIIGWTRGNTA 420
Db 361 QGYPSPFYGDYGIPTHGVPAMKSKIDPILFARQKAYAGQNDYLDHNNIIGWTRGNTA 420
Qy 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTINADGNGNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTINADGNGNFSVNGGSVS 480
Qy 481 IWYWK 485
Db 481 IWYWK 485

RESULT 3

US-09-925-576C-12
; Sequence 12, Application US/09925576C
; Publication No. US20030129718A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Carsten
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Nielsen, Bjarne Ronfeldt
; TITLE OF INVENTION: Amylase Variants
; FILE REFERENCE: 10004 204-US
; CURRENT APPLICATION NUMBER: US/09/925,576C
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-925-576C-12

Query Match 100.0%; Score 2708; DB 10; Length 485;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Db 1 HNGTNGTMMQYFEWYLPNDGNHNRRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
Qy 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAAVNALKSGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAAVNALKSGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQVSGEYITIAWTKFDPPGRGNTHSNFKRWYHFDGVDWDQSRKLNNRIYKF 180
Db 121 EVNPNRNQVSGEYITIAWTKFDPPGRGNTHSNFKRWYHFDGVDWDQSRKLNNRIYKF 180
Qy 181 RGDGKGDWEVDYDENGNDYDLYADIDMDHDPVNVNELRWGQVWYNTLTGLDGFIDAVKH 240
Db 181 RGDGKGDWEVDYDENGNDYDLYADIDMDHDPVNVNELRWGQVWYNTLTGLDGFIDAVKH 240
Qy 241 IKYSFTRDWINHVRSAATGKMFVAEFWKNLDLGAIEYLNKTNWNHVSFVDPVPLHYNLYNA 300
Db 241 IKYSFTRDWINHVRSAATGKMFVAEFWKNLDLGAIEYLNKTNWNHVSFVDPVPLHYNLYNA 300
Qy 301 SKSGGNDYMDROIENGTVVQRHPHMAVTFVDNHDSDPEEALSFVEEFKPLAYALTLTRE 360
Db 301 SKSGGNDYMDROIENGTVVQRHPHMAVTFVDNHDSDPEEALSFVEEFKPLAYALTLTRE 360
Qy 361 QGYPSPFYGDYGIPTHGVPAMKSKIDPILFARQKAYAGQNDYLDHNNIIGWTRGNTA 420
Db 361 QGYPSPFYGDYGIPTHGVPAMKSKIDPILFARQKAYAGQNDYLDHNNIIGWTRGNTA 420
Qy 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTINADGNGNFSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTVTINADGNGNFSVNGGSVS 480
Qy 481 IWYWK 485
Db 481 IWYWK 485

RESULT 4

US-10-327-837-24
; Sequence 24, Application US/10327837
; Publication No. US20030211958A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hock, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-327-837-24

Query Match 100.0%; Score 2708; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSASNLKDKGISAVWIPPAWKASQNDVGGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSASNLKDKGISAVWIPPAWKASQNDVGGA 60
Qy 61 YDLVDFEFNQKGTIRTKYGTNRNQLQAAVNAKLSNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLVDFEFNQKGTIRTKYGTNRNQLQAAVNAKLSNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQEVSGEYTTTEAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 180
Db 121 EVNPNRNQEVSGEYTTTEAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 180
Qy 181 RGDGKGWDWEVDTEGNYDYLMAADIDMDHPEVNVNLRNMGVWYTTNTLGLDGFRIIDAVKH 240
Db 181 RGDGKGWDWEVDTEGNYDYLMAADIDMDHPEVNVNLRNMGVWYTTNTLGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAIENYLNKTNWNSHVSFVDFPLHYNLYNA 300
Db 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAIENYLNKTNWNSHVSFVDFPLHYNLYNA 300
Qy 301 SKSGNVDMDQIFNGTVVQRHPMAVTFVDNHDSPBEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGNVDMDQIFNGTVVQRHPMAVTFVDNHDSPBEALESFVEEWFKPLAYALTITRE 360
Qy 361 QGYPSVFGYGYGIPTHGVPAKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTRGNTA 420
Db 361 QGYPSVFGYGYGIPTHGVPAKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTRGNTA 420
Qy 421 HPNSGLATIMSDGAGGNKMFVGRNKGAGQVWTDITGNRAGVTITNADGWGNSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGRNKGAGQVWTDITGNRAGVTITNADGWGNSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 5

US-10-327-837-26
; Sequence 26, Application US/10327837
; Publication No. US20030211958A1

; GENERAL INFORMATION:

; APPLICANT: Svendsen, Allan
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Bisgard-Frantzen Henrik
; APPLICANT: Outtrup, Helle
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Nielsen, Vibeke Skovgaard
; APPLICANT: Hock, Lisbeth Hedegaard
; TITLE OF INVENTION: Novel -Amylase And -Amylase Mutants
; FILE REFERENCE: 5276.400-US
; CURRENT APPLICATION NUMBER: US/10327,837
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US/09/290,734
; PRIOR FILING DATE: 1999-04-13
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-327-837-26

Query Match 100.0%; Score 2708; DB 12; Length 485;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSASNLKDKGISAVWIPPAWKASQNDVGGA 60
Db 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSASNLKDKGISAVWIPPAWKASQNDVGGA 60
Qy 61 YDLVDFEFNQKGTIRTKYGTNRNQLQAAVNAKLSNGIQVYGDVVMNHKGGADATEMVRV 120
Db 61 YDLVDFEFNQKGTIRTKYGTNRNQLQAAVNAKLSNGIQVYGDVVMNHKGGADATEMVRV 120
Qy 121 EVNPNRNQEVSGEYTTTEAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 180
Db 121 EVNPNRNQEVSGEYTTTEAWTKDFPGRGNTHSNFKRWYHFDGVDWDSRKLNNRIYKF 180
Qy 181 RGDGKGWDWEVDTEGNYDYLMAADIDMDHPEVNVNLRNMGVWYTTNTLGLDGFRIIDAVKH 240
Db 181 RGDGKGWDWEVDTEGNYDYLMAADIDMDHPEVNVNLRNMGVWYTTNTLGLDGFRIIDAVKH 240
Qy 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAIENYLNKTNWNSHVSFVDFPLHYNLYNA 300
Db 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAIENYLNKTNWNSHVSFVDFPLHYNLYNA 300
Qy 301 SKSGNVDMDQIFNGTVVQRHPMAVTFVDNHDSPBEALESFVEEWFKPLAYALTITRE 360
Db 301 SKSGNVDMDQIFNGTVVQRHPMAVTFVDNHDSPBEALESFVEEWFKPLAYALTITRE 360
Qy 361 QGYPSVFGYGYGIPTHGVPAKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTRGNTA 420
Db 361 QGYPSVFGYGYGIPTHGVPAKSKIDPILAEARQKAYGRQNDYLDHNNIIGWTRGNTA 420
Qy 421 HPNSGLATIMSDGAGGNKMFVGRNKGAGQVWTDITGNRAGVTITNADGWGNSVNGGSVS 480
Db 421 HPNSGLATIMSDGAGGNKMFVGRNKGAGQVWTDITGNRAGVTITNADGWGNSVNGGSVS 480
Qy 481 IWVWK 485
Db 481 IWVWK 485

RESULT 6

US-10-209-812-5
; Sequence 5, Application US/10209812
; Publication No. US20030087785A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Arne Agerlin
; APPLICANT: Osten, Claus von der
; APPLICANT: Andersen, Kim Vilbour
; APPLICANT: Ernst, Steffen
; APPLICANT: Roggen, Erwin Ludo

```
; TITLE OF INVENTION: A Modified Polypeptide
; FILE REFERENCE: 5666.200-US
; CURRENT APPLICATION NUMBER: US/10/209,812
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/417,359
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: PA 1998 01301
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: PA 1999 01418
; PRIOR FILING DATE: 1999-10-04
; PRIOR APPLICATION NUMBER: 60/105,624
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/157,426
; PRIOR FILING DATE: 1999-10-04
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-209-812-5

Query Match      100.0%; Score 2708; DB 14; Length 485;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
DB 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAANVNAKLSNGIQVYGDVVMNHKGGADATEMVR 120
DB 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAANVNAKLSNGIQVYGDVVMNHKGGADATEMVR 120
QY 121 EVNPNNRNQEVSGEYITIAWTKFDPGGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
DB 121 EVNPNNRNQEVSGEYITIAWTKFDPGGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
QY 181 RGDKGWDWEVDTEGNGYDLYMADIDMDHPVVNLRNNGVWYTNLTGLDGRIDAVKH 240
DB 181 RGDKGWDWEVDTEGNGYDLYMADIDMDHPVVNLRNNGVWYTNLTGLDGRIDAVKH 240
QY 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLNKTNWNHVSFVDFVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLNKTNWNHVSFVDFVPLHYNLYNA 300
QY 301 SKSGGNDYMRQIFNGTVVQRHPMHAFTFVDNHDSDPEEALSFVEEWFKPLAYALTIRE 360
DB 301 SKSGGNDYMRQIFNGTVVQRHPMHAFTFVDNHDSDPEEALSFVEEWFKPLAYALTIRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPILAEARQKYAYGRQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPILAEARQKYAYGRQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 7
US-10-477-725-12
; Sequence 12, Application US/10477725
; Publication No. US20040096952A1
; GENERAL INFORMATION:
; APPLICANT: NOVOZYMES A/S
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Thisted, Thomas
; APPLICANT: von der Osten, Claus
```

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; TITLE OF INVENTION: Alpha-amylase variant with altered properties
; FILE REFERENCE: 10182.204-US
; CURRENT APPLICATION NUMBER: US/10/477,725
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-10-477-725-12

Query Match      100.0%; Score 2708; DB 16; Length 485;
Best Local Similarity 100.0%; Pred. No. 1e-242;
Matches 485; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
DB 1 HHNGTGTMMQYFEWYLPNDGNHNRLRSDASNLKDKGISAVWIPPAWKASQNDVGYGA 60
QY 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAANVNAKLSNGIQVYGDVVMNHKGGADATEMVR 120
DB 61 YDLYDLGEFNGKGTIRTKYGTNRQLQAANVNAKLSNGIQVYGDVVMNHKGGADATEMVR 120
QY 121 EVNPNNRNQEVSGEYITIAWTKFDPGGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
DB 121 EVNPNNRNQEVSGEYITIAWTKFDPGGRGNTHSNFKRWYHFDGVDWQSRKLNRIYKF 180
QY 181 RGDKGWDWEVDTEGNGYDLYMADIDMDHPVVNLRNNGVWYTNLTGLDGRIDAVKH 240
DB 181 RGDKGWDWEVDTEGNGYDLYMADIDMDHPVVNLRNNGVWYTNLTGLDGRIDAVKH 240
QY 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLNKTNWNHVSFVDFVPLHYNLYNA 300
DB 241 IKYSFTRDWINHVSATGKNMFAVAEFWKNDLGAENYLNKTNWNHVSFVDFVPLHYNLYNA 300
QY 301 SKSGGNDYMRQIFNGTVVQRHPMHAFTFVDNHDSDPEEALSFVEEWFKPLAYALTIRE 360
DB 301 SKSGGNDYMRQIFNGTVVQRHPMHAFTFVDNHDSDPEEALSFVEEWFKPLAYALTIRE 360
QY 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPILAEARQKYAYGRQNDYLDHNNIIGWTREGNTA 420
DB 361 QGYPSVFYGDYGIPTHGVPAMKSKIDPILAEARQKYAYGRQNDYLDHNNIIGWTREGNTA 420
QY 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
DB 421 HPNSGLATIMSDGAGGNKMFVGRNKGQVWTDITGNRAGTGTINADGWNFSVNGGSVS 480
QY 481 IWVWK 485
DB 481 IWVWK 485

RESULT 8
US-09-769-864-6
; Sequence 6, Application US/09769864
; Patent No. US20010039253A1
; GENERAL INFORMATION:
; APPLICANT: Borchert, Torben V.
; APPLICANT: Svendsen, Allan
; APPLICANT: Andersen, Carsten
; APPLICANT: Nielsen, Bjarne
; APPLICANT: Nissen, Torben L.
; APPLICANT: Kjaerulff, Soren
; TITLE OF INVENTION: Alpha-Amulase Mutants
; FILE REFERENCE: 5368.200-US
; CURRENT APPLICATION NUMBER: US/09/769,864
; CURRENT FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/183,412
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 6
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